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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

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FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

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Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al.. (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

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In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

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Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) Arch. Pathol. Lab. Med. 124:966-978; Hamilton and Piccart (2000) Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) J. Clin. Oncol. 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer.

Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) <u>Clin. Cancer Res.</u> 6:1693-1701; Scholl, et al. (2000) <u>J. Immunother.</u> 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) <u>Clin. Chem.</u> 43:585-593. However, many patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

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Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are upand down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes,
and also as targets for screening for therapeutic compounds that modulate ovarian cancer,
such as hormones or antibodies. The methods of detecting nucleic acids of the invention or
their encoded proteins can be used for many purposes, e.g., early detection of ovarian
cancers, monitoring and early detection of relapse following treatment, monitoring response
to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting
therapy, determining tumor prognosis, treatment, or response to treatment (of primary or
metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the
invention will become apparent to the skilled artisan by the following description of the
invention.

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In one aspect, the present invention provides a method of detecting an ovarian cancerassociated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

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In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

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In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of:
(i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

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In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory, protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes.

Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

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In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

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Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math.

2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol.

Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc.

Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package,

Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990)

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J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

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A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

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Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5.235.033 and 5.034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g.,

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15 phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 20 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 25 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-30 4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) <u>J. Biomolecular NMR</u> 34:17-xx; Horn, et al. (1996) <u>Tetrahedron Lett.</u> 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) <u>Carbohydrate</u>

<u>Modifications in Antisense Research</u> ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) <u>Chem. Soc. Rev.</u> pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) <u>C&E News</u>. Each of these references is hereby expressly incorporated by reference.

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Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

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An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

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The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

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sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

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By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

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Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 100%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss.

"Tumor cell" refers to pre-cancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

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"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

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The identification of sequences that are differentially expressed in ovarian cancer versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

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An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

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The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

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The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

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Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical 20 Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

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The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

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The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

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Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in proteinprotein interaction. For example, Src-homology-2 (SH2) domains bind tyrosinephosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to prolinerich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

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In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on

the same molecule.

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The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

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A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

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In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silicabased materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

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In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

"operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

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In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, supra. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others. See Fernandez and Hoeffler, supra. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

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In one embodiment, ovarian cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

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Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of ovarian cancer protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

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Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) <u>CRC Crit. Rev. Biochem.</u> CRC Press.

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Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57; and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u>, 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

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In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

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In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a nonhuman species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

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In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, noncompetitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INFγ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

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In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

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"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

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In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

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In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

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The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out inTables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

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Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

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Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al.(1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al.(1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening.

Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

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In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

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After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

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Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins" or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

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Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

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Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present.

Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

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In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

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Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting ovarian cancer cell division is provided. The method comprises administration of an ovarian cancer inhibitor. In another embodiment, a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

20 Growth factor or serum dependence

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Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) <u>J. Nat'l Cancer Inst.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer Plenum</u>. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) <u>Sem Cancer Biol.</u> 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; and Freshney (1985) <u>Anticancer Res.</u> 5:111-130.

Invasiveness into Matrigel

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The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Nat'l Cancer Inst.</u> 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263-272; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturallyoccurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothicate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

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The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

Methods of identifying variant ovarian cancer-associated sequences

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Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

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The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) <u>J. Clin. Invest.</u> 95:341-

349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

used as adjuvants.

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Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptidemediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

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EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) <u>Nature</u> 403:672-676; Zhao, et al. (2000) <u>Genes Dev.</u> 14:981-993).

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TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID

Title: UniGene title
ratio: ratio tumor vs normal tissues

UGID Ex. Acon Title heparin-binding growth factor binding protein "serine (or cysteine) proteinase inhibitor, clade B(ovalbumi steroidogenic acute regulatory protein 423634 AW959908 Hs.1690 AW178761 Hs.227948 423017 40 432938 T27013 Hs.3132 445810 AW265700 Hs.155660 **ESTs** developmentally regulated GTP-binding protein 1 431938 AA938471 Hs.115242 *ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM Hs.51615 407112 AA070801 425650 NM_001944 Hs.1925 desmoglein 3 (pemphigus vulgaris antigen) 45 402075 predicted exon X03635 Hs.1657 400301 estrogen receptor 1

ratio

63.6

58.3

35.9

30.0

	402639	1.40500	1)- 444260	predicted exon	25.3
	421948	L42583	Hs.111758	keratin 6A	24.7 24.6
	414540	BE379050	Hs.89546	"gb:601236655F1 NIH_MGC_44 Homo sapiens cDNA clon	24.6 24.5
5	418994 401 <i>5</i> 75	AA296520	rts.09340	selectin E (endothelial adhesion molecule 1) predicted exon	23.6
	457024	AA397546	Hs.119151	ESTs	23.2
	440684	Al253123	Hs.127356	"ESTs, Highly similar to NEST_HUMAN NESTI [H.sapien	23.1
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	400964			predicted exon	22.5
10	402421			predicted exon	20.9
	437329	AA811977	Hs.291761	ESTs	20.8
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA clon	20.7
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapiens	20.4
15	401283		11 000000	predicted exon	20.3
15	440633	AI140686	Hs.263320	ESTS	19.9
	445603	H08345	Hs.106234	ESTs ·	19.7 19.7
	403786	AW604381	Hs.121121	predicted exon ESTs	19.6
	436508 459390	BE385725	115.121121	gb:601276347F1 NIH_MGC_20 Homo saplens cDNA clon	19.2
20	421823	N40850	Hs.28625	ESTs	19.0
20	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	18.9
	422525	AA758797	Hs.192807	ESTs	18.5
	458121	S42416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from JM c	18.3
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	18.1
25	450192	AA263143	Hs.24596	RAD51-interacting protein	18.0
	416839	H94900	Hs.17882	ESTs	17.9
	440788	AI806594	Hs.128577	ESTs	17.9
	451072	AA013451	Hs.117929	ESTs	17.7
00	402203			predicted exon	17.3
30	417611	AW993983		gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapiens	17.3
	438658	AJ222068	Hs.123571	ESTs	17.3
	403747		11 407047	predicted exon	17.2
	444958	AW292643	Hs.167047	ESTs	17.2 17.1
35	404097	00004770		predicted exon	16.9
22	459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo saplens cDNA clon gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapl	16.9
	443198	AI039813 AW452647	Hs.270482	ESTs	16.9
	441557 433871	W02410	Hs.205555	ESTs	16.8
	429163	AA884766	113.200000	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD	16.7
40	443406	AI056238	Hs.143316	ESTs	16.7
	400613	,		predicted exon	16.6
	448372	AW445166	Hs.170802	ESTs	16.5
	410929	H47233	Hs.30643	ESTs	16.5
	445887	Al263105	Hs.145597	ESTs ·	16.1
45	422036	AA302647	Hs.271891	ESTs	16.0
	404767			predicted exon	15.9
	420831	AA280824	Hs.190035	ESTs	15.8
	405196	414420442		predicted exon	15.8 15.8
50	452947	AW130413	Hs.139322	*gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clo small proline-rich protein 3	15.8
50	429538 435313	BE182592 Al769400	Hs.189729	ESTs	15.7
	449635	A1989942	Hs.232150	ESTs	15.6
	424098	AF077374	Hs.139322	small proline-rich protein 3	15.4
	411660	AW855718	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	*gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens c	15.4
55	442653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	443534	Al076123 ·		gb:oy92e04.x1 Soares_fetal_liver_splean_1NFLS_S1 Homo	15.4
	458012	Al424899	Hs.188211	ESTs .	15.3
	441018	AI809587	Hs.148782	ESTs	15.1
60	425972	BE391563	Hs.165433	"ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1
60	418092	R45154	Hs.106604	ESTS	15.1 15.1
	410909	AW898161	Hs.53112	*ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	15.0
	458234	BE551408 T92641	Hs.127196 Hs.127648	ESTs hypothetical protein PRO2176	15.0
	434208 403177	132041	113.121070	predicted exon	15.0
65	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	14.9
03	425090	AA350552	110.102121	gb:EST57886 Infant brain Homo sapiens cDNA 5' end, mR	14.7
	409723	AW885757	Hs.257862	ESTs	14.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens cDNA 5'	14.6
	444266	AI424984	Hs.125465	ESTs ·	14.5
70	443341	AW631480	Hs.8688	ESTs ·	14.4
	457336	AW969657	Hs.291029	ESTs ·	14.4
	440500	AA972165	Hs.150308	ESTs	14.4
	446292	AF081497	Hs.279682	Rh type C glycoprotein	14.3
75	438086	AA336519	Hs.301167	"Homo sapiens cDNA: FLJ21545 fis, clone COL06195"	14.3
75	434715	BE005346	Hs.116410	ESTs	14.2
	409387	AW384900	Hs.123526	ESTs	14.2 14.2
	409272	AB014569	Hs.52526	KIAA0669 gene product "gb:RC6-CN0014-080300-012-B09 CN0014 Homo saplens	14.2
	454913 439846	AW841462 T63959	Hs.228320		14.0
80	409695	AA296961	1 13.220320	"gb:EST112514 Adrenal gland tumor Homo sapiens cDNA	13.9
-	422897	AA679784	Hs.4290	ESTs	13.9
	404664			predicted exon	13.9
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3', mRNA	13.8
	407327	AA487182	Hs.269414	ESTs	13.8

	455435	AW939445		"gb:QV1-DT0072-310100-056-b07 DT0072 Homo sapiens	13.7
	449327	AI638743	Hs.224672	ESTs	13.7
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo saplens	13.7
-	407463	AJ272034		gb:Homo sapiens mRNA for putative capacitative calcium c	13.6
5	446767	Al380107	Hs.158954	ESTs	13.6
	433040	H70423	Hs.300511	ESTs	13.5
	435209	AW027809	Hs.187698	*ESTs, Highly similar to cytomegalovirus partial fusion rece	13.5
	441459	Al919142	Hs.214233	ESTs	13.5
10	401269	A1400575	LIA 452070	predicted exon ESTs	13.4 13.4
10	438663 426698	Al199575 AA394104	Hs.153070 Hs.97489	ESTs	13.4
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from clon	13.2
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clon	13.2
	456714	AW897265	110.2.1000	gb:CM0-NN0057-150400-335-a04 NN0057 Homo sapiens	13.2
15	458356	A1024855	Hs.131575 .		13.2
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	13.1
	454822	AW833793		*gb:QV4-TT0008-130100-080-a06 TT0008 Homo saplens c	13.1
	453358	A1990738	Hs.240066	ESTs	13.1
20	435542	AA687376	Hs.269533	ESTs	13.1
20	421286	AA806584	Hs.187895	ESTs	13.0
	452799	A1948829	Hs.213786	ESTs	13.0 13.0
	444355	BE383686	Hs.191621	ESTs . ESTs	12.9
	444271 443860	AW452569 AW866632	Hs.149804	"gb:QV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9
25	428719	AA358193	Hs.193128	hypothetical protein FLJ10805	12.9
23	418282	AA215535	Hs.98133	ESTs	12.8
	437308	AA749417	Hs.292353	ESTs	12.7
	400584			predicted exon	12.7
••	426306	AA447310	Hs.164059	"Homo sapiens cDNA FLJ13338 fis, clone OVARC100188	12.7
30	448466	Al522109	Hs.171066	ESTs	12.7
	402738			predicted exon	12.7
	451531	AA018311	Hs.114762	ESTs	12.6
	435243	AW292886	Hs.261373	adenosine A2b receptor pseudogene	12.6 12.6
35	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	12.5
33	425108	A1000489	Hs.96967 Hs.115263	ESTs epiregulin	12.5
	422330 432949	D30783 AA570749	Hs.298866	ESTs	12.5
	417009	AA191719	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA	12.4
	456378	AA843387	Hs.87279	ESTs	12.4
40	432966	AA650114		gb:ns92h09.s1 NCI_CGAP_Pr3 Homo saplens cDNA clon	12.4
	440571	AA904461	Hs.130798	ESTs	12.3
	411178	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo saplens c	12.3
	445934	AF131737	Hs.13475	hypothetical protein	12.3
15	433917	A1809325	Hs.122814	Human DNA sequence from clone RP5-1028D15 on chrom	12.2
45	402018	4 4 00 00 1		predicted exon	12.2
	424101	AA335394	11-04000	*gb:EST39787 Epididymus Homo sapiens cDNA 5' end, mR	12.2 12.1
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3 *gb:QV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1
	458154 440919	AW816379 AW291274	Hs.262826	ESTs	12.0
50	415747	AA381209	113.202020	"gb:EST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
50	411748	AW859920		gb:QV1-CT0364-260100-052-g05 CT0364 Homo sapiens	12.0
	452975	M85521	Hs.69469	dendritic cell protein	12.0
	427276	AA400269	Hs.49598	ESTs	12.0
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	12.0
55	450786	H86632	Hs.33654	ESTs	12.0
	402578	41.00-405		predicted exon	11.9
	459591	AL037185		gb:DKFZp564A1169_r1 564 (synonym: hfbr2) Homo saple	11.9 11.9
	433449 429108	AW772282 AA890521	Hs.126035	*gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA c ESTs	11:8
60	429100 454556	AW807073	110.120000	gb:MR4-ST0052-031199-018-d06 ST0062 Homo saplens	11.7
-00	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	11.7
	400385	NM_020389	Hs.283104	pulative capacitative calcium channel	11.6
	411725	AW858396		gb:CM0-CT0341-181299-130-c06 CT0341 Homo sapiens	11.5
	455174	AI694575	Hs.147801	ESTs	11.5
65	412402	AW984788		*gb:RC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5
	434205	AF119861	Hs.283032		11.5
	450496	AW449251	Hs.257131		11.5
	411149	N68715	Hs.269128	ESTS	11.5 11.4
70	414210	BE383592	Un 67726	*gb:601297871F1 NiH_MGC_19 Homo sapiens cDNA clon acetyl LDL receptor; SREC	11.3
70	409994 453845	D86864 AL157568	Hs.57735	gb:DKFZp761F0816_r1 761 (synonym: hamy2) Homo sapi	11.3
	404849	WE101000		predicted exon	11.3
	442824	BE178065	Hs.144081		11.3
	428548	AA430058	Hs.98649	EST	11.3
75	434804	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA do	11.3
-	430486	BE062109	Hs.241551	"chloride channel, calcium activated, family member 2"	11.3
	400174			predicted exon	11.2
	424324	AA346316		*gb:EST52440 Greater omentum tumor Homo sapiens cDN	11.2
00	447724	AW298375	Hs.24477	ESTs	11.2
80	457028	AW449838	Hs.97562	ESTs EST-	11.2 11.2
	429900	AA460421	Hs.30875	ESTs	11.2
	452240 458067	AI591147 AA393603	Hs.61232 Hs.36752	ESTs "Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314"	11.1
	402222	MUSCELLIN	1 13.00132	predicted exon	11.1
				F	

	440745	********	11- 450400	COT-	44.4
	446745 453060	AW118189 AW294092	Hs.156400 Hs.21594	ESTs ESTs	11.1 11.1
	443482	AW188093	Hs.250385	ESTs	11.1
	436843	AA824588	1 10.120000	*gb:oc83d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA c	11.0
5	416320	H47867	Hs.34024	ESTs	11.0
_	435772	AA700019	Hs.132992	*ATP-binding cassette, sub-family G (WHITE), member 5 (11.0
	451542	AA018365	Hs.32713	ESTs	11.0
	408522	Al541214	Hs.46320	"Small proline-rich protein SPRK [human, odontogenic kera	11.0
10	414712	N88858.comp	Hs.77039	ribosomal protein S3A	10.9
10	411940	AW876686	H- 254200	*gb:CM4-PT0031-180200-507-e05 PT0031 Homo saplens c	10.9 10.9
	408733	AW264812 AL137578	Hs.254290 Hs.27607	ESTs Homo saplens mRNA; cDNA DKFZp564N2464 (from clon	10.9
	452030 458175	AW296024	Hs.150434	ESTs _	10.9
	400612	ATTEGORET	16.100464	predicted exon	10.9
15	440159	Al637599	Hs.126127	ESTs	10.8
	429443	AB028967	Hs.202687	*potassium voltage-gated channel, Shal-related subfamily, m	10.8
	416319	AI815601	Hs.79197	*CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
	405783			predicted exon	10.7
20	405708	41000004	11- 000027	predicted exon	10.7
20	433266	A1863224	Hs.288677	Homo sapiens cDNA FLJ13872 fis, clone THYRO100132	10.6 10.6
	456900 432408	AA355442 N39127	Hs.169054 Hs.76391	ESTs "myxovirus (influenza) resistance 1, homolog of murine (int	10.6
	451702	AW665452	Hs.246503	ESTs	10.6
	418179	X51630	Hs.1145	Wilms tumor 1	10.6
25	408987	H85615		gb:yt03f11.r1_Soares retina N2b5HR Homo sapiens cDNA	10.6
	405285			predicted exon	10.5
	419276	BE165909	Hs.134682	"Homo sapiens cDNA: FLJ23161 fis, clone LNG09730"	10.5
	407287	AI678812	Hs.201658	*ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
20	403065	0500000		predicted exon	10.5 10.4
30	414195	BE263293 A1457286	Hs.143979	"gb:601144881F2 NIH_MGC_19 Homo sapiens cDNA clon "ESTs, Weakly similar to KIAA1276 protein [H.sapiens]"	10.4
	454258 412951	BE018611	Hs.251946	"Homo sapiens cDNA: FLJ23107 fls, clone LNG07738"	10.4
	428888	AA437010	Hs.266584	ESTs	10.4
	440834	AA907027	Hs.128606	ESTs	10.4
35	437096	AA744406		"gb:ny51h02.s1 NCI_CGAP_Pr18 Homo saplens cDNA clo	10.4
	400135			predicted exon	10.4
	447849	Al538147	Hs.164277	ESTs	10.3
	400593	A A 4000004	11- 000047	predicted exon	10.3 10.3
40	427469	AA403084	Hs.269347	ESTs predicted exon	10.3
40	402794 452743	AW965082	Hs.61455	ESTs	10.2
	448983	AI611654	Hs.224908	ESTs	10.2
	422696	AF242524	Hs.26323	hypothetical nuclear factor SB8!22	10.2
	428949	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 [H.sapiens]	10.2
45	409191	AW818390		"gb:RC1-ST0278-160200-014-d10 ST0278 Homo sapiens c	10.2
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	10.2 10.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone *gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA clon	10.2
	410626 445835	BE407727 AW290999	Hs.145534	chromosome 21 open reading frame 23	10.1
50	452507	AI904646		*gb:QV-BT065-020399-103 BT065 Homo sapiens cDNA, m	10.1
	433297	AV658581	Hs.282633	ESTs	10.1
•	426724	AA383623	Hs.293616	ESTs	10.0
	436659	A1217900	Hs.144464	ESTs	10.0
55	405675	DC444707	II- 00440E	predicted exon	10.0 10.0
23	413466 447198	BE141737 D61523	Hs.254105 Hs.283435	"enolase 1, (alpha)" ESTs	10.0
	403306	NM_006825	Hs.74368	"transmembrane protein (63kD), endoplasmic reticulum/Go	10.0
	413544	BE147225	110.11 1000	gb:PM2-HT0225-031299-003-f11 HT0225 Homo saplens	9.9
	437094	AW103746	Hs.136907	ESTs	9.9
60	401497			predicted exon	9.9
	416203	H27794	Hs.269055	ESTs	9.9
	426882	AA393108	Hs.97365	ESTS	9.9 9.9
	454874 406702	AW836407 Z20656	Hs.278432	*gb:PM3-LT0031-301299-002-b09 LT0031 Homo sapiens *myosin, heavy polypeptide 6, cardiac muscle, alpha (cardio	9.9
65	404952	220000	N3.270432	predicted exon	9.9
03	430691	C14187	Hs.103538	ESTs	9.9
	444518	AI160278	Hs.146884	ESTs	9.8
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen 1NFLS Homo sapie	9.8
70	438691	AA906288	Hs.212184	ESTs	9.8
70	405636		11 407040	predicted exon	9.8
	437242	AA747538	Hs.187942	ESTs	9.8 9.8
	425627 452226	AF019612 AA024898	Hs.297007 Hs.296002	ESTs .	9.8
	418986	Al123555	Hs.81796	ESTs	9.8
75	441139	AW449009	Hs.126647	ESTs	9.7
	427244	AA402400	Hs.178045	ESTs	9.7
	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clo	9.7
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
80	443526	AW792804	Hs.134002	ESTs.	9.6 9.6
٥U	440576	AW449775	Hs.126008	ESTs small nuclear ribonucleoprotein polypeptide G	9.6
	419088 454707	AI538323 AW814989	Hs.77496	*gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6
	446252	Al283125	Hs.150009	ESTs	9.6
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA d	9.6

	403093	414044000		predicted exon	9.6
	454633	AW811380		"gb:lL3-ST0143-290999-019-D05 ST0143 Homo saplens c	9.6
	407291	AA001464 AW865450		gb:ze45b01.r1 Soares retina N2b4HR Homo sapiens cDNA	9.5
5	455203 403647	AWODD45U		"gb:PM4-SN0020-010400-008-b09 SN0020 Homo saplens	9.5
,	403647			predicted exon predicted exon	9.5 9.5
	414281	BE269751	Hs.288995	hypothetical protein FLJ20813	9.5
	411057	AW815098	113.200333	"gb:QV4-ST0212-091199-023-f10 ST0212 Homo saplens c	9.5
	415953	H14425	Hs.27947	ESTs	9.5
10	450174	T82121	Hs.177285	ESTs	9.5
	422949	AA319435		"gb:EST21657 Adrenal gland turnor Horno saplens cDNA 5	9.5
	402112	R58624	Hs.2186	eukaryotic translation elongation factor 1 gamma	9.5
	457886	AA742279	Hs.293346	ESTs	9.4
	458145	Al239457	Hs.130794	ESTs	9.4
15	452332 ·	AW014859	Hs.101657	ESTs	9.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo sapien	9.3
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	9.3
	419968	X04430	Hs.93913	"interleukin 6 (interferon, beta 2)"	9.3
20	436211	AK001581	Hs.80961	"polymerase (DNA directed), gamma"	9.3
20	428412	AA428240	Hs.126083	ESTs	9.3
	449441	A1656040	Hs.196532	ESTs	9.3
	458771	AW295151	Hs.163612	ESTs	9.3
	458543	AA213403	Hs.257542	ESTS	9.3
25	414257 442826	AI828500 AI018777	Hs.21124 Hs.131241	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM ESTs	9.3 9.3
20	446740	Al611635	Hs.192605	ESTs ~	9.2
	408938	AA059013	Hs.22607	ESTs	9.2
	434157	AI538316	Hs.158451	ESTs	9.2
	408774	AW270899	Hs.254569	ESTs	9.2
30	424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on chromosome	9.2
	415715	F30364		gb:HSPD20786 HM3 Homo sapiens cDNA clone s400009	9.1
	405277			predicted exon	9.1
	412167	AW897230		*gb:CM0-NN0057-150400-335-a11 NN0057 Homo sapiens	9.1
25	442771	AW409808	Hs.101550	ESTs	9.1
35	404898			predicted exon	9.1
	401230			predicted exon	9.1
	400623			predicted exon	9.1
	418808	AI821836	Hs.10359	ESTs	9.1
40	436396	A1683487	Hs.299112	"Homo sapiens cDNA FLJ11441 fts, clone HEMBA100132	9.1
40	440466 437568	AA885871 Al954795	Hs.135727 Hs.156135	ESTS ESTS	9.0 9.0
	405382	71334733	(15.150155	predicted exon	9.0
	435673	AF202961	Hs.284200	"Homo sapiens uncharacterized gastric protein ZG12P mRN	9.0
	405848	74 202001	110.201200	predicted exon	9.0
45	437229	AW976005		gb:EST388114 MAGE resequences, MAGN Homo saplen	9.0
	417728	AW138437	Hs.24790	KIAA1573 protein	9.0
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.0
	427093	AA398118	Hs.97579	ESTs	9.0
c 0	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.0
50	440556	AW206958	Hs.125968	ESTs	9.0
	400163	41.040040	11 05040	predicted exon	8.9
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like 1	8.9
	417549	AA203651		gb:zx58f10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo predicted exon	8.9 8.9
55	406163 437918	AI761449	Hs.121629	ESTs	8.9
55	449419	R34910	Hs.119172	ESTs	8.9
	434683	AW298724	Hs.202639	ESTs	8.9
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	8.9
	454590	AW809762	Hs.222056	"Homo sapiens cDNA FLJ11572 fis, clone HEMBA100337	8.8
60	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapiens c	8.8
	441433	AA933809	Hs.42746	ESTs	8.8
	416858	AW979294	Hs.85634	ESTs	8.8
	421978	AJ243662	Hs.110196	NICE-1 protein	8.8
65	451528	AA018297	Hs.35493	ESTs	8.8
65	408751	N91553	Hs.258343	ESTs	8.7
	401862	AMM07212		predicted exon	8.7 8.7
	417344 454455	AW997313 AW752710		"gb:RC2-BN0048-250400-018-f12 BN0048 Homo saplens "gb:IL3-CT0219-281099-024-A03 CT0219 Homo saplens c	8.7
	455592	BE008002		"gb:QV0-BN0147-290400-214-h04 BN0147 Homo sapiens	8.7
70	417650	T05870	Hs.100640	ESTs	8.7
	456309	AA225423		*gb:nc24a12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	8.7
	432030	A1908400	Hs.143789	ESTs	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
~~	402576			predicted exon	8.7
75	426874	N67325	Hs.247132	ESTs	8.7
	403334			predicted exon	8.7
	408562	AI436323	Hs.31141	"Homo sapiens mRNA for KIAA1568 protein, partial cds"	8.7
	439443	AF086261	Hs.127892	ESTs	8.7
80	428600	AW863261	Hs.15036	"ESTs, Highly similar to AF161358 1 HSPC095 [H.sapiens	8.7
OV	414539	BE379046	Un 100754	"gb:601236646F1 NIH_MGC_44 Homo sapiens cDNA clon	8.6
	432527 403273	AW975028	Hs.102754	ESTS predicted exon	8.6 8.6
	452077	BE144949		"gb:RC2-HT0187-041099-011-d12 HT0187 Homo sapiens	8.6
	444598	Al288830	Hs.149924	ESTs	8.6
				,	

	434066	AF116649	Hs.283944	"Homo sapiens PR00566 mRNA, complete cds"	8.6
	429643	AA455889	Hs.187548	ESTs	8.6
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clon	8.6
~	446142	Al754693	Hs.145968	ESTs	8.6
5	417412	X16896	Hs.82112	"interleukin 1 receptor, type i"	8.6
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapiens	8.5
	451318	AA029888	Hs.95071	ESTs	8.5
	405547			predicted exon	8.5
10	423843	AA332652		gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' en	8.5
10	454145	AA046872	Hs.62798	ESTs	8.4
	401200			predicted exon	8.4
	404166			predicted exon	8.4
	412761	AW995092		gb:QV0-BN0041-030300-145-a10 BN0041 Homo sapiens	8.4
1.0	412333	AW937485		*gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapiens	8.4
15	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
	419281	H96452	Hs.42189	ESTs	8.4
	446171	Al374927		gb:ta66c04.x1 Soares_total_fetus_Nb2HF8_9w Homo sapie	8.3
	437362	AL359561	Hs.16493 ,	hypothetical protein DKFZp762N2316	8.3
00	402631 -			predicted exon	8.3
20	458573	AV653838	Hs.295131	ESTs	8.3
	439185	AF087976	Hs.233343	ESTs	8.3
	445881	A1263029	Hs.210689	ESTs	8.3
	449737	Al668581	Hs.246316	ESTs	8.3
0.5	401830	AJ004832	Hs.5038	neuropathy target esterase	8.3
25	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
	416996	W91892	Hs.59609	ESTs	8.2
	443626	A1540644	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
	407471	D55644		gb:Human spleen PABL (pseudoautosomal boundary-like se	8.2
20	402664			predicted exon	8.2
30	417682	W69561		gb:zd47a08.r1 Soares_fetal_heart_NbHH19W Homo sapien	8.2
	424983	A1742434	Hs.169911	ESTs	8.2
	434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	8.2
	453448	AL036710	Hs.209527	ESTs	8.2
26	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo sapiens	8.2
35	404270			predicted exon	8.1
	438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
	418122	R42778	Hs.22217	ESTs	8.1
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.1
40	400925			predicted exon	8.1
40	403350			predicted exon	8.1
	426116	AA868729	Hs.144694	ESTs	8.1
	441518	AW161697	Hs.294150	ESTs	8.1
	421888	AA299780	Hs.121036	ESTs	8.1
15	402745			predicted exon	8.1
45	402071			predicted exon	8.1
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
	430372	Al206173	Hs.211375	ESTs	8.0
	449867	A1672379	Hs.73919	"clathrin, light polypeptide (Lcb)"	8.0
50	422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone	8.0
50	413382	BE090689	11. 457077	*gb:RC1-BT0720-280300-011-f08 BT0720 Homo saplens c	8.0
	456502	A1798611	Hs.157277	ESTs	8.0
	405336			predicted exon	8.0
	405917	A104774C	11- 000400	predicted exon	8.0
55	436007	AI247716	Hs.232168	ESTs	8.0
33	439192	AW970536	Hs.105413	ESTs	8.0
	437724	AW444828 AW138937	Hs.184323	ESTs	8.0
	452755	AVV 130937	Hs.213436	ESTs	8.0 7.9
	401781			predicted exon	7.9
60	406057 406289	AW068311	Hs.82582	predicted exon "integrin, beta-like 1 (with EGF-like repeat domains)"	7.9 7.9
50	421459	AW000311 AI821539	Hs.97249	ESTs	7.9
	448251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fis, clone HEMBB100128	7.9
•				ESTs	7.9
	429125 440154	AA446854 BE077129	Hs.271004 Hs.126119	"Homo saplens cDNA FLJ13273 fis, clone OVARC100101	7.9
65	413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	7.9
03	438268	AA782163	Hs.293502	ESTs	7.9
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on chromosome 6	7.9
	441194	BE274581	113.20001	"gb:601120870F1 NIH_MGC_20 Homo sapiens cDNA clon	7.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	7.9
70	445090	AW205208	Hs.147293	ESTs	7.9
, 0	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromosome	7.9
	414266	BE267834	113.23 1733	"gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
	407839	AA045144	Hs.161566	ESTs	7.8
	456101	AA159478	113.101000	gb:zo74d06.s1 Stratagene pancreas (937208) Homo sapiens	7.8
75	455853	BE147225		"gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	7.8
, 5	414995	C18200		gb:C18200 Human placenta cDNA (TFujiwara) Homo sapie	7.8
	447247	AW369351	Hs.287955	"Homo sapiens cDNA FLJ13090 fis, clone NT2RP3002142	7.8 7.8
	416151	T26561	10.201300	"gb:AB65C7R Infant brain, LLNL array of Dr. M. Soares 1	7.8
	446435	AW206737	Hs.253582	ESTs	7.8
80	403698			predicted exon	7.8
	424914	AA348410	Hs.119065	ESTs	7.8
	409731	AA125985	Hs.56145	"thymosin, beta, identified in neuroblastoma cells"	7.8
	401604			predicted exon	7.8
	413025	AA805265	Hs.291646	ESTs	7.8
				•	

	Ansone			andialed area	70
	405896 454505	AW801365		predicted exon "gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapiens	7.8 7.7
	448283	A1340462	Hs.182979	ribosomal protein L12	7.7
_	434098	AA625499	110.1020.0	"gb:af69g08.r1 Soares_NhHMPu_S1 Homo saplens cDNA	7.7
5	431673	AW971302	Hs.293233	ESTs	7.7
	421029	AW057782	Hs.293053	ESTs	7.7
	408391	AW859276		"gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapiens	7.7
	422529	AW015128	Hs.256703	ESTs	7.7
10	454389	AW752571	11- 00000	*gb:iL3-CT0213-170100-055-F02 CT0213 Homo sapiens c	7.7
10	427821	AA470158	Hs.98202 Hs.191840	ESTs . ESTs	7.7 7.7
	434657 445628	AA641876 Al344166	Hs.155743	ESTs	7.7
	424872	AA347923	113.103/40	*gb:EST54302 Fetal heart II Homo sapiens cDNA 5' end, m	7.7
	439232	N48590	Hs.46693	ESTs	7.7
15	441417	AI733297	Hs.144474	ESTs	7.7
	453596	AA441838	Hs.62905	ESTs	7.7
	430440	X52599	Hs.2561	"nerve growth factor, beta polypeptide"	7.7
	413306	AW303544	Hs.118654	ESTs	7.7
20	400968			predicted exon	7.7
20	446726	AW300144	Hs.209209	"Homo sapiens cDNA FLJ11629 fis, clone HEMBA100424	7.7
	427504	AA776743	Hs.191589	ESTs	7.7 7.6
	405621 414127	Al431863	Hs.135270	predicted exon ESTs	7.6
	409866	AW502152	113.1002.10	gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_52 Homo sap	7.6
25	446232	AI281848	Hs.165547	ESTs	7.6
	403568			predicted exon	7.6
	451458	A1797558	Hs.270820	ESTs	7.6
	439157	AA912737	Hs.20160	ESTs	7.6
20	401793			predicted exon	7.6
30	429839	AJ190291	Hs.112143	ESTs	7.6
	445672	A1907438	Hs.282862	ESTs	7.6
	449444 447499	AW818436 AW262580	Hs.23590 Hs.147674	"solute carrier family 16 (monocarboxylic acid transporters) KIAA1621 protein	7.6 7.6
	421773	W69233	Hs.112457	ESTs	7.6
35	439706	AW872527	Hs.59761	ESTs	7.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clon	7.5
	402050			predicted exon	7.5
	429687	Al675749	Hs.211608	nucleoparin 153kD	7.5
40	423193	R07299	Hs.254837	"Homo saplens cDNA FLJ13502 fis, clone PLACE1004836	7.5
40	416548	H62953	11- 404400	gb:yr47f06.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.5
	443236	AI079496	Hs.134169	ESTs	7.5 7.4
	436053 437191	AI057224 NM_006846	Hs.15443 Hs.5476	ESTs "serine protease Inhibitor, Kazal type, 5"	7.4 7.4
	451829	AW964081	Hs.247377	ESTs	7.4
45	443151	Al827193	Hs.132714	ESTs	7.4
	452055	Al377431	Hs.293772	ESTs	7.4
	445265	Al218295	Hs.144942	ESTs	7.4
	401032			predicted exon	7.4
50	448184	BE541249	Hs.109697	ESTs	7.4
50	414808	T95945	U- 00077	gb:ye42e02.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.4 7.4
	418540	A1821597	Hs.90877	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.4 7.4
	410449 435568	AW748954 AA688048	Hs.18192 Hs.294080	Ser/Arg-related nuclear matrix protein (plenty of prolines 1 ESTs	7.4
	459160	AI904723	115234000	*gb:CM-BT066-120299-092 BT066 Homo sapiens cDNA,	7.4
55	419753	N42531		gb:yy11c12.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.4
	432383	AK000144	Hs.274449	"Homo sapiens cDNA FLJ20137 fis, clone COL07137"	7.4
	404893			predicted exon	7.4
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5-phosphate epimer	7.4
60	413864	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo saplens	7.3
60	426871	AA393041	Hs.216493	ESTS should by 1 at Course infant begin 1 NIB Home conions aDN	7.3 7.3
	415613 427025	R20233 AA397589	Hs.97523	gb:yg18h11.r1 Soares Infant brain 1NIB Homo sapiens cDN ESTs	7.3 7.3
	427025 444683	AL375101	Hs.158721	*ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
	447700	Al420183	Hs.171077	*ESTs, Weakly similar to similar to serine/threonine kinase	7.3
65 ·	412740	AW993984		*gb:RC1-8N0035-130400-013-a05 BN0035 Homo sapiens	7.3
•	416642	T96118	Hs.226313	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
	416506	H59879	Hs.237306	ESTS	7.3
	426130	AAB53282		gb:NHTBCae04f07r1 Normal Human Trabecular Bone Cell	7.3
70	407392	AB032369		"gb:Homo sapiens MIST mRNA, partial cds."	7.3
70	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	7.3
	451221	Al949701	Hs.210589	ESTs gb:ox48c08_x1 Soares_total_fetus_Nb2HF8_9w Homo sapi	7.3
	443161 418186	Al038316 BE541042	Hs.23240	"Homo sapiens cDNA FLJ13496 fis, clone PLACE1004471	7.3 7.3
	439152	H65014	1.0.20270	gb:yu66f10.r1 Weizmann Olfactory Epithelium Homo sapie	7.2
75	459534	BE386808	Hs.147905	ESTs	7.2
-	443326	BE156494	Hs.188478	ESTs	7.2
	417351	T90278	Hs.15049	ESTs	7.2
	454182	AW177335		*gb:CM1-CT0129-180899-006-b08 CT0129 Homo sapiens	7.2
0 Λ	402298	11847.55	11-41000-	predicted exon	7.2
80	458562	N34128	Hs.145268	ESTs	7.2 7.2
	407021 449276	U52077	Hs.252713	gb:Human mariner1 transposase gene, complete consensus ESTs	7.2 7.2
	418251	AW241510 AA832123	Hs.177723		7.2
	420788	AA937957	Hs.193367	ESTs	7.2
				00	

	401881			andiated over	7.2
	456436	AA251079	Hs.158386	predicted exon ESTs	7.2
	413425	F20956	113.130000	gb:HSPD05390 HM3 Homo saplens cDNA clone 032-X4-	7.2
_	448966	AW372914	Hs.287462	"Homo sapiens cDNA FLJ11875 fis, clone HEMBA100707	7.2
5	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (from clon	7.2
	406053			predicted exon	7.2
	405851			predicted exon	7.2
	431009	BE149762	Hs.248213	"gap junction protein, beta 6 (connexin 30)"	7.2
10	426662	AA879474	Hs.122710	ESTs	7.2
10	408536	AW381532	Hs.135188	ESTS	7.1.
	455013	BE073250	Un 402702	"gb:MR0-BT0551-060300-102-e05 BT0551 Homo saplens	7.1
	428910 424634	W03667 NM_003613	Hs.193792 Hs.151407	ESTs "cartilage intermediate layer protein, nucleotide pyrophosph	7.1 7.1
	449794	AW444502	Hs.256982	*ESTs, Highly similar to AF116865 1 hedgehog-interacting	7.1
15	423410	AF058989	Hs.128231	"G antigen, family B, 1 (prostate associated)"	7.1
	445460	AI797473	Hs.209468	ESTs ·	7.1
	447285	Al371849	Hs.200696	"ATPase, Class VI, type 11C"	7.1
	419750	AL079741	Hs.183114	"Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515	7.1
00	438986	AF085888	Hs.269307	ESTs	7.1
20	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; testicular	7.1
	432479	AL042B44	Hs.275675	kalanin p80 (WD40-containing) subunit 8 1	7.1
	449733	R74546	Hs.29438	"Homo sapiens cDNA FLJ12094 fis, clone HEMBB100260	7.1
	437846	AA773866	Hs.244569	ESTS	7.1
25	454934	AW846080	U- 047000	"gb:MR3-CT0176-081099-002-b09 CT0176 Homo sapiens	7.1
25	421929 401780	AA300543	Hs.247360	ESTs	7.1 7.0
	448106	A1800470	Hs.171941	ESTs -	7.0
	448835	BE277929	Hs.11081	*ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sap	7.0
	400842	002	1.0111001	predicted exon	7.0
30	429364	AA451797	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0
	454963	AW847647		gb:IL3-CT0213-280100-056-A06 CT0213 Homo sapiens c	7.0
	423891	AK002042	Hs.134795	"Homo sapiens cDNA FLI11180 fis, clone PLACE1007452	7.0
	407506	U71600		"gb:Human zinc finger protein zfp31 (zf31) mRNA, partial	7.0
25	413802	AW964490	Hs.32241	ESTs	7.0
35	440051	BE559980		"gb:601345293F1 NIH_MGC_8 Homo saplens cDNA clone	7.0
	446283	AI948801	Hs.171073	ESTS .	7.0
	419236 405472	AA330447	Hs.135159	"Homo saplens cDNA FLJ11481 fis, clone HEMBA100180 predicted exon	7.0 7.0
	435024	AI863518	Hs.127743	"ESTs, Weakly similar to V-ATPase G-subunit like protein	7.0
40	453969	AW090783	Hs.301731	"Homo sapiens cDNA FLJ11738 fis, clone HEMBA100547	7.0
10	404992	A11030100	113.001701	predicted exon	7.0
	428129	Al244311	Hs.26912	ESTs	7.0
	414315	Z24878		"gb:HSB65D052 STRATAGENE Human skeletal muscle cD	7.0
4.5	400491	H25530	Hs.50868	"solute carrier family 22 (organic cation transporter), memb	6.9
45	459275	AI808913	Hs.118321	ESTs	6.9
	450853	AA479629	Hs.44243	ESTs	6.9
	457460	Al143312	Hs.164004	ESTs	6.9
	434168	AI204525	Hs.116156	ESTS	6.9
50	445153 450028	Al214671 Al912012	Hs.200737	"gb:qm32d02.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clo ESTs	6.9 6.9
50	414954	D81402	NS.200131	gb:HUM162A03B Human fetal brain (TFujiwara) Homo sa	6.9
	459478	AW195566	Hs.253182	ESTs	6.9
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clon	6.9
	401050			predicted exon	6.9
55	447588	Al394154	Hs.279659	"ESTs, Weakly similar to unknown protein [H.sapiens]"	6.9
	449002	Al620018	Hs.117461	ESTs	6.9
	452759	AW590773	Hs.258996	ESTs	6.9
	443220	R85304	Hs.132032	"Homo saplens cDNA FLJ11683 ffs, clone HEMBA100490	6.9
60	400749			predicted exon predicted exon	6.8 6.8
00	406277	DEDA4E03	Do 112704		
	433785 434129	BE044593 Al807757	Hs.112704 Hs.221041	ESTs ESTs	6.8 6.8
	453369	BE551550	Hs.232630	ESTs	6.8
	411722	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapiens	6.8
65	455152	AW858621		gb:CM0-CT0342-021299-115-f04 CT0342 Homo saplens	6.8
	412670	AA115456		gb:zk89b05.r1 Soares_pregnant_uterus_NbHPU Homo sapi	6.8
	419054	N40340	Hs.191510	"ESTs, Weakly similar to ORF2 [M.musculus]"	6.8
	421316	AA287203	Hs.251397	SMA5	6.8
70	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone	6.8
70	458603	AW103046	Hs.6162	KIAA0771 protein	6.8
	439527	AW298119	Hs.202536	ESTs	6.8
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2	6.8
	439127 434890	AW978465 AF161345	Hs.292368 Hs.283930	ESTs *Homo sapiens HSPC082 mRNA, partial cds*	6.8 6.8
75	429413	NM_014058	Hs.201877	DESC1 protein	6.7
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.7
	447252	R90916		gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo saplen	6.7
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo sapiens	6.7
	439509	AF086332	Hs.58314	ESTs	6.7
80	418858	AW961605	Hs.21145	"Homo sapiens cDNA: FLJ22489 fis, clone HRC10951"	6.7
	419323	AI092379	Hs.135275	ESTs	6.7
	415317	Z43388	Hs.5570	hypothetical protein FLJ10006	6.7
	418654	AA226334	Hs.154291	ESTS "abiliana agricos HDCCC21P mPNA complete ede "	6.7
	407413	AF067801		"gb:Homo sapiens HDCGC21P mRNA, complete cds."	6.7
				02	

	439694	AA843915	Hs.54707	ESTs	6.7
	451191	N67900	Hs.118446	ESTs	6.7
	454006	U12775			
			Hs.37006	agouti (mouse)-signaling protein	6.7
~	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen 1NFLS Homo sapien	6.7
5	455879	BE153275		*gb:PM0-HT0335-180400-008-e11 HT0335 Homo sapiens	6.7
	451368	BE242152	Hs.288417	protein serine threonine kinase Clk4	6.7
	453509	AL040021		gb:DKFZp434N1812_r1 434 (synonym; htes3) Homo saple	6.7
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
1Λ	423372	AI246375	Hs.154458	ESTs	6.7
10	450316	W84446	Hs.17850	ESTs ·	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo saplens	6.7
	405771	D401 1010		predicted exon	6.6
		414 M 4044 C			
15	411483	AW848115		*gb:IL3-CT0214-301299-048-C09 CT0214 Homo sapiens c	6.6
15	420271	A1954365	Hs.42892	ESTs	6.6
	431948	AA917706	Hs.194616	ESTs	6.6
	409629	AW449589	Hs.279724	ESTs	6.6
	458841	W28965		gb:54d10 Human retina cDNA randomly primed sublibrary	6.6
			Un 44070		6.6
20	416565	AW000960	Hs.44970	ESTs	
20	409097	AA677927	Hs.144269	ESTs	6.6
	441832	Al018249	Hs.128062	ESTs	6.6
	457285	A1038858	Hs.228780	"ESTs, Highly similar to AF199597 1 A-type potassium cha	6.6
	406504			predicted exon	6.6
	414606	BE387771		*gb:601283251F1 NIH_MGC_44 Homo sapiens cDNA clon	6.6
25			11- 004070		
23	452956	AW003578	Hs.231872	ESTs	6.6
	410743	AA089474	Hs.272153	ESTs	6.6
	404599			predicted exon	6.6
	423575	C18863	Hs.163443	"Homo sapiens cDNA FLJ11576 fis, clone HEMBA100354	6.6
	443027	AJ027847	Hs.253550	ESTs	6.6
30		AV658444	Hs.280776		6.6
50	458663			"Homo sapiens cDNA FLJ13684 fis, clone PLACE2000021	
	431277	AA501806	Hs.249965	ESTs	6.6
	445232	BE294357		"gb:601172878F1 NiH_MGC_17 Homo sapiens cDNA clon	6.6
	459170	Al905518		gb:RC-BT091-210199-098 BT091 Homo saplens cDNA, m	6.6
	437876	AA770151	Hs.126424	ESTs	6.6
35	406752	AI285598	Hs.217493	annexin A2	6.6
55		A1203330	115.217433		
	401245			predicted exon	6.6
	446102	AW168067	Hs.252956	ESTs	6.5
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.5
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (from clone	6.5
40	458831	H71739	Hs.200227	ESTs	6.5
	408914	AW450309		gb:UI-H-BI3-akz-g-08-0-UI.s1 NCI_CGAP_Sub5 Homo sa	6.5
					6.5
	411018	AW813428		*gb:MR3-ST0192-010200-210-c05 ST0192 Homo saplens c	
	436562	H71937	Hs.169756	"complement component 1, s subcomponent"	6.5
4	457620	AA602711		"gb:np03h06.s1 NCI_CGAP_Pr2 Homo saplens cDNA clon	6.5
45	438647	AA813118	Hs.163230	ESTs	6.5
	439570	179925	Hs.269165	ESTs	6.5
	419273	BE271180	Hs.293490	ESTs	6.5
					6.5
	443745	AB039670	Hs.9728	ALEX1 protein	
50	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
50	458695	AV660159	Hs.282284	ESTs	6.5
	410966	AW812088		*gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapiens c	6.4
	417135	AA422067	Hs.50547	ESTs	6.4
	416441	BE407197		*gb:601301552F1 NIH_MGC_21 Homo saplens cDNA clon	6.4
	413702	BE170313		gb:QV4-HT0536-040500-193-g02 HT0536 Homo sapiens	6.4
55					
"	452563	A1907552		gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4
	408956	AK001868	Hs.295306	*ESTs, Highly similar to unnamed protein product (H.sapien	6.4
	406349			predicted exon	6.4
	425420	BE536911	Hs.234545	*ESTs, Weakly similar to AF155135 1 novel retinal pigmen	6.4
	459430	AW662886		gb:hi82h11.x1 Soares_NFL_T_GBC_S1 Homo saplens cDN	6.4
60	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	6.4
55	458678	Al306162	Hs.170938	"ESTs, Weakly similar to KIAA0705 protein [H.sapiens]"	6.4
	429695	AA835714	Hs.293556	ESTs	6.4
	426872	AA410446	Hs.112011	"ESTs, Weakly similar to unknown [H.sapiens]"	6.4
	437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp566C0324 (from c	6.4
65	440517	AW139632	Hs.132246	ESTs	6.4
	450877	AI799608 1	Hs.29178	ESTs ·	6.4
	410664	NM_006033	Hs.65370	"lipase, endothelial"	6.4
		1414-000000	113.03370		
	405793			predicted exon	6.4
70	418709	AA227394		gb:zr17c10.r1 Stratagene NT2 neuronal precursor 937230 H	6.4
70	428684	AA431792	Hs.44784	ESTs	6.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.4
	400983			predicted exon	6.3
	422365	AF035537	Hs.115521	"REV3 (yeast homolog)-like, catalytic subunit of DNA poly	6.3
	425612	BE004257		gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapiens	6.3
75		DE00-401			6.3
13	401521	41707111	11. 4-44	predicted exon	
	430290	AI734110	Hs.136355	ESTs	6.3
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (from clon	6.3
	437939	AW298600	Hs.141840	*ESTs, Weakly similar to S59501 interferon receptor JFNA	6.3
	451842	AI820539	Hs.267087	*ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
80				predicted exon	6.3
00	405810	41/040000			
	443747	AV646352		gb:AV646352 GLC Homo sapiens cDNA clone GLCAME	6.3
	427287	NM_014903	Hs.174188	KIAA0938 protein	6.3
	413521	BE145814		gb:MR0-HT0208-101299-202-a04 HT0208 Homo sapiens	6.3
	429090	AW820278	Hs.99066	ESTs	6.3

	451488	H22999	Hs.208846	ESTs	6.3
	455713	BE069891		gb:QV4-BT0401-201299-064-b01 BT0401 Homo sapiens	6.3
	452161	R43077	Hs.221747	ESTs	6.3
_	428647	AA830050	Hs.124344	ESTs	6.3
5	445063	AI246275	Hs.149196	ESTs	6.3
•	456671	AB011142	Hs.114293	KIAA0570 gene product	6.3
	401508			predicted exon	6.3
	412677	AW029608	Hs.17384	ESTs	6.3
•	441720	AJ346487	Hs.28739	ESTs	6.3
10	418051	AW192535		ESTs	6.3
10			Hs.19479		
	438014	N71183	Hs.121806	"Homo sapiens cDNA FLJ11971 fis, clone HEMBB100120	. 6.3
	432101	Al918950	Hs.11092	*Homo sapiens cDNA FLJ14290 fis, clone PLACE1006795	6.3
	421032	AW293133	Hs.101340	ESTs	6.3
1.5	436532	AA721522		gb:nv54h12r1 NCI_CGAP_Ew1 Homo sapiens cDNA clo	6.3
15	431318	AA502700	Hs.293147	ESTs	6.3
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Homo sapiens c	6.3
	402425			predicted exon	6.3
	455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapiens	6.3
	400160			predicted exon	6.3
20	413795	AL040178	Hs.142003	ESTs	6.2
	405071		1.0111200	predicted exon	6.2
	403741			predicted exon	6.2
	432489	Al804855	Hs.207530	ESTs	6.2
		A1004033	N8.201330		6.2
25	402296	414/000400	11- 000407	predicted exon	
23	446091	AW022192	Hs.200197	ESTs	6.2
	444788	A1871122	Hs.202821	ESTs	6.2
	404972			predicted exon	6.2
	400227			predicted exon	6.2
20	433804	A1936561	Hs.112740	ESTs	6.2
30	448807	Al571940	Hs.7549	ESTs	6.2
	404340			predicted exon	6.2
	424632	AB014523	Hs.151406	KIAA0623 gene product	6.2
	449547	H93543	Hs.117963	ESTs	6.2
	406945	K01383	Hs.203967	metallothionein 1A (functional)	6.2
35	433663	AF083131	Hs.229535	CATX-15 protein	6.2
	407809	AW082279	Hs.244106	ESTs	6.2
	418342	BE002723	Hs.293504	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.2
	438007	AA133008	Hs.158675	ribosomal protein L14	6.2
	410536	N39533	113.130013	gb:yv27d04.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.2
40			Un 170270		6.2
40	448005	AW207437	Hs.170378	ESTs	6.2
	414083	AL121282	Hs.257786	ESTs	
	405362	11410 /0500	11. 070707	predicted exon	6.2
	410102	AW248508	Hs.279727	"Homo saplens cDNA FLJ14035 ffs, clone HEMBA100463	6.2
A E	457868	AW975133		gb:EST387239 MAGE resequences, MAGN Homo sapien	6.2
45	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, part	6.2
	443603	BE502601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H.sapiens]"	6.2
	430051	AA464611	Hs.52515	transducin (beta)-like 2	6.1
	434569	Al311295	Hs.58609	ESTs	6.1
	430481	AA479678	Hs.203269	"ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1
50	402859			predicted exon	6.1
	401260			predicted exon	6.1
	406544			predicted exon	6.1
	428446	AI024600 .	Hs.98612	ESTs	6.1
	412246	Al160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]"	6.1
55	400420	AJ277247	Hs.287369	interleukin 22	6.1
	455662	BE065387		*gb:RC1-BT0314-030500-016-d03 BT0314 Homo sapiens	6.1
	428613	AB037749	Hs.186928	KIAA1328 protein	6.1
	443267	AW450630	Hs.133851	ESTs	6.1
	433405	AW157566	Hs.156892	ESTs	6.1
60	416795	A1497778	Hs.168053	"ESTs, Highly similar to AF227948 1 HBV pX associated p	6.1
~	435706	W31254	Hs.7045	GL004 protein	6.1
	450769	AA057418	Hs.33654	ESTs	6.1
		AA398848	Hs.97541		6.1
	427174	AW974499	Hs.192183	ESTs ESTs	6.1
65	425389 416676	H73802	Hs.35381	ESTs	6.1
UJ	416675				
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	6.1 C.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
70	408523	AW833259	11-40111-	"gb:RC2-TT0007-131099-011-c01 TT0007 Homo saplens c	6.0
70	416515	N91716	Hs.194140	ESTs	6.0
	452591	BE173164	Hs.1516	Insulin-like growth factor-binding protein 4	6.0
	437146	AA730977		"gb:nw55f05.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clo	6.0
	450094	Al174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (from clon	6.0
~~	402529			predicted exon	6.0
75	430706	NM_003540	Hs.247816	"H4 histone family, member C"	6.0
	459186	A1908287	•	gb:RC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
	452158	Al699120	Hs.61198	ESTs	6.0
	411237	AW833676		"gb:QV4-TT0008-181199-038-h04 TT0008 Homo sapiens	6.0
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	6.0
80	439398	AA284267	Hs.221504	ESTs	. 6.0
	440862	H39048	Hs.127432	ESTs	6.0
	415451	H19415	Hs.268720	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.0
			110.200120	gb;zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sapi	6.0
	459587	AA031956			6.0
	456072	H54381		gb:yq89a03.s1 Soares fetal liver spleen 1NFLS Homo sapie	0.0

	409954	AW512770	Hs.266457	ESTS	6.0
	443488	A1073495	Hs.133912	"ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
	430825	AI734186	Hs.185105	ESTs	6.0
5	454466	AA984138	Hs.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
J	456506	AA278277	Hs.194212	ESTS	6.0
	449228	AJ403107	Hs.148590	*ESTs, Weakly similar to AF208846 1 BM-004 [H.saplens]	6.0
	457727 442440	AW974687 BE464435	Hs.146180	"gb:EST386776 MAGE resequences, MAGM Horno sapien "ESTs, Weakly similar to non-receptor protein tyrosine kina	6.0 5.9
	455110	BE154505	NS. 140 100	"gb:PM0-HT0343-281299-003-e06 HT0343 Homo sapiens	5.9
10	402790	DC104000		predicted exon	5.9
	409982	BE005839		gb:RC2-BN0120-250400-012-f03 BN0120 Homo sapiens	5.9
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	5.9
	408948	AW296713	Hs.221441	ESTs	5.9
	402046			predicted exon	5.9
15	416438	R89238	Hs.34262	ESTs	5.9
	403083			predicted exon	5.9
	402481			predicted exon	5.9
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52 Homo sap	5.9
20	420362	U79734	Hs.97206	huntinglin interacting protein 1	5.9
20	421375	AA489200	Hs.100595	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
	437630	AI252782	Hs.153029	ESTs	5.9
	443500	AV646388	Hs.137071	ESTs (Control of the control of the	5.9
	448995	A1613276	Hs.5662	"guanine nucleotide binding protein (G protein), beta polyp	5.9
25	438214	H06076 AW812795	Hs.26320 Hs.155381	TRABID protein	5.9 5.9
23	428046 431941	AK000106	Hs.272227	"ESTs, Moderately similar to 138022 hypothetical protein [H "Homo sapiens cDNA FLJ20099 fis, clone COL04544"	5.9
	403356	A1000100	(13.212221	predicted exon	5.9
	439031	AF075079		gb:Homo sapiens full length insert cDNA YQ80A08	5.9
	430032	AW936136	Hs.99610	ESTs	5.9
30	423457	F08208	Hs.155606	paired mesoderm homeo box 1	5.9
•	422158	L10343	Hs.112341	"protease inhibitor 3, skin-derived (SKALP)"	5.9
	406592	2.00.10		predicted exon	5.9
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo sapiens	5.8
	429399	AA452244	Hs.16727	ESTs	5.8
35	408590	AW238162	Hs.253873	ESTs	5.8
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
	417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129			predicted exon	5.8
40	434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
40	402800	A1417C2200	11- 40753	predicted exon	5.8
	436185	AW753380	Hs.49753	"Homo sapiens mRNA for KIAA1561 protein, partial cds"	5.8
	419519 452542	Al198719 AW812256	Hs.176376	ESTs *gb:RC0-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8 5.8
	427166	AA431576	Hs.155658	ESTs	5.8
45	416168	H23687	16.10000	gb:yn72d12.r1 Soares adult brain N2b5HB55Y Homo sapie	5.8
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (from clon	5.8
	421558	AB011125	Hs.105749	KIAA0553 protein	5.8
	458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLAS	5.8
~ ^	418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade 8 (ovalbumi	5.8
50	426544	AA492325		gb:ng81b11.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone	5.8
	433544	Al793211	Hs.165372	*ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
	442007	AA301116	Hs.142838	"Homo sapiens cDNA: FLJ23444 fis, clone HSI01343"	5.8
	443422	R10288	Hs.301529 Hs.266263	ESTS	5.8
55	434311 424966	BE543469 AU077312	Hs.153985	"Homo sapiens cDNA FLJ14115 fis, clone MAMMA10017 "solute carrier family 7 (cationic amino acid transporter, y+	5.8 5.8
55	441744	AA960922	Hs.200938	ESTs	5.8
	413101	BE065215	110.200000	"gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapiens c	5.7
	445687	W80382	Hs.149297	ESTs	5.7
	441369	AA931535		gb:oo56a04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clon	5.7
60	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
	431211	M86849	Hs.5566	"gap junction protein, beta 2, 26kD (connexin 26)"	5.7
	411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.7
	448612	Al696363	Hs.171285	ESTs	5.7
65	419118	AA234223	Hs.139204	ESTs	5.7
03	406322	4141074000		predicted excn	5.7
	454690	AW854639	11- 24000	"gb:MR1-CT0258-140100-203-d10 CT0258 Homo sapiens hypothetical protein FLJ10826	5.7
	450313	AI038989 AA179233	Hs.24809 Hs.42390	nasopharyngeal carcinoma susceptibility protein	5.7 5.7
	416292 449309	AW589823	Hs.224189	ESTs	5.7 5.7
70	408418	AW963897	Hs.44743	KIAA1435 protein	5.7
	416100	H18700	Hs.268799	ESTs	5.7
	437845	AA769578	Hs.90488	ESTs	5.7
	443345	A1052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
26	418407	AL044818	Hs.84928	"nuclear transcription factor Y, beta"	5.7
75	434557	AW855466	Hs.271866	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
	431688	AA513906		"gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clo	5.7
	437641	AA811452	Hs.291911	ESTs	5.7
	409319	AW752736	Hs.33565	ESTs	5.7
80	403967	AF030107	Hs.17165	regulator of G-protein signalling 13	5.7
30	445189	Al936450	Hs.147482 Hs.154188	ESTs ESTs	5.7 5.7
	414418 446563	H62943 BE326588	Hs.141454	ESTS	5.7 5.7
	446075	AW451457	Hs.279179	ESTs	5.7
	428068	AW016437	Hs.233462	ESTs	5.7
				•	

	438425	AW292922	Hs.293170	ESTs	5.7
	415532	R14780	Hs.12826	ESTs	5.7
	441442	AL043282	Hs.131824	ESTs	5.7
	443380	A1792478	Hs.135377	ESTs	5.7
5	445527	W39694	Hs.83286	ESTs	5.7
	414376	BE393856	Hs.66915	"ESTs, Weakly similar to 16.7Kd protein [H.sapiens]"	5.7
	457960	AA771881	Hs.298149	ESTs	5.6
	453293	AA382267	Hs.10653	ESTs	5.6
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	5.6
10	405227			predicted exon	5.6
	442257	AW503831		gb:UI-HF-BN0-alb-b-05-0-UI.r1 NIH_MGC_50 Homo sap	5.6
	403403			predicted exon	5.6
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6
	438656	H85310	Hs.209456	"ESTs, Weakly similar to NG22 [H.sapiens]"	· 5.6
15	419936	Al792788		*gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clo	5.6
	437267	AW511443	Hs.258110	ESTs	5.6
	430563	AA481269	Hs.178381	ESTs	5.6
	444835	Al198994	Hs.158479	ESTs	5.6
	444902	AJ132099	Hs.12114	vanin 1	5.6
20	451800	AW977435	Hs.31890	ESTs	5.6
	405465			predicted exon	5.6
	403891			predicted exon	5.6
	425557	A1694300	Hs.46730	ESTs	5.6
~-	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	5.6
25	450152	A1138635	Hs.22968	ESTs	5.6
	410053	AW579707	Hs.59332	ESTs	5.6
	421285	NM_000102	Hs.1363	"cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
	425264	AA353953	Hs.20369	"ESTs, Weakly similar to gonadotropin inducible transcript	5.6
20	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	5.6
30	429616	A1982722	Hs.120845	ESTs	5.6
	423528	AB011137	Hs.129740	KIAA0565 gene product	5.6
	403089		.1. 75050	predicted exon	5.6
	414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal	5.6
25	403687	1105500	11-04404	predicted exon	5.6
35	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.5
	432501	BE546532	Hs.287329	Fas binding protein 1	5.5 5.5
	403691	BE296182		predicted exon	5.5 5.5
	409545	AI015862	Hs.131793	*gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA clon ESTs	5.5 5.5
40	435990 444409	Al792140	Hs.49265	ESTs	5.5
70	435478	AA682622	113.43203	gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	5.5
	439981	Al348408	Hs.124675	"ESTs, Weakly similar to unnamed protein product (H.saple	5.5
	433644	AW342028	Hs.256112	ESTs	5.5
	441541	AA938663	Hs.199828	ESTs	5.5
45	400709	7 0 1000000	110.100020	predicted exon	5.5
	407615	AW753085		gb:PM1-CT0247-151299-005-a03 CT0247 Homo sapiens	5.5
	424153	AA451737	Hs.141496	MAGE-like 2	5.5
	452465	AA610211	Hs.34244	ESTs	5.5
	406030			predicted exon	5.5
50	431071	AA491379		"gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA cl	5.5
	418086	AA211791	Hs.269666	"Homo sapiens cDNA FLJ13415 fis, clone PLACE1001799	5.5
	453034	BE246010	Hs.184109	ribosomal protein L37a	5.5
	412953	Z45794	Hs.238809	ESTs	5.5
<i></i>	425351	Al206234	Hs.155924		. 5.5
55	406149			predicted exon	5.5
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	5.5
	458378	A1040535	Hs.150524	ESTs	5.5
	401213			predicted exon predicted exon	5.5 5.5
60	405904 445132	744014			· 5.5
UU	445132 405138	Z44811		gb:HSC29G031 normalized infant brain cDNA Homo saple predicted exon	5.5 5.5
	442238	AW135374	Hs.270949	ESTs .	5.5 5.5
	416852	AF283776	Hs.80285	Homo saplens mRNA; cDNA DKFZp586C1723 (from clon	_ 5.5
	448691	AA481119	Hs.283558	hypothetical protein PRO1855	5.5
65	452242	R50956	Hs.59503	*ESTs, Weakly similar to AF157318 1 AD-017 protein [H.s	5.5
	456994	AA383623	Hs.293616	ESTs	5.5
	440913	Al267491	Hs.160593	ESTs	5.5
	435380	AA679001	Hs.192221	ESTs	5.5
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
70	414035	Y00630	Hs.75716	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.4
	459084	H01699	Hs.27289	CGI-125 protein	5.4
	405867			predicted exon	5.4
	414093	BE544867		gb:601078872F1 NiH_MGC_12 Homo sapiens cDNA clon	5.4
76	447306	Al373163	Hs.170333	ESTs	5.4
75	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapiens	5.4
	404828			predicted exon	5.4
	402543			predicted exon	5.4
	421988	AW450481	Hs.161333	ESTs	5.4
90	413404	BE503463	Hs.297431	ESTs	5.4
80	459043	Al806444	Hs.208113	"ESTs, Weakly similar to N-WASP [H.sapiens]"	5.4
	404410	A A 470C40		predicted exon	5.4 5.4
	430264	AA470519	Un DEOCCE	"gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clon	5.4 5.4
	431499	NM_001514 AW962574	Hs.258561	general transcription factor IIB "gb:EST374647 MAGE resequences, MAGG Homo sapten	5.4
	412566	PICSOFF		30-50-10-10-1 MNOC reservations, MNOG House Sahier	J.4

	454239	BE176420	Hs.8177	ESTs	5.4
	458163	AA884304	Hs.131163	ESTs	5.4
	446205	AW172662	Hs.149479	ESTs	5.4
_	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo sapien	5.4
5	415579	AA165232	Hs.222069	ESTs	5.4
	423200	AA323073	Hs.289083	ESTs	5.4
	440052	AI633744	Hs.195648	ESTs	5.4
	424717	H03754	Hs.152213	"wingless-type MMTV integration site family, member 5A"	5.4
	420111	AA255652	•	gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA do	5.4
10	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	5.4
	414904	AA157881	Hs.143056	ESTs	5.4
	409479	BE163800	Hs.136912	ESTs	5.4
	404727	00.00000		predicted exon	5.4
	446011	AI623778	Hs.145809	ESTs	5.4
15	456083	U46922	Hs.77252	fragile histidine triad gene	5.4
10	424834	AK001432	Hs.153408	*Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	5.4
					5.4
	425071	NM_013989	Hs.154424	"deiodinase, iodothyronine, type II"	5.4 5.4
	426065	N32049	II- 405575	gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W	
20	415602	F12920	Hs.165575	ESTs	5.4
20	432839	AA579465	Hs.287332	ESTs	5.4
	416879	H98899	Hs.42599	ESTs	5.4
	456088	BE177320	Hs.156148	"Homo sapiens cDNA: FLJ23082 fis, clone LNG06451"	5.4
	423175	W27595	Hs.18653	ESTs	5.4
25	424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	5.3
25	452281	T93500	Hs.28792	"Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405	5.3
	424323	AA338791	Hs.146763	nascent-polypeptide-associated complex alpha polypeptide	5.3
	426701	Al968103	Hs.209461	"Homo saplens cDNA FLJ 12836 fis, clone NT2RP2003206	5.3
	447645	AW897321	Hs.159699	ESTs	5.3
20	402974			predicted exon	5.3
30	436607	AW661783	Hs.211061	ESTs	5.3
	428873	AI701609	Hs.98908	ESTs	5.3
	405454			predicted exon	5.3
	431867	AA523660	Hs.191727	ESTs	5.3
	442768	AL048534	Hs.48458	*ESTs, Wealdy similar to ALU8_HUMAN ALU SUBFAM	5.3
35	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	5.3
	435098	AF174394	Hs.177461	*Homo sapiens apoptotic-related protein PCAR mRNA, par	5.3
	421284	U62435	Hs.103128	"cholinergic receptor, nicotinic, alpha polypeptide 6"	5.3
	435711	AF226667	Hs.58553	CTP synthase II	5.3
	405292	/ W	. 10.00000	predicted exon	5.3
40	410123	T16981	Hs.21963	ESTs	5.3
. •	435435	T89473	Hs.192328	ESTs	5.3
	417071	N58820	Hs.275133	ESTs	5.3
	438958	H50167	Hs.33113	ESTs	5.3
	457405	AA504860	115.55115	gb:ab03a10.s1 Stratagene fetal retina 937202 Homo sapiens	5.3
45				gb:PM1-HT0345-121199-001-c08 HT0345 Homo sapiens	5.3
43	413642	BE154837		gb:ng38g06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clo	5.3
	433868	AA612960	Un 25070	ESTs	5.3
	444461	R53734	Hs.25978		5.3
	427088	AA398085	Hs.142390 Hs.211516	ESTs ESTs	5.3
50	451307	AW293207	ns.211010		5.3
50	403831			predicted exon	5.3
	402892	41074000	11 000004	predicted exon	5.3 5.3
	433420	A1674093	Hs.293961	ESTS	
	455759	BE080469	11 40004	gb:QV1-BT0630-280200-086-d06 BT0630 Homo sapiens	5.3 5.3
55	411379	AI816344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	
22	428483	AI908539	Hs.184592	KIAA0344 gene product	5.3
	429208	AA447990	Hs.190478	ESTs	5.3
	447572	A1631546	Hs.159732	ESTs	5.3
	434896	AW022054	Hs.136591	ESTs	5.3
60	417616	R07728	Hs.268668	ESTS	5.3
OU	411805	AW864183		"gb:PM0-SN0014-260400-002-d02 SN0014 Homo saplens	5.3
	419000	179855	Hs.268592	ESTs	5.3
	413488	BE144017	Hs.184693	"transcription elongation factor B (SIII), polypeptide 1 (15k	5.3
	400975			predicted exon	5.3
C =	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy chain (5.3
65	430757	A1458623		"gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clo	5.3
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide 8"	5.2
	401877	AB011094	Hs.129892	KIAA0522 protein	5.2
	457122	AI026157	Hs.33728	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.2
~	410706	A1732404	Hs.68846	ESTs	5.2
70	435807	A1033299	Hs.113614	ESTs	5.2
	428398	AI249368	Hs.98558	ESTs	5.2
	401088			predicted exon	5.2
	414501	N43991	Hs.171984	ESTs	5.2
-	419083	A1479560	Hs.98613	*Homo sapiens cDNA FLJ12292 fis, clone MAMMA10018	5.2
75	421107	AA283822	Hs.55606	*ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER P	5.2
	411489	AW848346		"gb:IL3-CT0214-150200-076-F03 CT0214 Homo sapiens c	5.2
	419249	X14767	Hs.89768	"gamma-aminobutyric acid (GABA) A receptor, beta 1"	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	5.2
80	451686	AA059246	Hs.110293	ESTs	5.2
	453867	Al929383	Hs.108196	HSPC037 protein	5.2
	419985	H66373	Hs.15973	"ESTs, Highly similar to bA393J16.3 [H.sapiens]"	5.2
	426650	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5' end, mRNA	5.2
	424115	AA335497	Hs.293965	ESTs	5.2

	105570			and the desire	
	405576	4.4070040		predicted exon	5.2
	409584	AA076010	11 470000	gb:zm89f12.s1 Stratagene ovarian cancer (937219) Homo sa	5.2
	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	5.2
5	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.2
)	439155	H81076	Hs.269001	ESTs	5.2
	432267	AK000872	Hs.274227	"Homo sapiens cDNA FLJ10010 fis, clone HEMBA100030	5.2
	459024	AA020799	Hs.179825	RAN binding protein 2-like 1	5.2
	404088			predicted exon	5.2
10	403525	41040747	11- 005455	predicted exon	5.2
10	445882	AI948717	Hs.225155	*ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATE	5.2
	448257	AW772070	Hs.253146	ESTs	5.2
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                             1242238_1
                                                AW846080 AW845074 AW846118 AW846130
AW847647 AW847659 AW847656 AW847653 AW847717 AW847786
BE073250 BE073378 BE073379 AW850533 AW850529
             454934
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                             1246752_1
1248899_1
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                             1252971_1
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                                                 BE152428 AW855572 AW855607
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                             1253955_1
                             1254339.1
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                             1255227_1
                                                 AW858621 AW937120
             455152
                             1259973_1
                                                 AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
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                                                AW977806 AW887923 AW886321
AW939445 AW939465 AW939604 AW939531 AW939530 AW939993
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                                                AW945954 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036
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                             1335196_1
1348141_1
1349206_1
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BE064059 BE063903 BE063838 BE063863 BE064056 BE063974 BE063904 BE063898 BE063896 BE063906 BE063980
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455640
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             455662
                                                 BE065387 BE065310 BE065391
                                                BE069891 BE158893 BE069898 BE158900
BE080469 BE080474 BE080477 BE080546 BE080545
BE146879 BE146914 BE146918
             455713
                             1352512_1
                             1359316_1
1375451_1
             455759
             455851
55
                                                BE147225 BE147205 BE147234
BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
BE179085 BE179084 BE179086 BE179264
             455853
                             1375671_1
             455879
                             1380017_1
1398665_1
             455993
                             1470256_1
                                                 H54381 H54463 BE393262
             456072
                                                H35431 H35463 BE393262

AA159478 AW901089 AA160437 AW593155

N51636 T51874 T51829

AA225423 AA225369 BE144153 AW801549

AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794
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                             177026_1
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457620
                                                 AA504860 AA504911
AA602711 BE078290
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                                                 AW974687 AA649656 AA652145
                                                 AW975133 AA729943 AA805813
AW816379 AA888282 AA879046 AA879195
AL157625 N72696 BE622492
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             458154
                             491768_1
                             75803_1
773443_1
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             458829
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                                                 W28965 W28971
AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
             458841
                             784186_1
                             920051_1
920646_1
             459160
             459170
                                                 Al908287 BE064074 BE068820 BE068823 BE068822 BE068826
             459186
                             922888_1
75
             TABLE 1C:
```

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

80 Strand: Indicates DNA strand from which exons were predicted Nt_position: Indicates nucleotide positions of predicted exons

				•
	Pkey	Dof	Classed	Nt_position
		Ref	Strand	
	400584	9887612	Minus	18398-18573
	400593	9887642	Minus	25013-25127 _ -
_	400612	9929646	Minus	151513-151662
5	400613	9864507	Pius	92278-92472
_	400623	7228177	Plus	74195-74335,74653-74827
	400709	7249204	Plus	153075-154680
	400749	7331445	Minus	9162-9293
10	400842	1927148	Plus	90462-90673
10	400925	7651921	Plus	38183-38391,43900-44086
	400964	7139719	Minus	155282-155403
	400968	7923967	Plus	19938-20043
	400975	7139779	Minus	108473-108847
	400983		Plus	
15		8081198		107903-108832
15	401032	8117525	Minus	68451-68555
	401050	8117628	Minus	78449-79425
	401088	8492704	Plus	194659-195179
	401129	8699792	Minus	62022-62242,62326-62451,62543-62710,63072-63167
	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
20	401213	9858408	Plus	
20				98243-98380,98489-98619
	401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
	401245	4827300	Minus	59373-59531
	401260	8076883	Minus	86008-86355
	401269	8954206	Plus	2259-2591 `
25	401283	9800093	Minus	47256-47456 _~
	401497	7381770	Plus	92607-92813
	401508	7534110	Minus	110779-110983
	401521	7705251	Plus	9127-9234
20	401530	7770649	Plus	41468-42406
30	401575	7229804	Minus	76253-76364
	401604	7689963	Minus	119835-120185
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401793	7263888	Minus	102945-103083
35				
33	401809	7342191	Minus	107548-108298
	401862	7770606	Minus	55839-55993,59145-59293
	401881	8122429	Minus	148470-148651,153418-153618,154282-154438
	402018	7528100	Plus	168728-168859
	402046	8072415	Plus	166394-166556,168167-168395
40	402050	8076908	Minus	130105-130227
	402071	8117361	Plus	85924-86039
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402131	7704961	Minus	33114-33209,33496-33678
4.5	402203	8576119	Minus	8124-8285
45	402222	9958106	Plus	3261-3834,3939-4269
	402296	6598824	Plus	22587-23723
	402298	6598824	Plus	36758-37953
	402421	9796341	Minus	46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924
	402425	9796347	Minus	50224-50395
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50	402481	9797406	Plus	87891-88991
	402529	7630937	Minus	165-917
	402543	9838066	Minus	89684-90893
	402576	7230225	Minus	1867-2247
	402578	9884928	Plus	66350-66498
55	402628	9931216	Plus	31753-31966
-	402631	9931231	Minus	115658-116580 ·
	402639	9958129	Minus	
				20167-22383
	402664	8077024	Plus	70318-70846
60	402709	8901246	Minus	56847-57055
60	402738	7331557	Minus	8725-8859
	402745	9212200	Minus	76516-76690
	402790	4835258	Minus	147744-147861
	402794	6136940	Minus	131034-131794
	402800	6010175	Plus	43921-44049,46181-46273
65	402859	9588237	Minus	69821-75323
••	402892	8086844	Minus	194384-194645
	402974	9663349	Plus	124035-124321
	403041	3171152	Plus	70527-71019
70	403065	8954197	Minus	71615-71773,73930-74144
70	403083	8954241	Plus	163070-163351
	403089	8954241	Plus	171964-172239
	403093	8954241	Plus	177083-177373,177464-177751
	403177	9838213	Minus	142560-142726
	403273	8018055	Plus	133809-134099
75				
13	403334	8568877 .	Minus	137205-137350
	403350	8569775	Minus	135374-135523
	403356	8569930	Plus	92839-93036
	403403	9438460	Plus	21240-21399
	403525	7960440	Plus	152431-153243
80	403568	8101145	Minus	85509-85658
	403647	8699843	Minus	35849-36204
	403687	7387384	Plus	9009-9534
	403691	7387384	Minus	88280-88463
	403698	4263532	Plus	.10464-10907

	403741	7630932	Minus	2833-3468
	403747	7658395	Minus	20493-20621
	403786	8083636	Minus	73028-73217
5	403831 403891	7249249	Minus	61468-61575 191508-193220
,	403091	7331467 7711864	Minus Minus	129213-129415
	403963	8568150	Plus	149466-149665
	404070	2996642	Plus	7210-7414,10043-10195
	404088	9958257	Plus	184131-184295
10	404097	7770701	Plus	55512-55781
	404166	7596822	Plus	86147-86509
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
	404340	7630856	Plus	10898-11506
15	404410	7342122	Plus	49052-49176,56177-56273,59384-59488
15	404599	8705107	Plus	110443-110733
	404638	9796751	Minus Minus	99433-99528,100035-100161 104257-105215
	404664 404727	9797142 8081050	Plus	115534-115747
	404767	7882827	Minus	23244-23759
20	404828	6580415	Minus	26291-27253
	404849	7706886	Plus	144843-144964,149846-150121
	404893	6850447	Plus	65083-65223
	404898	7331420	Minus	177015-177328
0.5	404952	7382669	Minus	136326-136618
25	404972	3213020	Plus	48711-49524.,
	404992	4662677	Minus	106104-106199,111659-111781
	405071	7708797	Minus Plus	11115-11552 90303-90516
	405138 405196	8576241 7230083	Minus	135716-135851
30	405227	6731245	Minus	22550-22802
50	405277	3980473	Pius	23471-23572
	405285	6139075	Minus	55744-55903,57080-57170,61478-61560
	405292	3845420	Plus	33227-33442
25	405336	6094635	Plus	33267-33563
35	405362	2337862	Minus	105008-105142,105980-106091,140445-140556,142519-142641
	405382	6552767	Plus	31923-32311
	405454 405465	7656675 7767904	Plus Plus	133807-134053 8935-9073,12242-12367,13364-13506,14965-15493
	405465	8439781	Plus	106297-106447,108462-108596
40	405547	1054740	Plus	124361-124520,124914-125050
	405576	4003382	Plus	84000-85009
	405621	5523811	Plus	59362-59607
	405636	5123990	Plus	56384-56587
15	405675	4557087	Plus	70304-70630
45	405708	4156182	Plus	55030-55604
	405771 405783	7018349 5738434	Plus Minus	91191-91254,91510-91589 27238-27885
	405783	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
50	405810	4938307	Minus	64543-64966
	405848	7651809	Minus	28135-28244
	405851	6164995	Minus	26407-27151
	405867	6758731	Minus	74553-75173
.55	405896	6758795	Plus	57311-57874 16375 16594
.55	405904 405917	7705118 7712162	Minus Minus	16375-16584 106829-107213
	405982	8247790	Minus	36028-36408
	406030	8312328	Minus	96123-96547
	406053	6758997	Plus	30921-31532
60	406057	6691254	Minus	20830-21222
	406149	7144791	Minus	44464-45164
	406163	7158901	Plus	66690-66835
	406277	5686030	Minus	4759-5490
65	406322	9212102	Minus	130230-130418 21251-21526
05	406349	9256007 7711360	Minus Minus	21251-21526 107068-107277
	406504 406544	7711508	Plus	46576-46757
	406589	8224211	Plus	38806-38989
	406592	4567182	Plus	352560-352963
70				

TABLE 2A lists about 187 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., ig, fn3, egf, 7tm domains).

TABLE 2A: ABOUT 187 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains
ratio: tumor vs. normal tissues

80

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	Pkey	Ex. Acon No.	UGID	Title	PFAM domain	ratio
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase Inhibito	serpin	63.6
•	431938	AA938471	Hs.115242	developmentally regulated GTP-bindi	SCP	32.0
5	425650 418994	NM_001944	Hs.1925 Hs.89546	desmoglein 3 (pemphigus vulgaris ant	cadherin EGF;lectin_c;sushi	30.0 24.5
<i>J</i>	410554	AA296520 AW130413	rts.09540	selectin E (endothelial adhesion molec gb:xf50f04.x1 NCI_CGAP_Gas4 Hom	alpha-amylase	15.8
	418092	R45154	Hs.106604	ESTs	pkinase;Activin_recp	15.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	Cys_knot	12.6
10	422330	D30783	Hs.115263	epiregulin	EGF	12.5
10	446745 416319	AW118189 Al815601	Hs.156400 Hs.79197	ESTs CD83 antigen (activated B lymphocyt	vwa ig	11.1 10.8
	432408	N39127	Hs.76391	myxovirus (influenza) resistance 1, ho	ion_trans;K_tetra	10.6
	405285			predicted exon	A2M;A2M_N	10.5
15	405636			predicted exon	EGF;ldl_recept_a;ldl_recept_b	9.8
15	403093 446740	AI611635	Hs.192605	predicted exon ESTs	fn3 Rydr_itpr	9.6 9.2
	405547	A1011033	113.132003	predicted exon	ABC_tran;ABC_membrane	8.5
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT	7tm_1	8.4
20	404270			predicted exon	SCP	8.1
20	402745 452755	AW138937	Hs.213436	predicted exon ESTs	EGF;ldl_recept_b;thyroglobulin_1 cystatin	8.1 8.0
	421459	Al821539	Hs.97249	ESTs	disintegrin;Reprolysin	7.9
	416151	T26661		gb:AB65C7R Infant brain, LLNL arra	laminin_G;EGF	7.8
25	446232	Al281848	Hs.165547	ESTs	7tm_3 _	7.6
25	431009 424634	BE149762	Hs.248213 Hs.151407	gap junction protein, beta 6 (connexin cartilage intermediate layer protein, n	connexin	7.2 7.1
	400749	NM_003613	FIS. 15 1407	predicted exon	lg;lsp_1 fn3;ldl_recept_a;ldl_recept_b	6.8
	419054	N40340	Hs.191510	ESTs, Weakly similar to ORF2 [M.m	lg;SPRY	6.8
20	459170	Al905518		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran;ABC_membrane	6.6
30	416441 410664	BE407197	Hs.65370	gb:601301552F1 NIH_MGC_21 Hom	SDF Ribosomal_L22	6.4 6.4
	402425	NM_006033	rs.03370	lipase, endothelial predicted exon	ion_trans	6.3
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_H	Ephrin	6.0
25	403083			predicted exon	fn3_	5.9
35	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G	SDF	5.9
	418345 424966	AJ001696 AU077312	Hs.241407 Hs.153985	serine (or cysteine) proteinase inhibito solute carrier family 7 (cationic amino	serpin aa_permeases	5.8 5.8
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (co	connexin	5.7
40	430563	AA481269	Hs.178381	ESTs	ABC_tran;ABC_membrane	5.6
40	450152 418844	Al138635 M62982	Hs.22968 Hs.1200	ESTs	łg;pkinase lipoxygenase;PLAT	5.6 5.6
	403089	M02302	FIS. 1200	arachidonate 12-lipoxygenase predicted exon	fn3	5.6
	403687			predicted exon	tsp_1;Reprolysin	5.6
45	403691			predicted exon	tsp_1;Reprolysin	5.5
43	414035 421284	Y00630 U62435	Hs.75716 Hs.103128	serine (or cysteine) proteinase inhibito cholinergic receptor, nicotinic, alpha p	serpin neur_chan	5.4 5.3
	435435	T89473	Hs.192328	ESTs	lipase;PLAT	5.3
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUM	lipoxygenase;PLAT	5.2
50	419249 425698	X14767	Hs.89768 Hs.159241	gamma-aminobutyric acid (GABA) A	neur_chan ·	5.2 5.2
50	431117	NM_016112 AF003522	Hs.250500	polycystic kidney disease 2-like 1 delta (Drosophila)-like 1	ion_trans EGF;DSL	5.2 5.1
	457948	Al498640	Hs.159354	ESTs	G-alpha;arf	5.1
	435174	AA687378	Hs.194624	ESTs	SPRY	5.0
55	408170 434351	AW204516 AW974991	Hs.31835 Hs.191852	ESTs ESTs, Weakly similar to ALU1_HUM	arf;ras arf;ras	5.0 4.9
55	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	7tm_1	4.8
	422597	BE245909		. ATP-binding cassette, sub-family B (M	ABC_tran;ABC_membrane	4.8
	405545	4100440	11- 470000	- predicted exon	ABC_tran;ABC_membrane	4.8
60	426471 409632	M22440 W74001	Hs.170009 Hs.55279	transforming growth factor, alpha serine (or cysteine) proteinase inhibito	EGF semin	4.7 4.7
00	420206	M91463	Hs.95958	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	Kunitz_BPTI;G-gamma	4.6
	424402	M63108	Hs.1769	luteinizing hormone/choriogonadotrop	7tm_1	4.5
65	436480 430226	AJ271643 BE245562	Hs.87469 Hs.2551	putative acid-sensing ion channel adrenergic, beta-2-, receptor, surface	ASC 7tm_1	4.5 4.4
05	436126	AW449757	Hs.163036	ESTs	SNF	4.4
	406812	AF000575	Hs.67846	feukocyte immunoglobulin-like recep	ig	4.4
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (TIMP	4.3
70	449184 410555	AW296295 U92649	Hs.196491 Hs.64311	ESTs a disintegrin and metalloproteinase do	TNFR_c6 disintegrin;Reprotysin	4.3 4.3
70	422389	AF240635	Hs.115897	protocadherin 12	cadhein	4.3
	405281			predicted exon	A2M;A2M_N	4.3
	413548	BE147555	Hs.288541	Homo sapiens mRNA for KIAA1558	EGF;ldi_recept_a;ldi_recept_b	4.3
75	449535 425864	W15267 U56420	Hs.23672 Hs.159903	low density lipoprotein receptor-relate olfactory receptor, family 5, subfamily	kdl_recept_a;EGF;kdl_recept_b 7tm_1	4.3 4.3
. •	410611	AW954134	Hs.20924	KIAA 1628 protein	Peptidase_S9	4.2
	430686	NM_001942	Hs.2633	desmoglein 1	cadherin;Cadherin_C_term	4.1
	418693	A1750878	Hs.87409	thrombospondin 1	vwc;TSPN	4.0
80	445924 457148	A1264671 AF091035	Hs.164166 Hs.184627	ESTs KIAA0118 protein	sugar_tr arf;ras	3.9 3.9
	428568	AC004755	Hs.184922	one cut domain, family member 3	E1-E2_ATPase	3.9
	412170	D16532	Hs.73729	very low density lipoprotein receptor	EGF;ldl_recept_a;ldl_recept_b	3.8
	442566	R37337	Hs.12111	ESTs	ank;death;RHD;TIG 7tm_1	3.8 3.8
	403763			•	יווני	3.0

	403074	DE4-6044		predicted exon	fn3	3.8
	413605	BE152644	Ll= 004000	gb:CM1-HT0329-250200-128-f09 HT	alpha-amylase	3.8 3.7
	442295 403661	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, c predicted exon	Collagen;COLFI 7tm_3;ANF_receptor	3.7 3.7
5	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Hom	pkinase;Sema;Plexin_repeat;TIG	3.7
•	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocortic	7tm_1	3.7
	431176	AI026984	Hs.293662	ESTs	laminin_EGF;laminin_B	3.6
	436233	AI742878	Hs.124116	ESTs	lg	3.6
• •	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived g	EGF	3.6
10	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	zf-C2H2	3.6
	400380	NM_018485	Hs.283079	G protein-coupled receptor C5L2	7tm_1	3.6
	453893	NM_000835	Hs.36451	glutamate receptor, ionotropic, N-met	lig_chan	3.5 3.5
	409402 421166	AF208234 AA305407	Hs.695 Hs.102308	cystatin B (stefin B) potassium inwardly-rectifying channe	cystalin IRK	3.5 3.5
15	445575	Z25368	Hs.172004	filin	fn3	3.5
13	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway p	tsp_1;vwc;IGFBP	3.5
	403909	NM_016255	Hs.95260	Homo sapiens mRNA; cDNA DKFZp	Na_H_Exchanger	3.5
	403077			predicted exon	fn3	3.5
	455612	BE042896	Hs.274848	ESTs	ABC_tran;ABC_membrane	3.5
20	424091	AF235097	Hs.139263	calcium channel, voltage-dependent, a	ion_trans	3.5
	403956	W28077	Hs.79389	nel (chicken)-like 2	cadherin;Cadherin_C_term	3.4
	457470	AB040973	Hs.272385	G protein-coupled receptor 72	7tm_1	3.4 3.4
	401522 404886	N47812	Hs.81360	CGI-35 protein predicted exon	disintegrin;Reprolysin ion_trans	3.4
25	437692	AA176959	Hs.172004	titin	fn3	3.4
	407944	R34008	Hs.239727	desmocollin 2	cadherin	3.4
	407393	AB038237		gb:Homo sapiens mRNA for G protei	7tm_1	3.3
	436936	AL134451	Hs.197478	ESTs	EGF;laminin_G	3.3
••	423309	BE006775	Hs.126782	sushi-repeat protein	sushi;HYR	3.3
30	402172			predicted exon	ig .	3.3
	447420	AI378628	U- 20026	gb:tc72g07.x1 Soares_NhHMPu_S1 H	ank;pkinase;death	3.3 3.3
	438901 424362	AF085834 AL137646	Hs.29036 Hs.146001	ESTS	sushi trypsin;sushi;CUB	3.3
	430453	BE387060	Hs.3903	Homo sapiens mRNA; cDNA DKFZp Cdc42 effector protein 4; binder of Rh	fn3	3.3
35	416631	H69466	113.0300	gb:yr88f07.r1 Soares fetal liver spleen	kdl_recept_a;MACPF	3.3
-	453174	AI633529	Hs.135238	ESTs	7tm_1	3.3
	433848	AF095719	Hs.93764	carboxypeptidase A3	Zr_carbOpept;Propep_M14	3.2
	408546	W49512	Hs.46348	bradykinin receptor B1	7tm_1	3.2
40	423573	AA328504		gb:EST31993 Embryo, 12 week I Hom	7tm_1	3.2
40	458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5	7tm_3;ANF_receptor	3.2
	433430	AI863735	Hs.186755	ESTs EST	thyroglobulin_1;IGFBP ank;pkinase;death	3.2 3.2
	438850 420783	R33727 Al659838	Hs.24688 Hs.99923	lectin, galactoside-binding, soluble, 7	Gal-bind_lectin	3.2
	409968	U56102	Hs.57699	adhesion glycoprotein	ig	3.1
45	430630	AW269920	Hs.2621	cystatin A (stefin A)	7tm_3;ANF_receptor	3.1
• •	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfa	TNF	3.1
	422279	H69644	Hs.114231	C-type lectin-like receptor-2	tectin_c	3.1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromely	hemopexin;Peptidase_M10	3.1
50	412597	AU077051	Hs.74561	alpha-2-macroglobulin	A2M;A2M_N	3.1 3.1
30	453420	AJ003459		gb:AJ003459 Selected chromosome 2	!RK zf-C3HC4;SPRY;zf-B_box	3.1
	404243 449987	AW079749	Hs.184719	predicted exon ESTs, Weakly similar to AF116721 1	ABC_tran;ABC_membrane	3.1
	422471	AA311027	Hs.271894	ESTs	lg	3.0
	400464			predicted exon	Peptidase_S9	3.0
55	458713	BE044496	Hs.282707	ESTs	EGF	3.0
	421340	F07783	Hs.1369	decay accelerating factor for complem	sushi	3.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7tm_1	3.0
	400704	41.000.450	11- 40040	predicted exon	lig_chan;ANF_receptor E1-E2_ATPase;Hydrolase	3.0 3.0
60	416239 433664	AL038450 AW292176	Hs.48948 Hs.245834	ESTs ESTs	Ricin_B_lectin	3.0
UU	423994	X01057	Hs.1724	interleukin 2 receptor, alpha	mi Tani Doggi	2.9
	447726	AL137638	Hs.19368	Homo sapiens mRNA; cDNA DKFZp	wa	2.9
	425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat 2 (FA	EGF;cadherin;laminin_G	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglut_core;Transglutamin_N	2.9
65	401537			predicted exon	ig;pkinase;LRRNT;LRRCT	2.9
	405790	1140400	11- 440400	predicted exon	Sema;Plexin_repeat;TIG	2.9
	422669 430793	H12402	Hs.119122 Hs.247940	ribosomal protein L13a 5-hydroxytryptamine (serotonin) recep	arf;ras;Ribosomal_S17 7tm_1	2.9 2.9
	403411	M83181	(13.247 340	predicted exon	ABC_tran;ABC_membrane	2.8
70	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide ep	Transglutamin_N;Transglut_core	2.8
, •	414482	S57498	Hs.76252	endothelin receptor type A	7tm_1	2.8
	427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	COX68	2.8
	404187		:	predicted exon	ig .	2.8
75	443537	D13305	Hs.203	cholecystokinin B receptor	7tm_1	2.8
75	428701	NM_013276	Hs.190207	carbohydrate kinase-like	vwa;integrin_A;P2X_receptor	2.7
	411213	AA676939	Hs.69285	neuropilin 1	CUB;MAM;F5_F8_type_C	2.7 2.7
	453999 401244	BE328153	Hs.240087	ESTs predicted exon	kazal vwa;vwd;TIL	2.7
	401244 458930	NM_003612	Hs.24640	sema domain, Immunoglobulin domai	Sema	2.7
80	434411	AA632649	Hs.201372	ESTs .	sushi	2.7
	400421	AF263537	Hs.287370	fibroblast growth factor 23	FGF ·	2.7
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	2.7
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosoma	ion_trans	2.6
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	pkinase;ig	2.6

					•	
	401657			predicted exon	7tm_1	2.6
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2	sushi;trypsin;CUB	2.6
	432042	AW971345	Hs.292715		sugar_tr	2.6 ·
						2.6
5	433138	AB029496	Hs.59729	semaphorin sem2	ig;Sema ABC_tran;ABC_membrane	2.6
,	452530	Al905518	11- 400000	gb:RC-BT091-210199-098 BT091 Ho		2.6
	426418	M90464	Hs.169825		Collagen;C4	2.6
	403796			predicted exon	cadherin	
	431728	NM_007351	Hs.268107		EGF;C1q	2.6
10	441595	AW206035	Hs.192123		sugar_tr	2.6
10	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	EGF;MAM	2.6
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2H	SDF	2.5
	428765	X54150	Hs.193122		ig	2.5
	450245	AA007536	· Hs.271767		ig	2.5
1.5	416429	H54658	Hs.268942		E1-E2_ATPase;Hydrolase	2.5
15	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneurona	sugar_tr	2.5
	433182	AB039920	Hs.127821		ion_trans	2.5
	403092			predicted exon	fn3	2.5
	406850	AI624300	Hs.172928		vwc;Collagen;COLFI	2.5
	438698	AW297855	Hs.125815		lipoxygenase;PLAT	2.5 .
20	456815	NM_013348	Hs.144011	potassium inwardly-rectifying channe	IRK	2.5
				·	•	
	TABLE 2B:					
	Pkey: Unio	ue Eos probese	t identifier nur	nber		
		er: Gene cluster		•		
25	Accession:	Genbank acces	sion numbers			
				•		
	Pkey	CAT Number	Accession			
	409385	112523_1	AA071267	T65940 T64515 AA071334		
	412333	1289037_1	AW937485	AW937589 AW937658 AW937654 AW937492		
30	413605	1379792_1		BE152712 BE152668 BE152659 BE152810 BE15281		
		_	BE152669	BE152661 BE152672 BE152653 BE152716 BE15265	1 BE152767 BE152677 BE152652	BE152714 BE152708 BE152665 BE152679
•			BE152771	BE152775 BE152666 BE152768 BE152813 BE15266	4 BE152676 BE152681 BE152709	BE152667 BE152814 BE152808 BE152711
			BE152707	BE152815 BE152678 BE152673 BE152782 BE15267	1 BE152682 BE152760 BE152809	BE152778 BE152780 BE152762 BE152776
				BE152774 BE152763 BE152769		·
35	416151	1573926_1		4135 H23016		
-	416441	159480_1		AA182474 AA180369 BE275628 BE276131		
	416631	1605019_1		33884 N59684		
	423573	229714_1		AA327783 AW962370		
	447197	711623_1		366546 R36167		
40	447420	721207_1		N32350 H85772		
. •	452530	920646_1		Al905516 Al905457 Al905515 AW176013 AW176037		
	452947	939810_1	AW130413			
	453420	966433_1	AJ003459			
	459170	920646_1		Al905516 Al905457 Al905515 AW176013 AW176037		•
45		0200 10_1				
	TABLE 20	:				
		que number com	esponding to	en Eos probeset		
	Ref: Segu	ence source. Th	e 7 digit num	bers in this column are Genbank Identifier (GI) number	s. "Dunham I. et al." refers to the p	publication entitled "The DNA sequence of
				, et al. (1999) Nature 402:489-495		•
50	Strand: Indicates DNA strand from which exons were predicted					
•				ns of predicted exons		
			,			
	Pkey	Ref	Strand	Nt_position		
	400464	9929570		22074-22214		
55	400704	8118864		63110-63241		
-	400749	7331445		9162-9293		
	401244	4827300		55359-56376		
	401537	7960358		186786-187029,190607-190779,198218-198348		
	401657	9100664		7312-8163		
60	402172	8575911		143378-143671		
	402425	9796347		50224-50395		
	402745	9212200		76516-76690		
	403074	8954241		143375-143561		
	403077	8954241		146923-147222,147326-147628	•	
65	403083	8954241		163070-163351		
	403089	8954241		171964-172239		
	403092	8954241		174720-175016.175104-175406.175508-175813		
	403093	8954241		177083-177373,177464-177751		
	403411	9438635		104247-104420		
70	403661	8705027		30268-30482		
. •	403687	7387384		9009-9534		
	403691	7387384		88280-88463		
	403763	7229888		43575-43887		
	403796	8099896		75073-77664		•
75	404187	4481839		7644-7991		
	404243	5672609		74695-75123		
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965		•
	404886	4884062	Plus	30058-30596		
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-4595	8,47296-47457,49549-49658,4979	0-49904,50231-50342,53583-53667,54111-
80				54279		
	405285	6139075	Minus	55744-55903,57080-57170,61478-61560		
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823		
	405547	1054740	Plus	124361-124520,124914-125050		
	405636	5123990	Plus	56384-56587		
				107		

405790 1203968 Plus 136364-136509,136579-136699,136805-136941

TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained. 5

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: Unigene Title
PFAM domains

10

ratio: tumor vs. normal tissues

	ratio: turr	ior vs. normai us	sues		
15	Pkey	Ex. Acon No.	UGID	Title	ratio
10	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	219.9
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	165.0
	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psorlasis-associated)	161.5
20	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	150.2
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odontogenic k	149.5
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	- 136.6
25	428471	X57348	Hs.184510	stratifin	129.5
25	421978	AJ243662	Hs.110196	NICE-1 protein	108.7
	437191	NM_006846	Hs.5476	serine protease inhibitor, Kazal type, 5	106.2 105.5
	407788	BE514982	Hs.38991	\$100 calcium-binding protein A2 solute carrier family 2 (facilitated glucose transporter),	103.5
	441565 431211	AW953575 M86849	Hs.169902 Hs.5566	gap junction protein, beta 2, 26kD (connexin 26)	102.1
30	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	95.3
50	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus d	87.0
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	86.1
	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	85.0
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated protein	84.8
35	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	84.5
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced product u	84.4
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	83.8
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	81.0
40	432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	81.0
40	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	77.8
	409453	AI885516	Hs.95612	ESTs	75.3
	424670	W61215	Hs.116651	epithelial V-like antigen 1	67.5 67.0
•	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium protein, calv	65.7
45	423634 442379	AW959908	Hs.1690 Hs.8265	heparin-binding growth factor binding protein transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7
73	456898	NM_004613 NM_001928	Hs.155597	D component of complement (adipsin)	64.6
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, clade 8 (ovalbu	63.6
	447990	8E048821	Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	60.7
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from	60.3
50	414438	A1879277	Hs.76136	thioredoxin .	59.9
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	58.9
	433336	AF017986	Hs.31386	ESTs, Highly similar to JE0174 frizzled prolein-2 [H.sa	58.8
	403741			predicted exon	57.0
<i>E E</i>	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	56.1
55	424098	AF077374	Hs.139322	small proline-rich protein 3	55.8 55.6
	441591	AF055992	Hs.183	Duffy blood group	55.6 55.6
	426521	AF161445	Hs.170219	hypothetical protein	55.5 55.3
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	54.1
60	406725 422168	D51245	Hs.288061 Hs.112408	actin, beta S100 calcium-binding protein A7 (psoriasin 1)	54.1
00	406755	AA586894 N80129	Hs.94360	metallothionein 1L	54.0
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	53.3
	442257	AW503831	12.1000	gb:UI-HF-BN0-alb-b-05-0-UI.r1 NIH_MGC_50 Homo	53.1
	421957	AW068637	Hs.109857	hypothetical protein DKFZp434H0820	52.3
65	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemotactic pro	51.2
	406722	H27498	Hs.283305	Homo sapiens SNC73 protein (SNC73) mRNA, comple	51.0
	427223	BE208189	Hs.174031	cytochrome c oxidase subunit VIb	51.0
	414420	AA043424	Hs.76095	immediate early response 3	50.9
70	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.3
70	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	49.5
	436906	H95990	Hs.181244	major histocompatibility complex, class I, A	49.0
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	49.0
	414035	Y00530	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	48.8 48.8
75	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma cluster 4 antig	48.7
13	421948	AL036058	Hs.111758 Hs.76807	keratin 6A major histocompatibility complex, class II, DR alpha	48.5
	414662 425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	48.5
	404767	1414[012203	113.134424	predicted exon	48.4
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor 1	48.2
80	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	47.7
-	414183	AW957446	Hs.301711	ESTs	47.2
	400163			predicted exon	47.0
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	46.9
	423457		Hs.155606	paired mesoderm homeo box 1	46.6
				100	

	414085	AA114016	Hs.75746	aldehyde dehydrogenase 6	46.0
	423189	M59371	Hs.171596	EphA2	45.6
	438240	N92638	Hs.124004	ESTs	45.5
-	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	45.3
5	412774	AA120865	Hs.23136	ESTs	45.1
	407242	M18728		gb:Human nonspecific crossreacting antigen mRNA, co	44.8
	431292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromos	44.8
	403695			predicted exon	43.5
10	417365	D50683	Hs.82028	transforming growth factor, beta receptor II (70-80kD)	43.4
10	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (from c	43.4
	424479	AF064238	Hs.149098	smoothelin	43.3
	444726	NM_006147	Hs.11801	interferon regulatory factor 6	43.2
	432314	AA533447	Hs.285173	ESTs	43.2
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotaclin)	43.1
15	441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP1001	42.7
	412969	Al373162	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	42.6
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL02160	42.5
	400111			predicted exon	42.4
	407207	T03651	Hs.179661	tubulin, beta polypeptide	42.4
20	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	41.9
	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
	406657	A1678644	Hs.277477	major histocompatibility complex, class I, C	41.8
25	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	41.6
25	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5
	428785	Al015953	Hs.125265	ESTs	41.3
	450988	BE618571	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
20	414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	40.8
30	405022			predicted exon	40.8
	408221	AA912183	Hs.47447	ESTs	40.8
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	40.7
	421416	BE302950	Hs.104125	adenylyl cyclase-associated protein	40.6
36.	412247	AF022375	Hs.73793	vascular endothelial growth factor	40.5
35	410541	AA065003	Hs.64179	hypothetical protein ,	40.5
	406658	Al920965	Hs.77961	major histocompatibility complex, class I, B	40.0
	420225	AW243046	Hs.94789	ESTs	40.0
	406825	Al982529	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	39.4
40	443623	AA345519	Hs.9641	complement component 1, q subcomponent, alpha poly	39.4
40	404201	AF059566	Hs.103983	solute carrier family 5 (sodium lodide symporter), mem	39.3
	40513B			predicted exon	39.1
	408733	AW264812	Hs.254290	ESTs	39.0
	414044	BE614194	Hs.75721	profilin 1	38.9
4 5	430152	AB001325	Hs.234642	aquaporin 3	38.8
45	428121	AB006622	Hs.182536	Homo saplens cDNA: FLJ21370 fis, clone COL03092	38.8
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MAMMA10	38.7
	406140			predicted exon	38.5
	432918	AF077200	Hs.279813	hypothetical protein	38.4
50	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	38.4
50	427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	38.1
	448835	BE277929	Hs.11081	ESTs, Weakly similar to S57447 HPBRII-7 protein [H.	38.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010	37.9
	428383	BE616599	Hs.184029	hypothetical protein DKFZp761A052	37.7
55	436258	AW867491	Hs.107125	ESTs, Weakly similar to S57447 HPBRII-7 protein [H.	37.7
55	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis palm	37.7
	400327	M18679	Hs.247942	Human variant 5S rRNA-like gene and ORF, complete	37.6
	401781	4140770070	11- 000440	predicted exon	37.6 37.3
	448257	AW772070	Hs.253146	ESTS	
60	428415 424206	AA337211 NM_003734 ,	Hs.184222 Hs.198241	Down syndrome critical region gene 1 amine oxidase, copper containing 3 (vascular adhesion p	37.2 37.2
OO			Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (37.2
	406812 425882	AF000575	Hs.161002	absent in melanoma 1	37.2
	432501	U83115 BE546532	Hs.287329	Fas binding protein 1	37.1
	421786	Al188653	Hs.21351	ESTs	37.1
65	427781	BE275986	Hs.181311	asparaginyl-tRNA synthetase	37.0
05	410143	AA188169	Hs.288819	Homo sapiens cDNA: FLJ21022 fis, clone CAE06383	36.8
	451328	AW853606	Hs.109012	ESTs	36.7
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	36.7
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
70	401785	WAARDOOGO	113.70550	predicted exon	36.5
, ,	411469	T09997	Hs.70327	cysteine-rich protein 2	36.2
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulator 3	36.1
	417039	AA302180	Hs.80986	ATP synthase, H+ transporting, mitochondrial F0 comp	36.1
	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	36.0
75	402543	· AMADOED	1.0.105710	predicted exon	36.0
, ,	408669	Al493591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	35.9
	414987	AA524394	Hs.165544	ESTs	35.9
	445810	AW265700	Hs.155660	ESTs ·	35.9
	406653	AA574074	Hs.77961	major histocompatibility complex, class I, B	35.7
80	407498	U28131		gb:Human HMGI-C chimeric transcript mRNA, partial	35.6
55	412524	AA417813	Hs.11177	ESTs	35.5
	401521			predicted exon	35.4
	408948	AW296713	Hs.221441	ESTs	35.1
	406728	AI986345	Hs.183704	ubiquitin C	34.9
	.00.20				

				· · · · · · · · · · · · · · · · · · ·	
	440669	Al206964		gb:qr30g06.x1 NCI_CGAP_GC6 Homo sapiens cDNA	34.8
	422658	AF231981	Hs.250175	homolog of yeast long chain polyunsaturated falty acid	34.8
	452924	AW580939	Hs.97199	complement component C1q receptor	34.7
_	428600	AW863261	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC095 [H.sapi	34.7
5	409828	AW501137		gb:UI-HF-BP0p-ait-e-12-0-UI.r1 NIH_MGC_51 Homo	34.5
	459390	BE385725	11 400074	gb:601276347F1 NIH_MGC_20 Homo sapiens cDNA	34.5
	445055	BE512856	Hs.109051	glycoprotein, synaptic 2	34.3
	411789	AF245505	Hs.72157	Homo sapiens adiican mRNA, complete cds	34.3
10	410626	BE407727	Un C0046	gb:601299771F1 NIH_MGC_21 Homo sapiens cDNA	34.2
10	410706 419273	A1732404 BE271180	Hs.68846 Hs.293490	ESTs ESTs	34.2 34.2
	407839	AA045144	Hs.161566	ESTS	34.0
	444286	Al625304	Hs.190312	ESTS	34.0
	449226	AB002365	Hs.23311	KIAA0367 protein	34.0
15	414290	Al568801	Hs.71721	ESTs	33.9
	401245	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		predicted exon	33.9
	425222	M85430	Hs.155191	villin 2 (ezrin)	33.8
	409950	R42678	Hs.301669	KIAA0564 protein	33.8
	437201	F29279	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II,	33.7
20	406566	AF088886	Hs.11590	cathepsin F	33.7
	405071			predicted exon	33.7
	455426	AW937792		gb:QV3-DT0045-140200-082-b07 DT0045 Homo sapi	33.6
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen 1NFLS Homo s	33.5
25	424995	Z45023		gb:HSC2FA041 normalized infant brain cDNA Homo s	33.5
25	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019	33.5
	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	33.4
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal type I, pro	33.3
	417409	BE272506	Hs.82109	syndecan 1	33.3
30	425389	AW974499	Hs.192183	ESTs	33.3
30	434658	A1624436 AA306049	Hs.194488	ESTs DVEZBA340135 aminin	33.2 33.1
	456562 447111		Hs.102669 Hs.17409	DKFZP4340125 protein cysteine-rich protein 1 (intestinal)	33.0
	432360	AI017574 BE045243	Hs.274416	NADH dehydrogenase (ubiquinone) 1 alpha subcomple	32.9
	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	32.7
35	419968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	32.7
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	32.6
	451541	BE279383	Hs.26557	plakophilin 3	32.6
	424499	N90344	Hs.149436	kinesin family member 5B	32.4
40	402144			predicted exon	32.4
40	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	32.4
	400231			predicted exon	32.3
	437712	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1	32.3
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	32.2
45	419659	AB023206	Hs.92186	Leman coiled-coil protein	32.0
73	428582 421401	BE336699 AW410478	Hs.185055 Hs.104019	BENE protein transforming, acidic coiled-coil containing protein 3	32.0 32.0
	414064	BE245289	Hs.16165	expressed in activated T/LAK lymphocytes	32.0
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
	411930	F06485	113.110242	gb:HSC19G051 normalized infant brain cDNA Homo s	31.9
50	428150	AW950547	Hs.182684	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
	401887			predicted exon	31.8
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta polypeptide	31.7
	422738	X80915	Hs.1573	growth differentiation factor 5 (cartilage-derived morph	31.6
	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed intermediate filam	31.5
55	413924	AL119964	Hs.75616	KIAA0018 gene product	31.4
	420231	R06866	Hs.19813	ESTs .	31.3
	434715	BE005346	Hs.116410	ESTs	31.3
	422831	R02504	11- 00000	gb:ye86f06.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
60	416854	H40164 ·	Hs.80296	Purkinje cell protein 4	31.2 31.1
UU	422976 426356	AU076657 BE536836	Hs.1600	sec61 homolog ab:601064837F1 NIH MGC 10 Homo sapiens cDNA	31.0
	433935	AF112208	Hs.44163	13kDa differentiation-associated protein	30.8
	430040	AW503115	Hs.227823	pM5 protein	30.8
	406340	AA299679	Hs.180370	cofilin 1 (non-muscle)	30.8
65	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription factor, epith	30.7
	425105	BE280066	Hs.24956	hypothetical protein FLJ22056	30.7
	402066			predicted exon	30.7
	429538	BE182592	Hs.139322	small proline-rich protein 3	30.6
70	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.4
70	421251	Z28913	Hs.102948	enigma (LIM domain protein)	30.3
	456084	AA155859	Hs.79708	ESTs	30.3
	402023			predicted exon	30.3
	404356	R24707	Hs.260201	predicted exon ESTs	30.2 30.2
75	415973 445983	Al269107	Hs.132219	ESTs	30.2
, 5	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	30.1
	458789	AL157468	Hs.20157	Homo sapiens cDNA FLJ20848 fis, clone ADKA01732	30.1
	400842	/\L10/400	110.60101	predicted exon	30.1
	406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	30.0
80	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (from c	30.0
-	451383	AW239364	Hs.20242	hypothetical protein FLJ12788	30.0
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	30.0
	459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens cDNA	30.0
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	30.0

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membrane protein	29.9
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
	436651	BE045962	Hs.275998	ESTs	29.6
_	419766	BE243101	Hs.22391	chromosome 20open reading frame 3	29.5
5	420747	BE294407	Hs.99910	phosphofructokinase, platelet	29.5
-	436895	AF037335	Hs.5338	carbonic anhydrase XII	29.5
	412765	AK000620	Hs.74571	ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD9 antigen (p24)	29.4
	413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
10	447795	AW295151	Hs.163612	ESTs	29.4
10	431103		Hs.44		29.4
		M57399		pleiotrophin (heparin binding growth factor 8, neurite g	29.4
	415314	N88802	Hs.5422	glycoprotein M6B	
	428411	AW291464	Hs.10338	ESTs .	29.3
15	430580	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
15	430451	AA836472	Hs.249982	cathepsin B	29.2
	453949	AU077146	Hs.36927	heat shock 105kD	29.2
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme 4	29.2
	407845	AL036518	Hs.118598	ESTs	29.1
	453500	A1478427	Hs.43125	ESTs	29.1
20	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0
	453467	Al535997	Hs.30089	ESTs	29.0
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	W69233	Hs.112457	ESTs	28.9
	423621	BE002904	180.112407	gb:QV4-BN0090-070400-163-c07 BN0090 Homo sapi	28.8
25	408935	BE539706	Hs.285363	ESTs	28.8
20	450847	NM_003155	Hs.25590	stanniocalcin 1	28.8
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	28.7
		AA852604			28.7
	423225		Hs.125359	Thy-1 cell surface antigen th: HSC3DG061 complized infant brein cDNA Home	28.7
30	433469	F12741		gb:HSC3DG061 normalized Infant brain cDNA Homo	
3 0	405783	1100700	11-04000	predicted exon	28.7
	417308	H60720	Hs.81892	KIAA0101 gene product	28.7
	400749			predicted exon	28.7
	413442	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo saplens c	28.6
	404828			predicted exon	28.6
35	407453	AJ132087		gb:Homo saplens mRNA for axonemal dynein heavy ch	28.6
	418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6
	413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	28.5
	450690	AA296696	Hs.25334	FXYD domain-containing ion transport regulator 5	28.5
	402430			predicted exon	28.4
40	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
	406086			predicted exon	28.2
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	28.2
	417055	N39489	Hs.7258	Homo sapiens cDNA: FLJ22021 fis, clone HEP08253	28.1
45	449184	AW296295	Hs.196491	ESTs	28.1
43	446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW997986	113.10203	gb:RC1-BN0056-230200-021-e11 BN0056 Homo sapie	28.0
	452818	W21909	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	28.0
	402869	1421303	110.0012	predicted exon	27.9
50		A A 3E 2044	Un 5224		27.9
50	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	27.9
	402075	007457	II- 0000 A	predicted exon	
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecul	27.8
E E	439766	AB033492	Hs.301241	Homo saplens mRNA; cDNA DKFZp586A0424 (from	27.7
55	424482	BE268621	Hs.149155	voltage-dependent anion channel 1	27.6
	420737	L08096	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7	27.6
	414663	BE396326		gb:601289258F1 NIH_MGC_8 Homo sapiens cDNA c	27.6
	409703	NM_006187	Hs.56009	2'-5'oligoadenylate synthetase 3	27.6
~	446108	AL036596	Hs.102773	ESTs	27.5
60	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	A1248205	Hs.153244	ESTs	27.5
	405411			predicted exon	27.5
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
65	450455	AL117424	Hs.25035	chloride intracellular channel 4	27.3
	414855	AA156986	Hs.104640	HIV-1 Inducer of short transcripts binding protein	27.2
	433578	BE336886	Hs.3416	adipose differentiation-related protein	27.2
	401994	,		predicted exon	27.2
	445033	AV652402	Hs.155145	ESTs	27.2
70	402277			predicted exon	27.1
	428106	BE620016	Hs.182470	PTD010 protein	27.1
	448625	AW970786	Hs.178470	Homo saplens cDNA: FLJ22662 fis, clone HSI08080	27.1
	422587	A1879352	Hs.118625	hexokinase 1	27.0
	457204	BE264152	Hs.221994	ESTs	27.0
75	444094	Al695764	Hs.202394	ESTs	27.0
	414053	BE391635	Hs.75725	transgelin 2	26.9
			Hs.2575	calpain 1, (mu/l) large subunit	26.9
	430511	BE018156			26.9
	434039	L32977	Hs.3712	ubiquinol-cytochrome c reductase, Rieske iron-sulfur po Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
80	424939	AK000059	Hs.153881		
OU	414539	BE379046		gb:601236646F1 NiH_MGC_44 Homo sapiens cDNA	26.9
	404675		41. 44005-	predicted exon	26.8
	401597	AA172106	Hs.110950	Rag C protein	26.8
	401405			predicted exon	26.8
	411541	W03940		gb:za62b02.r1 Soares fetal liver spleen 1NFLS Homo sa	26.8
				111	

	440000				~~ ~
	412025	AI827451	Hs.24143	ESTS	26.7 26.7
	414276 444065	BE297862 AW449415	Hs.10260	gb:601174780F1 NIH_MGC_17 Homo sapiens cDNA Homo sapiens cDNA FLJ11341 fis, clone PLACE1010	26.7
	447981	R53772	Hs.8929	hypothetical protein FLJ11362	26.7
5	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	26.5
	400982	_		predicted exon	26.5
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone HRC08686	26.5
	407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	26.4
10	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
10	448218 413511	Al188489 Al627178	Hs.75412	gb:qd09b12.x1 Soares_placenta_8to9weeks_2NbHP8to Arginine-rich protein	26.3 26.2
	459511	Al142379	110.110412	gb:gg64c01.r1 Soares_testis_NHT Homo sapiens cDNA	26.2
	410668	BE379794	Hs.65403	hypothetical protein	26.2
	458662	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	26.2
15	451219	AA054209	Hs.167904	ESTs	26.2
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	26.2
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
	446342 421177	BE298665 AW070211	Hs.14846 Hs.102415	Homo saplens mRNA; cDNA DKFZp564D016 (from c Homo saplens mRNA; cDNA DKFZp586N0121 (from	26.2 26.1
20	433848	AF095719	Hs.93764	carboxypeptidase A3	26.1
	448497	BE613269	Hs.21893	ESTs, Weakly similar to glycerol 3-phosphate permease	26.1
	415279	F04237	Hs.1447	glial fibrillary acidic protein	26.0
	419323	A1092379	Hs.135275	ESTs	26.0
25	430265	L36033	Hs.237356	stromal cell-derived factor 1	25.9
25	437679	NM_014214	Hs.5753	Inositol(myo)=1(or 4)-monophosphatase 2	25.9 25.8
	425535 412923	AB007937 AA179922	Hs.158287 Hs.75056	KIAA0468 gene product adaptor-related protein complex 3, delta 1 subunit	25.8
	447980	Al703397	Hs.202355	ESTs	25.8
	419118	AA234223	Hs.139204	ESTs	25.8
30	421224	AW402154	Hs.125812	ESTs	25,8
	414890	BE281095	Hs.77573	uridine phosphorylase	25.8
	447330	BE279949	Hs.18141	ladinin 1	25.7 25.7
•	405610 447604	AW089933	Hs.293674	predicted exon ESTs	25.7 25.7
35	445677	H96577	Hs.6838	ras homolog gene family, member E	25.7
	456088	BE177320	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone LNG06451	25.7
	417120	N79687	Hs.46616	ESTs	25.6
	405194			predicted exon	25.6
40	410687	U24389	Hs.65436	lysyl oxidase-like 1	25.6 25.6
40	421888 420459	AA299780 AF016045	Hs.121036 Hs.97905	ESTs ovo (Drosophila) homotog-like 1	25.5
	416323	N72630	Hs.33981 ·	Homo sapiens genomic DNA, chromosome 21q, section	25.5
	446292	AF081497	Hs.279682	Rh type C glycoprotein	25.5
4.5	416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	25.5
45	430028	BE564110	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
	438450 400215	AI050866	Hs.65853	nodal, mouse, homolog predicted exon	25.5 25.4
	430014	H59354	Hs.182485	actinin, alpha 4	25.4
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	25.4
50	405867			predicted exon	25.4
	459170	Al905518		gb:RC-BT091-210199-098 BT091 Homo sapiens cDNA	25.4
	407944	R34008	Hs.239727 Hs.979	desmocollin 2	25.4 25.3
	415748 423287	D90086 H38340	HS.9/9	pyruvate dehydrogenase (lipcamide) beta gb:yp70h07.r1 Scares adult brain N2b4HB55Y Homo s	> 25.3
55	450944	AA554989	Hs.209061	sudD (suppressor of bimD6, Aspergillus nidulans) homo	25.3
	432906	BE265489	Hs.3123	lethal glant larvae (Drosophila) homolog 2	25.3
	400104			predicted exon	25.3
	449019	AI949095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
60	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
60	402639 447147	AA910353	Hs.292815	predicted exon ESTs	25.3 25.3
	453379	AA035261	Hs.61753	ESTs	25.3
	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone LNG09846	25.3
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
65	406685			gb:Human nonspecific crossreacting antigen mRNA, co	25.3
	444747	AW450407	Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2 25.2
	417883 430235	R22519 BE268048	Hs.23398 Hs.236494	ESTs RAB10, member RAS oncogene family	25.2
	459001	AI761313	Hs.204605	ESTs	25.2
70	434368	AW519020	Hs.212640	Homo saplens cDNA FLJ13265 fis, clone OVARC1000	25.2
	415917	Z43912		gb:HSC1OA111 normalized infant brain cDNA Homo	25.2
-	444409		Hs.49265	ESTs	25.2
	428578 433417	BE391797 AA587773	Hs.82148 Hs.136494	hypothetical protein ESTs	25.1 25.1
75	426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeplide 21	25.1
	402131	5250-1000		predicted exon	25.1
	450545	AW135582	Hs.201767	ESTs	25.0
	434162		Hs.116136	ESTs	25.0
οΛ	406571	********	11- 4-0	predicted exon	24.9
80	427600		Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P cystatin B (stefin B)	24.9 24.9
	409402 400135		Hs.695	predicted exon	24.9
	428403		Hs.239894	leucine rich repeat (in FLII) interacting protein 1	24.9
	403223			.predicted exon	24.8

	435236	T03890	Hs.157208	ESTs, Highly similar to Arx homeoprotein [M.musculu	24.8
	457439	AW410408	Hs.271167	L-pipecolic acid oxidase	24.8
	448667	Z78394	Hs.4895	Homo sapiens cDNA: FLJ22046 fis, clone HEP09276	24.8
_	440605	Z40094	Hs.185698	ESTs	24.8
5	426724	AA383623	Hs.293616	ESTs	24.8
	403359			predicted exon	24.7
	442826	AI018777	Hs.131241	ESTs .	24.7
	411503	AW190338	Hs.28029	purinergic receptor P2X, ligand-gated ion channel, 4	24.6
10	414540	BE379050	() 400000	gb:601236655F1 NIH_MGC_44 Homo saplens cDNA	24.6
10	421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV00180	24.5
	438802	AA825976	Hs.136954	ESTs	24.5
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation transporter), me	24.5
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
15	426383	BE537380 AA219321	LI- 472204	gb:601064570F1 NIH_MGC_10 Homo sapiens cDNA	24.4 24.4
13	418408		Hs.173294	ESTs ·	
	416186 416908	W87575 AA333990	Hs.269177	ESTs coagulation factor XIII, A1 polypeptide	24.4 24.4
	453857	AL080235	Hs.80424 Hs.35861	DKFZP586E1621 protein	24.4
	439706	AW872527	Hs.59761	ESTs	24.4
20	441619	NM_014056	Hs.7917	DKFZP564K247 protein	24.4
20	417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
	433662	W07162	Hs.150826	CATX-8 protein	24.3
	453986	M13232	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
	457123	AA770021	Hs.16332	ESTs	24.3
25	433864	AA931550	Hs.192785	ESTs	24.3
	409865	AW502208		gb:UI-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_52 Hom	24.3
	448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	24.3
	406277			predicted exon	24.3
	451957	Al796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PLACE1006	24.3
30	408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fis, clone ADKA0320	24.2
	401757			predicted exon	24.2
	444751	Al207406	Hs.11866	hypothetical protein PRO1197	24.2
	408647	AW245831		gb:2822937.5prime NIH_MGC_7 Homo saplens cDNA	24.2
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	24.2
35	436913	AA789074	Hs.187478	ESTs	24.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to HuEMAP [H.sapiens]	24.2
	451743	AW074266	Hs.23071	ESTs	24.2
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	24.2
40	407926	AW956382	Hs.59771	ESTs	24.1
40	413973	BE279858	Hs.128417	Homo sapiens cDNA FLJ14009 fis, clone Y79AA1002	24.1
	439078 401913	AF085936		gb:Homo sapiens full length insert cDNA clone YR58F	24.1 24.1
	435138	BE314734		predicted exon gb:601152976F1 NIH_MGC_19 Homo saplens cDNA	24.1
	405311	00014104		predicted exon	24.0
45	413127	BE066529	Hs.83484	SRY (sex determining region Y)-box 4	24.0
	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) receptor 1A	24.0
	434445	Al349306	Hs.11782	ESTs	24.0
	418166	AI754416	Hs.260024	Cdc42 effector protein 3	24.0
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
50	401167			predicted exon	23.9
	454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	23.9
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/	23.9
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	23.9
	450796	NM_001988	Hs.25482	envoplakin	23.8
55	442199	BE277633	Hs.286027	etoposide-induced mRNA	23.8
	402699			predicted exon	23.8
	426143	BE379836	Hs.167106	proteasome (prosome, macropain) subunit, alpha type, 3	23.8
	437592	NM_003851	Hs.5710	cellular repressor of E1A-slimulated genes	23.8
60	433598	Al762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU	23.8
00	401088 445924	Al264671	Hs.164166	predicted exon ESTs	23.8 23.8
	420902	AA742277	ns.104100	gb:ny28e09.s1 NCI_CGAP_GCB1 Homo sapiens cDN	23.8
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	23.8
	458698	AW452189	Hs.257528	ESTs	23.7
65	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	23.7
05	413460	R61610	Hs.21527	ESTs, Weakly similar to KIAA0918 protein [H.sapiens	23.6
	401575		110121021	predicted exon	23.6
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	23.6
	427276	AA400269	Hs.49598	ESTs	23.6
70	417069	AA442192	Hs.81097	cytochrome c oxidase subunit VIII	23.5
	400161			predicted exon	23.5
	417190	NM_001359	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondrial	23.5
	443667	Al129066	Hs.135457	ESTs	23.5
75	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapie	23.5
75	400685			predicted exon	23.5
	422090	W05345	Hs.293884	ESTs	23.4
	432517	AF275816	Hs.283096	PR domain containing 9	23.4
	405307	1140000		predicted exon	23.4
80	416328	H48389	Hs.268886	ESTs	23.4
٥U	427174	AA398848	Hs.97541	ESTs	23.4
	426148	AI751071	Hs.167135	Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001	23.3
	452544 404890	AW851888		gb:QV0-CT0225-131099-034-d05 CT0225 Homo sapie predicted exon	23.3 23.3
	404650	AA131539	Hs.15669	ESTs	23.3
	700120		113,13003	70.0	20.0

	400000	44400		FOT	
	428362 425349	AA426555 AA425234	Hs.169333 Hs.79886	ESTs ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3 23.3
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11 (aldose redu	23.3
_	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	23.2
5	411796	AA807197	Hs.6918	ESTs	23.2
	458954	AW379075	Hs.141742	Homo sapiens cDNA FLJ12211 fis, clone MAMMA10	23.2
	408896	AI610447	Hs.48778	niban protein	23.2 23.2
	457024 414591	AA397546 AI888490	Hs.119151 Hs.55902	ESTs ESTs	23.2
10	437846	AA773866	Hs.244569	ESTs	23.2
	401220			predicted exon	23.1
	421747	Al816224	Hs.107747	DKFZP566C243 protein	23.1
	452950	AA428123	Hs.7745	17kD fetal brain protein	23.1 23.1
15	414327 405256	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protein [R.norvegic predicted exon	23.1
10	452416	AA026115	Hs.114777	ESTs	23.1
	440684	Al253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI [H.sap	23.1
	445603	H08345	Hs.106234	ESTs	23.1
20	436306 434867	AA805939 AF159442	Hs.117927 Hs.103382	ESTs phospholipid scramblase 3	23.1 23.0
20	404727	AF 133442	ns. 103362	predicted exon	23.0
	407317	A1204033	Hs.271461	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	23.0
	405580			predicted exon	23.0
25	437898	W81260	Hs.43410	ESTs	22.9
25	448781 457297	AW243419 AW968188	Hs.254048 Hs.290999	ESTs STS	22.9 22.9
	405545	A44200 100	115.230333	predicted exon	22.9
	431562	Al884334	Hs.11637	ESTs	22.9
20	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from c	22.9
30	439848	AW979249	U- 204077	gb:EST391359 MAGE resequences, MAGP Homo sap	22.9
	418149 439332	AA811473 AW842747	Hs.291877 Hs.293314	ESTs ESTs, Highly similar to unnamed protein product [H.sa	22.9 22.8
	401566	A11042141	13.233314	predicted exon	22.8
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
35	406684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecul	22.8
	421651	AW860612	Hs.283586	ESTs	22.8
	421064 441249	Al245432 AA971585	Hs.101382 Hs.166250	tumor necrosis factor, alpha-induced protein 2 ESTs	22.8 22.8
	457624	AA809159	Hs.287581	Homo saplens cDNA FLJ13544 fis, clone PLACE1006	22.8
40	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33) mRNA, p	22.8
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
	436827	H72187	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
	418174 418307	L20688 U70867	Hs.83656 Hs.83974	Rho GDP dissociation inhibitor (GDI) beta solute carrier family 21 (prostaglandin transporter), mem	22.7 22.7
45	456035	N54956	Hs.271726	ESTs	22.7
	457867	AA045767	Hs.5300	bladder cancer associated protein	22.7
	440401	Al126341	Hs.143887	ESTs	22.7
	400126	4K000343	Hs.77646	predicted exon	22.7 22.7
50	414931 406719	AK000342 Al832962	Hs.169476	Homo sapiens mRNA; cDNA DKFZp761M0223 (from glyceraldehyde-3-phosphate dehydrogenase	22.6
-	439875	W95357	Hs.138860	Rho GTPase activating protein 1	22.6
	456058	N94587	Hs.55063	ESTs	22.6
	441926	AI015051	Hs.130953	ESTs	22.6
55	428423 438518	AU076517 BE561958	Hs.184276 Hs.285823	solute carrier family 9 (sodium/hydrogen exchanger), is immunoglobulin heavy constant mu	22.6 22.6
JJ	420674	NM_000055	Hs.1327	butyrylcholinesterase	22.6
	422160	AW582898		gb:ia07e04.y1 Human Pancreatic Islets Homo sapiens c	22.5
	412408	D51103	Hs.73851	ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
60	400964	A1A/04E44E	No 407700	predicted exon	22.5 22.5
JU	434360 427977	AW015415 AW630727	Hs.127780 Hs.181307	ESTs H3 histone, family 3A	22.5
	450339	A1693281	Hs.54547	ESTs	22.4
	424059	AW451266	Hs.107418	ESTs	22.4
65	414626	BE410589		gb:601303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4
65	401991	NILE COTOLO	LL Danna	predicted exon	22.4 22.3
	419741 457952	NM_007019 U25750	Hs.93002 Hs.210783	ubiquitin carrier protein E2-C Hurnan chromosome 17g21 mRNA clone 1046:1-1	22.3 22.3
	422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
-	429504		Hs.204238	lipocalin 2 (oncogene 24p3)	22.3
70	447306	AI373163	Hs.170333	ESTs	22.3
	424966		Hs.153985 Hs.119591	solute carrier family 7 (cationic amino acid transporter,	22.3 22.2
	422739 432504		Hs.277704	adaptor-related protein complex 2, sigma 1 subunit oxygen regulated protein (150kD)	22.2
	423804		Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
75	404683	AI924294	Hs.173259	uncharacterized bone marrow protein BM033	22.2
	441624		Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
	425751 453076		Hs.1940	crystallin, alpha B ESTs	22.2 22.2
	452976 414642		Hs.101189	gb:zi03h01.r1 Soares_pregnant_uterus_NbHPU Homo	22.2
80	437452		Hs.7104	Homo sapiens mRNA; cDNA DKFZp761P06121 (from	22.2
	417426	NM_002291	Hs.82124	laminin, beta 1	22.2
	414774		Hs.77274	plasminogen activator, urokinase	22.1
	424631 413967		Hs.179808 Hs.117853	ESTs ESTs	22.1 22.1
	410007	A11204401	119.111030		
				114	

	400174			predicted exon	22.1
	431837	T79326	Hs.298262	ESTs, Wealdy similar to dJ88J8.1 [H.sapiens]	22.1
	401628 418374	AJ011916	U- 04250	predicted exon	22.1
5	429297	X82494	Hs.84359 Hs.198862	hypothetical protein fibulin 2	22.0 22.0
_	403508	A02434	135.130002	predicted exon	22.0
	432638	Al017717	Hs.126525	chromosome 21 open reading frame 15	22.0
	407382	AA503620		gb:ne49b08.s1 NCI_CGAP_Co3 Homo saplens cDNA	22.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	22.0
·10	420185	AL044056	Hs.158047	ESTs .	22.0
	409545	BE296182		gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA	22.0
	426662	AA879474	Hs.122710	ESTs	22.0
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	22.0
15	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDNA clone EU	21.9
19	422447 421574	AA310711 AJ000152	Hs.124340 Hs.105924	ESTs defensin, beta 2	21.9 21.9
	435302	A1076259	Hs.190337	ESTs	21.9
	414527	BE241739	Hs.76359	catalase	21.9
	441436	AW137772	Hs.185980	ESTs	21.9
20	454178	AW177274		gb:CM2-CT0128-230899-005-a02 CT0128 Homo sapie	21.8
	448838	BE614761		gb:601281335F1 NIH_MGC_39 Homo sapiens cDNA	21.8
	427889	Al400968	Hs.181046	dual specificity phosphatase 3 (vaccinia virus phosphat	21.8
	441114	AA917466	Hs.126600	ESTs	21.8
25	451831	NM_001674	Hs.460	activating transcription factor 3	21.8
25	405600			predicted exorg	21.8
	446981	AI652743	Hs.197497	ESTs	21.8
	432839	AA579465	Hs.287332	ESTs	21.8
	405208 435025	T08990	Hs.4742	predicted exon	21.8 21.7
30	413976	BE295452	Hs.75655	anchor attachment protein 1 (Gaa1p, yeast) homolog procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	21.7
50	423515	AA327017	Hs.162204	ESTs	21.7
	452329	N36626	Hs.29106	mitogen-activated protein kinase phosphatase x	21.7
	423050	AA320946		gb:EST23529 Adipose tissue, brown Homo saptens cD	21,7
	413679	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo saple	21.7
35	442166	AW845280	Hs.204723	ESTs	21.6
	445585	AI243836	Hs.147086	ESTs	21.6
	406160			predicted exon	21.6
		AA374743	Hs.279920	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas	21.6
40	446598	AW250546	Un 121574	gb:2821774.5prime NIH_MGC_7 Homo sapiens cDNA	21.6 21.6
70	434493 429582	AA635305 AI569068	Hs.121574 Hs.22247	ESTS ESTS	21.6
•	403796	A1303000	113.22241	predicted exon	21.6
	405028			predicted exon	21.6
	426597	AA382250	Hs.145601	ESTs	21.6
45	437308	AA749417	Hs.292353	ESTs	21.6
	447384	Al377221	Hs.40528	ESTs	21.6
	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	21.6
	437068		Hs.291427	ESTs	21.6
50	418509	AB028624	Hs.85539	ATP synthase, H+ transporting, mitochondrial F0 comp	21.5
50	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	21.5
	407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	21.5
	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.5 21.5
	413605 427286	BE152644 AW732802	Hs.2132	gb:CM1-HT0329-250200-128-f09 HT0329 Homo saple epidermal growth factor receptor pathway substrate 8	21.5
55	405226	A11102002	113.2102	predicted exon	21.4
33	402570			predicted exon	21.4
	457960	AA771881	Hs.298149	ESTs	21.4
	400684			predicted exon	21.4
	425943	H46986	Hs.31861	ESTs	21.4
60	434240	AF119912	Hs.258119	hypothetical protein PRO3073	21.4
	448376	A1494332	Hs.196963	ESTs	21.4
	408089	H59799	Hs.42644	thloredoxin-like	21.4
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33) mRNA, part	21.4 21.4
65	412652 428373	A1801777 A1751656	Hs.6774 Hs.183986	ESTs	21.4
05	416138	C18946	Hs.79026	poliovirus receptor-related 2 (herpesvirus entry mediato myeloid leukemia factor 2	21.3
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen included)	21.3
	411028	AW813703	1.0	gb:RC3-ST0197-130100-014-h09 ST0197 Homo sapien	21.3
	417438	Z43989	Hs.82141	Human clone 23612 mRNA sequence	21.3
70	417534	NM_004998	Hs.82251	myosin IC	21.3
	427767	Al879283	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	21.2
	433300	AA582307		gb:nn49d09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA	21.2
	452061	A1074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	21.2
75	411939	Al365585	Hs.146246	ESTs	21.2
75	435060	AI422719	Hs.233349	ESTs, Weakly similar to fork head like protein [H.saple	21.2
	432412 407491	AI470549 S82769	Hs.162201	ESTs gb:GABAA receptor gamma 3 subunit [human, fetal bra	21.2 21.2
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mobility group p	21.2
	426254	BE018103	Hs.168541	Homo saplens mRNA full length insert cDNA clone EU	21.1
80	458188	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	21.1
	406215			predicted exon	21.1
	425461	AK000602	Hs.157938	hypothetical protein FLJ20595	21.1
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT2RM4002	21.1
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone CAE07155	21.1
				•	

		•			
	408546	W49512	Hs.46348	bradykinin receptor B1	21.1
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	21,1
	430998	AF128847			
			Hs.204038	indolethylamine N-methyltransferase	21.1
_	438901	AF085834	Hs.29036	ESTs	21.1
5	440500	AA972165	Hs.150308	ESTs .	21.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo sapie	21.1
	447452	BE618258	Hs.102480	ESTs	21.1
	412446	Al768015	Hs.92127	ESTs	21.1
10	418975	T75496	Hs.296980	ESTs	21.0
10	454961	AW847807		gb:IL3-CT0213-190200-040-E12 CT0213 Homo saplen	21.0
	401072			predicted exon	21.0
	401204			predicted exon	21.0
	433626	AF078859	Hs.86347	hypothetical protein	21.0
16	418047	R37633	Hs.4847	ESTs	21.0
15	443380	AJ792478	Hs.135377	ESTs	21.0
	427424	AA402453	Hs.113011	ESTs	21.0
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	20.9
20	435656	R93409	Hs.120759	ESTs	20.9
20	413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
	418874	T60872		gb:yb72h11.s1 Stratagene ovary (937217) Homo sapien	20.9
	452574	AF127481	Hs.35093	lymphoid blast crisis oncogene	20.9
	400332	\$66407	Hs.248032	FLT4	20.9
	402421	000-101	TIOLE TOOLE	predicted exon	20.9
25		1177001	11- 470747		
23	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 28	20.9
	432038	AA524746	Hs.162110	ESTs	20.8
	423711	AF059194	Hs.131953	v-maf musculoaponeurotic fibrosarcoma (avian) oncoge	20.8
	402297			predicted exon	20.8
	405133			predicted exon	20.8
30	436661	Al125270	Hs.128069		20.8
50				ESTs, Weakly similar to similar to collagen [C.elegans]	
	437836	BE269291	Hs.292458	ESTs	20.8
	437329	AA811977	Hs.291761	ESTs	20.8
	445830	H10451	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT2RM4002	20.8
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of major histocom	20.7
35	421271	AW170057	Hs.133179	ESTs	20.7
55	400256	711110001	16.100170		
				predicted exon	20.7
	414028	AA782576	Hs.4944	Homo saplens cDNA FLJ12783 fls, clone NT2RP2001	20.7
	456728	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
	417707	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
40	438713	H16902	Hs.6749	ESTs	20.7
	450306	AL080080	Hs.24766	DKFZP564E1962 protein	20.7
	438898	AI819863	Hs.106243	ESTs	20.7
	403273			predicted exon	20.7
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens cDNA	20.7
45	401283			predicted exon	20.7
	403703			predicted exon	20.6
	416969	A101E443	Un 202404		
		AI815443	Hs.283404	organic cation transporter	20.6
	442400	AW381148	Hs.3593	ESTs	20.6
	447563	BE536115	Hs.160983	ESTs	20.5
50	419754	H52299	Hs.75243	bromodomain-containing 2	20.5
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member 3	20.5
	450507	AW295603	Hs.250891	ESTs	20.5
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	20.5
			H3.202001		
<i></i>	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo sapie	20.5
55	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	20.5
	400642			predicted exon	20.4
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	20.4
	442724	AA355525	Hs.159604	cysteinyl-tRNA synthetase	20,4
60	417861	AA334551	Hs.82767	sperm specific antigen 2	20.4
00	402948			predicted exon	20.4
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapie	20.4
	435478	AA682622		gb:zj20f09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Ho	20.4
	447955	BE544271	Hs.288390	Homo sapiens cDNA: FLJ22795 fis, clone KAIA2543	20.3
	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog) 1	20.3
65	420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
05					
	449482	Al784266	Hs.28774	ESTs	20.3
	400807			predicted exon	20.3
	419942	U25138	Hs.93841	potassium large conductance calcium-activated channel	20.3
	420783	AI659838	Hs.99923	tectin, galactoside-binding, soluble, 7 (galectin 7)	20.3
70	402986	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)	20.3
	451375	. Al792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from 2	20.3
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musculus]	20.3
	433090	AI720050	Hs.145362	immortalization-upregulated protein	20.3
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast	20.3
75	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
	409738	BE222975	Hs.56205	insulin induced gene 1	20.3
	428245				20.3
		AF151048	Hs.183180	hypothetical protein	
	412582	BE270631	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
00	406207			predicted exon	20.2
80	400931			predicted exon	20.2
	410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFZp434M1827 (from	20.2
	428438	NM_001955	Hs.2271	endothelin 1	20.2
	446918	AL135125	Hs.13913	KIAA1577 protein	20.2
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G	20.2
	414511	AA148725	Hs.12969	hypothetical prolein	20.2
	451546	AF051782	Hs.26584	Homo sapiens clone CDABP0038 mRNA sequence	20.1
-	441899	Al372588	Hs.8022	TU3A protein	20.1
5	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	20.1
	411014	AW816072		gb:MR3-ST0220-070100-021-h07 ST0220 Homo saple	20.1
	451400	BE160479		gb:QV1-HT0413-210200-081-g05 HT0413 Homo sapi	20.1
	459247	N46243	Hs.110373	ESTs	20.1
4.0	441633	AW958544	Hs.112242	ESTs	20.1
10	427466	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
	406893	M22406		gb:Human intestinal mucin mRNA, partial cds, clone SM	20.0
	406268			predicted exon	20.0
	403348			predicted exon	20.0
	400970			predicted exon	20.0
15	414045	NM_002951	Hs.75722	ribophorin II	20.0
	427169	AA398823	Hs.97549	EST	20.0
	405586			predicted exon	20.0
	445834	AI913290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	20.0
~~	422525	AA758797	Hs.192807	ESTs	20.0
20	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like 1	20.0
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HEMBA100	20.0
	411529	AA430348	Hs.288837	Homo saplens cDNA FLJ12927 fis, done NT2RP2004	20.0
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	20.0
0.5	403234			predicted exon	19.9
25	427267	Al201185	Hs.119164	ESTs .,	19.9
	400203			predicted exon	19.9
	449296	AL137257	Hs.23458	Homo sapiens mRNA; cDNA DKFZp434C1613 (from	19.9
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	19.9
20	423083	AA321774	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTEIN PH	19.9
30	422112	BE540240	Hs.111783	Lsm1 protein	19.9
	413282	BE078159		gb:CM0-BT0615-140200-175-e06 BT0615 Homo saple	19.9
	453702	AA037637	Hs.42128	ESTs	19.9
	403065			predicted exon	19.9
~~	440633	AJ140686	Hs.263320	ESTs	19.9
35	456994	AA383623	Hs.293616	ESTs	19.9
	458260	R41782	Hs.22279	ESTs	19.9
	452388	BE019696	Hs.29287	retinoblastoma-binding protein 8	19.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	19.9
40	441989	AA306207	Hs.286241	Homo saplens cDNA: FLJ22698 fis, clone HSI12044	19.9
40	418758	AW959311	Hs.87019	ESTs	19.9
	406646	M33600	Hs.180255	major histocompatibility complex, class II, DR beta 1	19.8
	433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	19.8
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid ceramidase)	19.8
45	452321	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen	19.8
45	449713	AW027025	Hs.239262	ESTs	19.8
	458827	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone HSI08080	19.8
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
	441730	A1243276	Hs.149017	ESTs	19.8
50	420701	N42919	Hs.88630	ESTs, Weakly similar to AC007228 1 R31665 2 [H.sap	19.8
50	403642	******		predicted exon	19.8
	408987	H85615	11- 000000	gb:yt03f11.r1 Soares retina N2b5HR Homo sapiens cD	19.8
	446712	AW204789	Hs.209828	ESTs	19.8
	403286		400500	predicted exon	19.8
55	434439	AI022360	Hs.190583	ESTs	19.8
JJ	404067	0000000		predicted exon	19.7 19.7
	455694	BE067300		gb:PM2-BT0349-161299-001-h10 BT0349 Homo sapie	19.7
	403287	A1490E07	Hs.120915	predicted exon ESTs	19.7
	434633	AI189587	Hs.15396		19.7
60	408199 420080	AA132637 M94065	Hs.94925	ESTs dihydroorotate dehydrogenase	19.7
00	408852	AW291435	Hs.254961	ESTs	19.7
	403786	A1123 1403	113.207001	predicted exon	19.7
	416839	H94900	Hs.17882	ESTs .	19.7
	434385	AA631946	Hs.259580	ESTs	19.7
65	446845	Al343645	Hs.156108	ESTs	19.7
05	425612	BE004257	118.100100	gb:CM0-BN0103-180300-296-c04 BN0103 Homo sapi	19.7
	402520	DE004237		predicted exon	19.6
	436098	R20597	Hs.9739	ESTs .	19.6
	438974	AF089816	Hs.6454	chromosome 19 open reading frame 3	19.6
70	430974	AA339541	Hs.24956	hypothetical protein FLJ22056	19.6
70	451310	AW250651	Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.sapiens]	19.6
	435961	BE293127	Hs.283722	GTT1 protein	19.6
	452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
	404850	JE-11000	. 10.200070	predicted exon	19.6
75	438360	H74149	Hs.288193	hypothetical protein FLJ10375	19.6
, 5	436508	AW604381	Hs.121121	ESTs	19.6
	430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	19.6
	407824	AA147884	Hs.9812	ESTs	19.6
	406388		113.3012	predicted exon	19.6
80	430204	AA618335	Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
	457560	Al801934	Hs.163909	ESTs	19.5
	429521	BE048708	Hs.50949	ESTs	19.5
	429758	AW137722	Hs.246804	ESTs	19.5
	441473		Hs.184846	ESTs, Wealty similar to R28830 1 [H.sapiens]	19.5

	411724	AA770559	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L (7.	19.5
	450453	AA009883	Hs.50186	ESTs	19.5
	419687	A1638859	Hs.227699	ESTs, Weakly similar to Yhr217cp [S.cerevisiae]	19.5
5	442162	AW294966	Hs.150849	ESTs	19.5
5	435056	AW023337	Hs.5422	glycoprotein M6B	19.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
	413825 422687	BE299181 AW068823	Hs.75564 Hs.119206	CD151 antigen	19.4 19.4
	435551	AF212365	Hs.5470	insulin-like growth factor binding protein 7 IL-17B receptor	19.4
10	440069	BE617892	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)	19.4
10	432277	AI669790	Hs.161825	ESTs	19.4
	428044	AA093322	Hs.182225	RNA binding motif protein 3	19.4
	456064	AA256213	Hs.72010	ESTs	19.4
	424897	D63216	Hs.153684	frizzied-related protein	19.4
15	424673	AA345051	Hs.294092	ESTs	19.4
	403852	70.0001	110.20 1002	predicted exon	19.3
	405699			predicted exon	19.3
	433096	AU076803	Hs.282975	carboxylesterase 2 (intestine, liver)	19.3
	400344	NM_012368	Hs.258574		19.3
20	417501	AL041219	Hs.82222	sema domain, immunoglobutin domain (Ig), short basic	19.3
	400449			predicted exon	19.3
	453801	AL134751	Hs.23450	mRNA for FLJ00023 protein	19.3
	435849	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
	454181	AW177377		gb:CM4-CT0129-190899-007-e09 CT0129 Homo saple	19.3
25	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	19.3
	406326			predicted exon	19.3
	421921	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
	416700	AW498958	Hs.79572	cathepsin D (lysosomal aspartyl protease)	19.2
20	458857	AI627342	Hs.224601	ESTs	19.2
30	405501			predicted exon	19.2
	416601	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
	425590	A1954686	Hs.158321	beaded filament structural protein 2, phakinin	19.2 19.2
35	428151	AA422028	Hs.169829	gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapiens cDN KIAA1180 protein	19.2
"	426420 414428	BE383808 BE296906	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
	404601	BE230300	115.102023	predicted exon	19.2
	403861			predicted exon	19.2
	448363	BE174595	Hs.366	6-pyruvoylletrahydropterin synthase	19.2
40	406655	M21533	Hs.181244	major histocompatibility complex, class I, A	19.1
	435372	AA809591	Hs.106486	ESTs, Highly similar to CIKG_HUMAN VOLTAGE-G	19.1
	413154	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo saple	19.1
	443021	AA368546	Hs.8904	lg superfamily protein	19.1
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated	19.1
45	412633	AF001691	Hs.74304	periplakin	19.1
	402071			predicted exon	19.1
	410387	A1277367	Hs.47094	ESTs	19.1
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasclclin I-like)	19.1
50	407032	U73799		gb:Human dynactin mRNA, partial cds.	19.0
50	404034			predicted exon	19.0
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudogene	19.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
	426410	BE298446	Hs.180372	BCL2-like 1	19.0 19.0
55	419618 457632	AA528295 AW292151	Hs.112689	gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens cDNA c ESTs	19.0
55	417138	AA193646	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
	417933	X02308	Hs.82962	thymidylate synthetase	19.0
	458808	AW134832	Hs.246295	ESTs	19.0
	415860	D56051	Hs.78888	diazepam binding inhibitor (GABA receptor modulator	18.9
60	440919	AW291274	Hs.262826	ESTs	18.9
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
	401747			predicted exon	18.9
	454209	AW179083		gb:MR4-ST0065-270899-006-A07 ST0065 Homo sapi	18.8
~	417661	T84155	Hs.15464	Homo sapiens cDNA: FLJ21351 fis, clone COL02762	18.8
65	426499	C14937	Hs.11169	Gene 33/Mig-6	18.8
	404240			predicted exon	18.8
	439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
	401789	******		predicted exon	18.8
70	456952	AW445081	Hs.301469	ESTs SOT-	18.8
70	439739	Al199391	Hs.124464	ESTs	18.8 18.8
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence mitogen-activated protein kinase 13	18.8
	427490	Z95152	Hs.178695	ESTs	18.8
	443482	AW188093 BE390652	Hs.250385	gb:601286820F1 NIH_MGC_44 Homo saplens cDNA	18.8
75	411420 435196	F35675	Hs.188128	ESTs, Moderately similar to ALUB_HUMAN !!!! ALU	18.8
, ,	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2	18.8
	413531	AL036958	Hs.75416	DAZ associated protein 2	18.7
	428981	BE313077	Hs.93135	ESTs	18.7
	421598	AW630942	Hs.106061	RD RNA-binding protein	18.7
80	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding protein	18.7
	406754	AA477223	Hs.75922	brain protein 13	18.7
	400661			predicted exon	18.7
	442638	AI088742	Hs.134713	ESTs	18.7
	434169	AA883752	Hs.179724	ESTs	18.7
				440	

	424126 408473	AA335635 BE259039	Hs.96917	ESTs	18.7 18.7
	401962	BE239039	Hs.129953	Ewing sarcoma breakpoint region 1 predicted exon	18.7
_	447326	AW002252	Hs.201395	ESTs	18.7
5	459053 403362	Al807052	Hs.210361	ESTs predicted exon	18.7 18.7
	427697	T18997	Hs.180372	BCL2-like 1	18.7
	402061	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
10	433785 405423	BE044593	Hs.112704	ESTs predicted exan	18.7 18.6
10	429259	AA420450	Hs.292911	ESTs	18.6
	444071	A1627808	Hs.110524	ESTs	18.6
	410512	AA085603	Hs.250570 Hs.236816	ESTs ESTs	18.6 18.6
15	440376 457353	A1024452 X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotropic hormone)	18.6
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily e	18.6
	415602	F12920	Hs.165575	ESTs endomucin-2	18.6 18.6
	407891 455910	AA486620 Z43712	Hs.41135	gb:HSC1JA121 normalized Infant brain cDNA Homo s	18.6
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig), short basic	18.6
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	18.6
	428125 406457	AA393071	Hs.182579	leucine aminopeplidase predicted exon	18.6 18.5
	446625	Al333070	Hs.156141	ESTs	18.5
25	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5 18.5
	423103 443549	AA322029 T89608	Hs.16601	gb:EST24685 Cerebellum II Homo sapiens cDNA 5' en ESTs	18.5
	419299	AI311085	Hs.62406	Homo saplens cDNA: FLJ22573 fis, clone HSI02387	18.5
20	411942	AW877015	11 440400	gb:QV2-PT0010-250300-096-f12 PT0010 Homo sapien	18.5
30	442440 454574	BE464435 AW809109	Hs.146180	ESTs, Weakly similar to non-receptor protein tyrosine k gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapie	18.5 18.5
	454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, tha	18.5 18.4
33	420603 401373	AB042636	Hs.4775	junctophilin 3 predicted exon	18.4
	402292			predicted exon	18.4
	444118	AA458542	Hs.10326	coatomer protein complex, subunit epsilon	18.4 18.4
40	408310 411236	AW179023 AW833752		gb:PM3-ST0036-170899-001-e08 ST0036 Homo saple gb:QV4-TT0008-130100-077-b07 TT0008 Homo saple	18.4
	431405	Al470895	Hs.252574	ribosomal protein L10a	18.4
	441408	A1733249	Hs.126897	ESTs	18.4 18.4
	453994 444518	BE180964 Al160278	Hs.165590 Hs.146884	ribosomal protein S13 ESTs	18.4
45	402407			predicted exon	18.4
	404270	AC054007	Un 442200	predicted exon	18.4 18.4
	409103 415198	AF251237 AW009480	Hs.112208 Hs.943	XAGE-1 protein natural killer cell transcript 4	18.3
	430771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3
50	432636	AA340864 NM_014874	Hs.278562 Hs.3363	claudin 7 KIAA0214 gene product	18.3 18.3
	433504 415606	W70022	15.5505	gb:zd51e10.r1 Soares_fetal_heart_NbHH19W Homo sa	18.3
	401401	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R28379	18.3
55	420758 457520	AW297536 AA553495	Hs.33053 Hs.162264	ESTs ESTs	18.3 18.3
55	432323	AK001409	Hs.274356	hypothetical protein FLJ10547	18.3
	404750			predicted exon	18.3
	450645	AL117441 . Al299144	Hs.25264 Hs.150797	DKFZP434N126 protein ESTs	18.3 18.3
60	445160 418461	BE242781	Hs.288037	Homo sapiens cDNA FLJ12999 fis, clone NT2RP3000	18.3
	401809			predicted exon	18.3
	458121 435106	S42416 AA100847	Hs.74647 Hs.193380	Human T-cell receptor active alpha-chain mRNA from ESTs, Highly similar to AF174600 1 F-box protein Fbx	18.3 18.3
	448398	AW444655	Hs.170838	ESTs	18.3
65	428145	BE243327	Hs.182626	chromosome 22 open reading frame 5	18.2
	445302		Hs.12488	hypothetical protein FLJ10675 gb:yp76h12.r1 Soares fetal liver spleen 1NFLS Homo s	18.2 18.2
	407352 413190		Hs.40368	adaptor-related protein complex 1, sigma 2 subunit	18.2
70	436371	Al821912	Hs.113912	ESTs	18.2
70	400965 433427		Hs.171889	predicted exon cholinephosphotransferase 1	18.2 18.2
	427504		Hs.191589	ESTs	18.2
	426759	A1590401	Hs.21213	ESTs	18.2
75	423792 406826		Hs.245854 Hs.84298	ESTs CD74 antigen (invariant polypeptide of major histocom	18.2 18.1
	406659		Hs.277477	major histocompatibility complex, class 1, C	18.1
	437453	AI761350	Hs.181391	hypothetical protein DKFZp761G2113	18.1
	409276 449628		Hs.278429 Hs.197713	hepatocellular carcinoma-associated antigen 59 ESTs	18.1 18.1
80	421043		Hs.89072	ESTs	18.1
	442344	AI022925	Hs.301212	ESTs	18.1
	448744 416062		Hs.9469 Hs.74427	phosphoinositol 3-phosphate binding protein-1 p53-induced protein	18.1 18.1
	414500		Hs.76285	DKFZP564B167 protein	18.1

				and the second second	
	427272	NM_001096	Hs.174140	ATP citrale lyase	18.1
	403964 433217	AB040914	Hs.278628	predicted exon KIAA1481 protein	18.1 18.1
	427902	AI809202	Hs.208343	ESTs, Weakly similar to cerebroside sulfotransferase [H	18.1
5	449586	Al863918	Hs.195078	ESTs	18.1
	430826	U10061	Hs.248019	POU domain, class 4, transcription factor 3	18.1
	414195	BE263293		gb:601144881F2 NIH_MGC_19 Homo saplens cDNA	18.1
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
10	411088	BE247593	Hs.145053	ESTs	18.1
10	419407 407938	AW410377 AA905097	Hs.41502	Homo sapiens cDNA: FLJ21276 fis, clone COL01829	18.1
	449360	A1640623	Hs.85050 Hs.252720	phospholamban ESTs	18.1 18.1
	417286	AA122237	Hs.81874	microsomal glutathlone S-transferase 2	18.0
	405515			predicted exon	18.0
15	439319	AW016401	Hs.233476	ESTs	18.0
	419387	BE379356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface antig	18.0
	414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C)	18.0
	447778 435523	BE620592 T62849	Hs.71190 Hs.11090	ESTs	18.0
20	429230	AF088991	Hs.198274	high affinity immunoglobulin epsilon receptor beta sub NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0 18.0
	457822	AA970001	Hs.150319	ESTs -	18.0
	442424	Al342715	Hs.129569	ESTs, Moderately similar to B34087 hypothetical prote	18.0
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	18.0
25	413477	Al815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein [M	18.0
25	405277	4 4 0004 40	11- 04500	predicted exon	18.0
	450192 442191	AA263143 W95186	Hs.24596 Hs.8136	RAD51-interacting protein endothelial PAS domain protein 1	18.0 18.0
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
	406744	AA554082	Hs.279860	hypothetical protein FLJ20030	17.9
30	425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
	414387	AL043148	Hs.186257	ESTs	17.9
	411811	AW864370	H- 2000	gb:PM4-SN0016-100500-004-h09 SN0016 Homo sapie	17.9
	433882 414333	U90441 BE274897	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro gb:601122959F1 NIH_MGC_20 Homo sapiens cDNA	17.9 17.9
35	403747	DC214031		predicted exon	17.9
	435542	AA687376	Hs.269533	ESTs	17.9
	403093			predicted exon	17.9
	412088	A1689496	Hs.108932	ESTs	17.9
40	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
40	404763 454633	A14/044200		predicted exon	17.9 17.9
	440788	AW811380 AI806594	Hs.128577	gb:IL3-ST0143-290999-019-D05 ST0143 Homo sapien ESTs	17.9
	411800	N39342	Hs.5184	TH1 drosophila homolog	17.9
4.5	441361	BE263308	Hs.7797	TERF1 (TRF1)-interacting nuclear factor 2	17.8
45	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof	17.8
	405333 408297	D17710	Un 112214	predicted exon ESTs	17.8 17.8
	403036	R17710	Hs.113314	predicted exon	17.8
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	17.8
50	417091	AA193283	Hs.291990	ESTs	17.8
	440789	AB007857	Hs.7416	KIAA0397 gene product	17.8
	438397	AA806478	Hs.123206	ESTS	17.8
	435948 450273	AA702675 AW296454	Hs.114135 Hs.24743	ESTs	17.8 17.8
55	435969	W85773	Hs.191386	hypothetical protein FLJ20171 ESTs	17.8
•	427031	AA397601	Hs.125147	ESTs	17.8
	454505	AW801365		gb:IL5-UM0067-240300-050-a01 UM0067 Homo sapi	17.8
	403447			predicted exon	17.8
60	433297	AV658581	Hs.282633	ESTS	17.8
UU	443326 448283	BE156494 Al340462	Hs.188478 Hs.182979	ESTs ribosomal protein L12	17.8 17.8
	458067	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22834 fis, clone KAIA4314	17.8
	452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	17.8
6	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo saplens cDN	17.8
65	450911	AA011586	Hs.272097	ESTs	17.7
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, receptor for, gamma	17.7 17.7
	407082 415271	Z47055 X94232	Hs.78335	gb:Human partial cDNA sequence, famesyl pyrophosph microtubule-associated protein, RP/EB family, member	17.7
	417413	AA197072	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.7
70	408937	AA210734	Hs.291386	ESTs	17.7
	433459	AA593498		gb:nn27b05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA	17.7
	459536	AI254723	Hs.145496	ESTS	17.7
	428500 433463	AI815395 R41963	Hs.184641 Hs.4197	delta-6 fatty acid desaturase ESTs	17.7 17.7
75	406537	141903	N5.4131	predicted exon	17.7
. –	410003	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo	17.7
	440857	AA907808	Hs.135556	ESTs	17.7
	451072	AA013451	Hs.117929	ESTs	17.7
90	418693	AI750878	Hs.87409	thrombospondin 1	17.7
80	443624	BE616129	Hs.9651	related RAS viral (r-ras) oncogene homolog	17.6
	422626 410756	AA344932 AB037820	Hs.118786 Hs.66159	metallothionein 2A KIAA1399 protein	17.6 17.6
	436621	A1266254	Hs.132929	ESTs	17.6
	453317	NM_002277	Hs.41696	keratin, hair, acidic,1	17.6
				•	

	456828	AF156889	Hs.148427	LIM homeobox protein 3	17.6
	421486	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.6
	428834	AW899713	Hs.10338	· ESTs	17.6
5	451419	R36309	Hs.174369	EST	17.6
5	448413	A1745379	Hs.42911	ESTs .	17.6
	424323 423943	AA338791	Hs.146763 Hs.135756	nascent-polypeptide-associated complex alpha polypept	17.6
	439423	AF163570 BE536678	Hs.147099	polymerase (DNA-directed) kappa ESTs	17.6 17.6
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
10	408246	N55669	Hs.43946	L13 protein	17.6
10	441579	AW468847	Hs.127194	ESTs	17.5
	420867	NM_014183	Hs.100002	HSPC162 protein	17.5
	453680	AL079647	Hs.14485	ESTs	17.5
_	400202			predicted exon	17.5
15	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	17.5
	409932	Al376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
	425563	AF084199	Hs.299837	ESTs	17.5
	440475	Al807671	Hs.128343	ESTs	17.5
20	452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
20	410570	Al133096	Hs.64593	ATP synthase, H+ transporting, mitochondrial F1F0, su	17.4
	419600	AA448958	Hs.91481	NEU1 protein	17.4
	419588	Al347205	Hs.91375	Human clone 23614 mRNA sequence	17.4
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase kinase 6	17.4
25	448928	Al350260	Hs.5384	Homo sapiens cDNA FLJ11743 fis, clone HEMBA100	17.4
23	403924	AA251600		predicted exon gb:zs10d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA	17.4 17.4
	419889 405023	AW408800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
	426065	N32049	113.104003	gb:yw96g08.s1 Soares_placenta_8to9weeks_2NbHP8to	17.4
	453199	Al336266	Hs.301854	Homo sapiens PRO0412 mRNA, complete cds	17.4
30	455132	AW857955		gb:PM0-CT0325-151299-002-A12 CT0325 Homo sapi	17.4
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger domain, 1A	17.4
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	17.3
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
	417935	R53697	Hs.170044	ESTs	17.3
35	430050	AA430993	Hs.227913	API5-like 1	17.3
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrate 1	17.3
	425996	W67330	Hs.81256	\$100 calcium-binding protein A4 (calcium protein, calv	17.3
	416964	D87467	Hs.80620	guanine nucleolide exchange factor for Rap1; M-Ras-re	17.3
40	437418	A1478954	Hs.59459	ESTs	17.3
40	447255 402203	AI884908	Hs.158607	ESTs predicted exon	17.3 17.3
	417611	AW993983		gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapie	17.3
	426560	AA381661	Hs.119878	ESTs	17.3
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010	17.3
45	445017	Al205493	Hs.176860	ESTs	17.3
	438658	AI222068	Hs.123571	ESTs ·	17.3
	442238	AW135374	Hs.270949	ESTs	17.3
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002	17.3
50	442609	AL020996	Hs.8518	selenoprotein N	17.2
50	416591	AA091976	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2 17.2
	403674 430514	AA318501	Hs.241587	predicted exon megakaryocyte-enhanced gene transcript 1 protein	17.2
	411696	AW857404	113.241301	gb:CM3-CT0313-291199-046-c11 CT0313 Homo saple	17.2
	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	17.2
55	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
	414364	D38521	Hs.75935	KIAA0077 protein	17.2
	409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
	425640	U34051	Hs.299204	ESTs, Highly similar to CD5S_HUMAN CYCLIN-DE	17.2
60	436044	BE247571	Hs.15627	Nit protein 2	17.2
60	401657	A1900440	11- 440044	predicted exon	17.2
	449763	AI822112	Hs.118241	ESTs	17.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2 17.2
	449636 444958	Al656608 AW292643	Hs.281328 Hs.167047	ESTs ESTs	17.2
65	429978	AA249027	Hs.241507	ribosomal protein S6	17.2
05	453043	AW136440	Hs.224277	ESTs	17.2
	458640	Al284935	110.227211	gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens cDNA	17.1
	456329	T41418		gb:ph1h3_19/1TV Outward Alu-primed hncDNA librar	17.1
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	17.1
70	403662			predicted exon	17.1
	411651	AW855392		gb:CM3-CT0275-191099-024-e12 CT0275 Homo saple	17.1
	404097			predicted exon	17.1
	447252	R90916		gb:yn01e10.r1 Soares adult brain N2b4HB55Y Homo s	17.1
75	430024	AI808780	Hs.227730	integrin, alpha 6	17.1
13	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerst ESTs	17.1 17.1
	444558 420869	AW181975 X58964	Hs.165892 Hs.123638	regulatory factor X, 1 (influences HLA class II expressi	17.1
	420859 448812	H30775	Hs.123636 Hs.22140	BM88 antigen	17.1
	431777	AA570296	Hs.105470	found in inflammatory zone 1	17.0
80	422007	A1739435	Hs.39168	ESTs	17.0
	403051			predicted exon	17.0
	402427			predicted exon	17.0
	417408	F17211	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.0
	450598	AF151076	Hs.25199	hypothetical protein	17.0

	404404			TOLANG	
	421121	AA459028	Hs.86228	TRIAD3 protein	17.0
	458488 417158	AL040565	Hs.209544 Hs.110062	ESTS	17.0
	439318	AW965223 AW837046	Hs.6527	ESTs, Weakly similar to ACR3_HUMAN 30 KD ADIP	17.0 17.0
5	428758	AA433988	Hs.98502	G protein-coupled receptor 56 Homo sapiens cDNA FLJ14303 fis, clone PLACE2000	17.0
•	447572	Al631546	Hs.159732	ESTs	17.0
	434434	AA633516	Hs.157201	ESTs	17.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	17.0
	408927	AW295650	Hs.255453	ESTs	17.0
10	439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	17.0
	454466	AA984138	Hs.279895	Homo sapiens mRNA for KIAA1578 protein, partial cd	17.0
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone HEP03447,	17.0
	436659	AI217900	Hs.144464	ESTS	17.0
15	422731	AL138411	11 400700	gb:DKFZp434A1229_r1 434 (synonym: htes3) Homo s	17.0
15	429294	AA095971	Hs.198793	KIAA0750 gene product	17.0
	432847	BE266941	Hs.279554	proteasome (prosome, macropain) 26S subunit, non-AT	16.9 16.9
	416977 406827	AW130242 AA971409	Hs.293476 Hs.84298	ESTs CD74 antigen (invariant polypeptide of major histocom	16.9
	453758	U83527	F15.04250	gb:HSU83527 Human fetal brain (M.Lovett) Homo sap	16.9
20	431314	AI732204	Hs.105423	ESTs	16.9
	423185	BE299590	·Hs.125078	omithine decarboxylase antizyme 1	16.9
	435086	AW975243	Hs.122596	ESTs	16.9
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapie	16.9
	456251	R13326	Hs.21303	ESTs	16.9
25	456327	H68741	Hs.38774	ESTs .	16.9
	450594	N31036		gb:yx51g04_r1 Soares melanocyte 2NbHM Homo saple	16.9
	428177	AA423967	Hs.178113	ESTs, Moderately similar to kinesin like protein 9 [M.m	16.9
	453250	AI346520	Hs.121619	chromosome 11 open reading frame 15	16.9
30	418294	AF061739	Hs.83954	protein associated with PRK1	16.9
υV	446546 421100	BE167687 AW351839	Hs.156628 Hs.124660	ESTs Homo sapiens cDNA: FLJ21763 fis, clone COLF6967	16.9 16.9
-	455993	BE179085	FIS. 124000	gb:RC0-HT0613-140300-021-d06 HT0613 Homo sapie	16.9
	459375	BE251770		gb:601112470F1 NIH_MGC_16 Homo sapiens cDNA	16.9
	454803	AW860148		gb:RC0-CT0379-290100-032-b10 CT0379 Homo sapie	16.9
35	445474	Al240014	Hs.259558	ESTs	16.9
	443198	AI039813		gb:ox49d06.x1 Soares_total_fetus_Nb2HF8_9w Homo	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glucose transporter),	16.9
40	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone HSi06009	16.9
40	416913	AW934714	Us 000Cf	gb:RC1-DT0001-031299-011-a11 DT0001 Homo sapie	16.9 16.9
	419355 452975	AA428520 M85521	Hs.90061 Hs.69469	progesterone binding protein dendritic cell protein	16.9
	432525	Al796096	Hs.109414	ESTs	16.8
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	16.8
45	437270	R18087	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmemb	16.8
	408007	AW135965	Hs.246783	ESTs	16.8
	450954	Al904740	Hs.25691	receptor (calcitonin) activity modifying protein 3	16.8
	402958		11: 04000	predicted exon	16.8
50	445656	W22050	Hs.21299 Hs.170298	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8 16.8
50	410684 437669	AA088500 Al358105	Hs.123164	ESTs ESTs, Weakly similar to match to ESTs AA667999 [H.	16.8
	447869	AW139113	Hs.164307	ESTs	16.8
	458025	Al275406		gb:ql63c10.x1 Soares_NhHMPu_S1 Homo saplens cDN	16.8
	445614	AV660763	Hs.110675	apolipoprotein C-IV	16.8
55	454610	AW810224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo saple	16.8
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	16.8
	422105	AI929700	Hs.111680	endosulfine alpha	16.8
	444788	AI871122	Hs.202821	ESTs	16.8
60	414057	AI815559	Hs.75730	signal recognition particle receptor ('docking protein')	16.8
UU	408822 433379	AW500715 AA586368	Hs.57079 Hs.190232	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000 ESTs	16.8 16.8
	441552	AA300300 AA937975	113,130232	gb:oc08e12.s1 NCI_CGAP_GCB1 Homo sapiens cDN	16.8
	403582	.4201313		predicted exon	16.8
	433871	W02410	Hs.205555	ESTs	16.8
65	439509	AF086332	Hs.58314	ESTs	16.8
	431639	AK000680	Hs.266175	phosphoprolein associated with GEMs	16.8
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	16.8
	401465			predicted exon	16.8
70	448913	AA194422	Hs.22564	myosin VI	16.8
70	410261	AF145713 BE244219	Hs.61490	schwannomin interacting protein 1	16.8 16.7
	421199 450489	A1697990	Hs.102497 Hs.224375	paxillin ESTs	16.7
	410186	AW602528	110.224010	gb:RC5-BT0562-260100-011-A02 BT0562 Homo sapi	16.7
	447224	BE617125		gb:601441664F1 NIH_MGC_65 Homo sapiens cDNA	16.7
75	403010			predicted exon	16.7
	404881	·		predicted exon	16.7
	445572	A1243445	Hs.189654	ESTs	16.7
	419440	AB020689	Hs.90419	KIAA0882 protein	16.7
80	443406	A1056238	Hs.143316	ESTs ESTs Highly similar to d 1745C22 1 fH septence	16.7
90	457901 448364	AW207023 T08958	Hs.250497 Hs.16561	ESTs, Highly similar to dJ745C22.1 [H.sapiens] HSPC141 protein	16.7 16.6
	446364	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (16.6
	401847			predicted exon	16.6
	429523	AK000788	Hs.205280	Homo saplens cDNA FLJ20781 fis, clone COL04235	16.6
			•		

	432845	Al989751	Hs.150378	ESTs	16.6
	400246			predicted exon	16.6
	404971			predicted exon	16.6
_	422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
5	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
	432201	AI538613	Hs.135657	ESTs	16.6
	456993	AL134577	Hs.200302	ESTs	16.6
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
	444060	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fis, clone COL09512	16.6
10	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
10	448199	Al953278	Hs.170557	ESTs	16.6
	443422	R10288	Hs.301529	ESTs	16.6
		K10200	113.301323	predicted exon	16.6
	401117				16.6
15	400613	4.400.4004	14-050044	predicted exon	16.6
13	431214	AA294921	Hs.250811	v-ral simian leukemia viral oncogene homolog B (ras re	
	431649	AL133077	Hs.266746	Homo sapiens cDNA: FLJ22615 fis, clone HSI05118	16.5
	421335	X99977	Hs.103505	ARS component B	16.5
	427154	AL137262	Hs.288991	Homo sapiens cDNA: FLJ22523 fis, clone HRC12507	16.5
20	401010			predicted exon	16.5
20	436678	BE512828	Hs.5273	NADH dehydrogenase (ublquinone) Fe-S protein 3 (30k	16.5
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-Inducible protein CG12-1	16.5
0.5	437623	D63880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
25	401244			predicted exon	16.5
	415167	AA160784	Hs.26410	ESTs	16.5
	438291	BE514605	Hs.289092	Homo saplens cDNA: FLJ22380 fis, clone HRC07453,	16.5
	405183			predicted exon	16.5
\	436480	AJ271643	Hs.87469	putative acid-sensing Ion channel	16.5
30	456691	Al023428	Hs.205696	ESTs	16.5
	418332	R34976	Hs.78293	ESTs	16.5
	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
	444859	AW449137	Hs.157487	ESTs	16.5
	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
35	400891	A11370100	1 2.7 0000	predicted exon	16.5
55	448372	AW445166	Hs.170802	ESTs	16.5
	425798	AA364002	1 10.170002	gb:EST74529 Pineal gland II Homo saplens cDNA 5' en	16.5
	459253	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (from c	16.5
			Hs.197488	ESTs	16.4
40	420746	AW195932	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
-1 0	414717	BE271039	FIS.77000		16.4
	400727	NIA 00220E	Un 440254	predicted exon	16.4
	422691	NM_003365	Hs.119251	ubiquinol-cytochrome c reductase core protein I	
	405639	0.5000504		predicted exon	16.4
15	414444	BE298594	11- T000F	gb:601119754F1 NIH_MGC_17 Homo saplens cDNA	16.4
45	456146	AL034349	Hs.79005	protein tyrosine phosphatase, receptor type, K	16.4
	414610	BE388044		gb:601283747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401268			predicted exon	16.4
5 0	403613			predicted exon	16.4
50	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4
	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	16.4
	452114	N22687	Hs.8236	ESTs	16.4
	404638	-		predicted exon	16.4
	404600			predicted exon	16.3
55	448855	AF070574	Hs.22316	Homo saplens clone 24819 mRNA sequence	16.3
	406629	AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
	450957	BE515202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
	449966	H60542	Hs.37848	ESTs	16.3
<i>c</i> c	402585			predicted exon	16.3
60	436008	Al078428	Hs.58785	ESTs	16.3
	401492		a	predicted exon	16.3
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405088			predicted exon	16.3
·	437345	BE259522	Hs.5556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
65	432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	16.3
	428801	AW277121	Hs.254881	ESTs	16.3
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
	452998	BE019681	Hs.6019	Homo saplens cDNA: FLJ21288 fis, clone COL01927	16.3
70	439938	Al147392	Hs.124607	ESTs	16.3
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	16.3
	.446081	AA972412	Hs.13755	F-box and WD-40 domain protein 2	16.3
	443534	AI076123		gb:oy92e04.x1 Soares_fetal_liver_spleen_1NFLS_S1 H	16.3
	459510	AA076706		gb:7801802 Chromosome 7 Fetal Brain cDNA Library	16.3
75	450517	AI523755	Hs.59236	ESTs, Weakly similar to B35049 ankyrin 1, erythrocyte	16.3
. •	451938	Al354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negative	16.3
	454478	AW805749		gb:QV1-UM0105-180400-162-f10 UM0105 Homo sap	16.2
	407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
	406580	· - 1.1,2070		predicted exon	16.2
80	409452	BE336714	Hs.289271	cytochrome c-1	16.2
00	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
			113.473733	gb:AV660856 GLC Homo sapiens cDNA clone GLCG	16.2
	458710	AV660856	Ue 25277	hypothetical protein FLJ21065	16.2
	450657	AK001579	Hs.25277		16.2
	404230			predicted exon	10.2
				102	

	439471	W69839	Hs.58033	ESTs	16.2
	400848	A A 400000	Ll= 402700	predicted exon	16.2
	428797 416272	AA496205 AA178882	Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (from c	16.2
5	444465	Al206592	Hs.143843	gb:zp38b09.r1 Stratagene muscle 937209 Homo sapiens ESTs	16.2 16.2
•	431257	AF039597	113.170070	gb:Homo sapiens Ku86 autoantigen related protein 1 (K	16.2
	447775	BE179318		gb:RC1-HT0615-290300-021-g05 HT0615 Homo sapie	16.2
	403833			predicted exon	16.2
10	444140	AV648089	Hs.282383	ESTs	16.2
10	446102	AW168067	Hs.252956	ESTs	16.2
	416475	T70298		gb:yd26g02.s1 Soares fetal liver spleen 1NFLS Homo s	16.2
	430783	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
	414070 444283	AW963783 Al138971	Hs.154636	gb:EST375856 MAGE resequences, MAGH Horno sap ESTs	16.2 16.2
15	405599	X92715	Hs.3057	zinc finger protein 74 (Cos52)	16.2
13	409427	AW389668	113.0001	gb:RC2-ST0168-071299-013-f06 ST0168 Homo sapien	16.2
	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
	435380	AA679001	Hs.192221	ESTs	16.2
20	406752	AI285598	Hs.217493	annexin A2	16.2
20	406096	F12200	Hs.5811	chromosome 21 open reading frame 59	16.2
	417551	Al816291	Hs.82273	hypothetical protein	16.2
	441252	AW360901	Hs.183047	ESTs, Weakly similar to unnamed protein product (H.s	16.2
	419608	AL037237	Hs.91586	transmembrane 9 superfamily member 1	16.1
25	438894 451287	Al630819 AK002158	Hs.300431 Hs.26194	ESTs hypothetical protein FLJ11296	16.1 16.1
	412499	AW956916	Hs.11238	KIAA0622 protein; Drosophila "multiple asters" (Mast	16.1
	433355	AI808235	110.11200	gb:wf44e01.x1 Soares_NFL_T_GBC_S1 Homo saplen	16.1
	416818	AI986408	Hs.204766	ESTs, Weakly similar to B48013 proline-rich proteogly	16.1
	438765	Al031888	Hs.132594	ESTs	16.1
30	424470	BE244261	Hs.5615	nuclear RNA export factor 1	16.1
	416194	H27114	Hs.301212	ESTs	16.1
	446702	R44518	Hs.143496	ESTs	16.1
	414222	AL135173	Hs.878 Hs.209022	sorbitol dehydrogenase	16.1
35	443122 448648	AI806656 BE614345	Hs.159089	ESTs, Weakly similar to Pro-Pol-dUTPase polyprotein ESTs	16.1 16.1
33	456394	W28506	(13.103003	gb:48f1 Human relina cDNA randomly primed sublibra	16.1
	445887	AI263105	Hs.145597	ESTs	16.1
	412332	AW937661	Hs.288324	Homo sapiens cDNA FLJ13283 fis, clone OVARC1001	16.1
40	403912			predicted exon	16.1
40	441446	R66269	Hs.28714	ESTs	16.1
	403153	A)ACTOCOC	11- 440500	predicted exon	16.0
	444907 421946	AW772596	Hs.148586 Hs.109773	ESTs	16.0 16.0
	421940	R99629 AW410681	Hs.5648	hypothetical protein FLJ20625 proteasome (prosome, macropain) 26S subunit, non-AT	16.0
45	407752	AA573581	Hs.13328	ESTs	16.0
	447953	AI804218	Hs.209614	Homo saplens cDNA: FLJ22343 fis, clone HRC06043	16.0
	425708	AK001342	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone HRC12866	16.0
	421449	AA713491	Hs.291501	ESTs	16.0
50	418323	NM_002118	Hs.1162	major histocompatibility complex, class II, DM beta	16.0
30	447787	BE620108	Hs.124475	gb:601483015F1 NIH_MGC_69 Homo sapiens cDNA ESTs	16.0
	422716 443958	AI702835 BE241880	Hs.10029	cathepsin C	16.0 16.0
	417908	AA207221	1.0.10020	gb:zq55h04.s1 Stratagene neuroepithelium (937231) Ho	16.0
	438542	AA810131	Hs.123317	ESTs	16.0
55	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor, alpha polypeptid	16.0
	456825	H67220	Hs.146406	nitrilase 1	16.0
	431360	NM_000427	Hs.251680	loricrin	16.0
	414266	BE267834	11- 400700	gb:601124428F1 NIH_MGC_8 Homo sapiens cDNA c	16.0
60	440571	AA904461	Hs.130798 Hs.270149	ESTs ESTs	16.0
00	426075 413488	AW513691 BE144017	Hs.270149 Hs.184693	transcription elongation factor 8 (SIII), polypeptide 1 (1	16.0 16.0
	446767	Al380107	Hs.158954	ESTs	16.0
	418008	W56044	Hs.211556	Homo sapiens cDNA: FLJ23378 ffs, clone HEP16248	16.0
	404239			predicted exon	16.0
65	458401	AW236939	Hs.172154	ESTs	16.0
	412955	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
	423072	A1792946	Hs.123116	solute carrier family 12 (sodium/potassium/chloride tran	15.9
	444954 449023	AW247076 Al623261	Hs.12163 Hs.248875	eukaryotic translation initiation factor 2, subunit 2 (beta ESTs	15.9 15.9
70	435729	BE048886	Hs.275017	EST	15.9
. •	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	15.9
	413047	H02209		gb:yj38c09.r1 Soares placenta Nb2HP Homo saplens cD	15.9
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	15.9
75	446863	AW614370	Hs.254620	ESTs	15.9
75	448564	AL044962	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3	15.9
	455640	BE064059	De 150150	gb:QV3-BT0296-010300-111-e04 BT0296 Homo sapie	15.9
	404345 418512	AA730407 AW498974	Hs.159156 Hs.89981	protocadherin 11 diacykriycerol kinase, zeta (104kD)	15.9 15.9
	411551	AW851309	110.00001	qb:IL3-CT0220-170200-067-C11 CT0220 Homo saplen	15.9
80	446726	AW300144	Hs.209209	Homo sapiens cDNA FLJ11629 fis, clone HEMBA100	15.9
	410748	BE383816	Hs.136005	ESTs, Highly similar to bG115G20.2 [H.sapiens]	15.9
	449618	AI076459	Hs.14366	Homo saplens cDNA FLJ12819 fis, clone NT2RP2002	15.9
	429697	AW296451	Hs.24605	ESTs	15.9
	424012	AW368377	Hs.137569	turnor protein 63 kDa with strong homology to p53	15.9
				104	

	100151				
	403151 452363	AIEOGTAG	Un 04052	predicted exon	15.8
	432303	AI582743 AF135024	Hs.94953 Hs.165296	ESTs, Highly similar to C1QC_HUMAN COMPLEME kallikrein 13	15.8 15.8
	432826	X75363	Hs.250770	kallikrein 15	15.8
5	431972	Al805145	Hs.191711	ESTs	15.8
	400269			predicted exon	15.8
	404703	Al904493	Hs.99890	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
	449335 418443	AW150717 NM_005239	Hs.296176 Hs.85146	STAT induced STAT inhibitor 3 v-ets avian erythrobiastosis virus E26 oncogene homolo	15.8 15.8
10	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (from	15.8
	433782	AF090945		gb:Homo sapiens clone HQ0670	15.8
	406473			predicted exon	15.8
	420831	AA280824	Hs.190035	ESTs	15.8
15	402939 405196			predicted exon predicted exon	15.8 15.8
13	452947	AW130413		gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	15.8
	414170	AA335996	Hs.3743	matrix metalloproteinase 24 (membrane-inserted)	15.B
	437133	AB018319	Hs.5460	KIAA0776 protein	15.8
20	458356	AI024855	Hs.131575	ESTs	15.8
20	407857 405687	Al928445	Hs.92254	hypothetical protein FLJ20163 predicted exon	15.8 15.8
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	15.8
	408662	AW247699	Hs.105897	ESTs	15.7
25	448338	A1492857		gb:th72h08.x1 Soares_NhHMPu_S1 Homo sapiens cDN	15.7
25	402694	414/07/47/	II- 000070	predicted exon	15.7
	430224 458792	AW675175 N56666	Hs.235975	hypothetical protein DKFZp434D0412 gb:yw75e02.r1 Soares_placenta_8to9weeks_2NbHP8to	15.7 15.7
	402944	1450000		predicted exon	15.7
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor 5A	15.7
30	408661	AW247625		gb:2820094.5prime NiH_MGC_7 Homo sapiens cDNA	15.7
	423238	AA323569	Hs.280482	ESTs	15.7
	421517 429865	AB018352	Hs.105399 Hs.225968	KIAA0809 protein	15.7 15.7
	440815	AB023217 AW071945	Hs.7436	KIAA1000 protein putative acyltransferase	15.7
35	400634		110111100	predicted exon	15.7
	451034	AL050341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	457571	Al375726	Hs.279918	hypothetical protein	15.7
	450105 407464	BE281124 AJ276396	Hs.288013	similar to yeast BET3 (S. cerevisiae) gb:Homo sapiens mRNA for matrix extracellular phosp	15.7 15.7
40	439465	AF086285		gb:Homo sapiens full length insert cDNA clone ZD47B	15.7
. •	451837	T92157	Hs.16970	ESTs	15.7
	435313	A1769400	Hs.189729	ESTs	15.7
	402738	*******		predicted exon	15.7
45	432966 457666	AA650114 AW470302	Hs.129663	gb:ns92h09.s1 NCI_CGAP_Pr3 Homo saplens cDNA c ESTs	15.7 15.7
73	401269	A1147 0302	113.123003	predicted exon	15.7
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
	418846	AI821602	Hs.115127	ESTs	15.6
50	448891	AI587332	Hs.209115	ESTs	15.6 15.6
50	445930 421254	AF055009 AK001724	Hs.13456 Hs.102950	Homo sapiens clone 24747 mRNA sequence coat protein gamma-cop	15.6
	447073	AW204821	Hs.157726	ESTs	15.6
	445438	AB014578	Hs.12707	KIAA0678 protein	15.6
55	432126	AA865239	Hs.55144 Hs.139263	ESTS	15.6 15.6
55	424091 440832	AF235097 Al057548	Hs.128224	calcium channel, voltage-dependent, alpha 1F subunit ESTs	15.6
	449228	AJ403107	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-004 [H.sapie	15.6
	434253	Al393345	Hs.116215	ESTs	15.6
60	459270	AL039604		gb:DKFZp434E2211_r1 434 (synonym: htes3) Homo s	15.6
60	454425 412055	AW300927 AA099907	Hs.27192 Hs.271806	hypothetical protein dJ1057B20.2 ESTs	15.6 15.6
	400837	AA033307	115.271000	predicted exon	15.6
	458866	BE616694	Hs.288042	Homo saplens cDNA FLJ14299 fis, clone PLACE1010	15.6
	417124	BE122762	Hs.25338	ESTs	15.6
65	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sapiens]	15.6
	418636 454128	AW749855 AL031259	Hs.41639	gb:QV4-BT0534-281299-053-c05 BT0534 Homo saple programmed cell death 2	15.6° 15.6
	441074	AW500001	Hs.4783	Homo sapiens cDNA: FLJ22035 fis, clone HEP08838	15.6
	451742	T77609	Hs.117970	ankyrin 2, neuronal	15.6
70	403687			predicted exon	15.6
	431838	AI097229	Hs.217484	ESTs	15.6
	402855 449635	Al989942	Hs.232150	predicted exon ESTs	15.6 15.6
	434392	AW983709	Hs.268051	ESTs	15.6
75	444301	AK000136	Hs.10760	hypothetical protein FLJ20129	15.6
	414973	C19089		gb:C19089 Human placenta cDNA (TFujiwara) Homo	15.5
	428374	AW405156	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5 15.5
	415745 432532		Hs.150790 Hs.162246	ESTs ESTs	15.5
80	417112			gb:zr41b09.s1 Soares_NhHMPu_S1 Horno sapiens cDN	15.5
-	418101	AL047476	Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110	AW384928	Hs.225160	Homo sapiens cDNA FLJ13102 fis, clone NT2RP3002	15.5
	458606 436989	AJ239397 AA741028	Hs.256155	gb:AJ239397 Uni-ZAP XR retinal pigment epithelium H ESTs	15.5 15.5
	-100303	1020	1.0.200100	F	.0.0

	407396	AF011757		gb:Homo sapiens RAGE binding protein (P12) mRNA,	15.5
	449684	AI659166	Hs.207144	ESTS	15.5
	454666 430492	AW812994	Hs.300803	gb:RC3-ST0186-230300-019-g02 ST0186 Homo sapien	15.5 15.5
5	439460	U15197 AA836220	Hs.13774	Human histo-blood group ABO protein mRNA, partial ESTs	15.5
•	449231	BE410360	113.13774	gb:601302340F1 NIH_MGC_21 Homo sapiens cDNA	15.5
	453060	AW294092	Hs.21594	ESTs	15.5
	416961	BE391476	Hs.80617	ribosomal protein S16	15.5
10	439988	AA860119	Hs.255976	ESTs	15.5
10	400917			predicted exon	15.5
	424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Homo	15.5
	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q3	15.5
	441680	AW444598	Hs.7940	RAP1, GTP-GDP dissociation stimulator 1	15.5 15.5
15	437830 409479	AB020658 BE163800	Hs.5867 Hs.136912	KIAA0851 protein ESTs	15.5
13	409885	AW503068	115.100512	gb:UI-HF-BP0p-aje-g-10-0-UI.r1 NIH_MGC_51 Homo	15.4
	459090	AA443323	Hs.107812	ESTs, Weakly similar to SPOP [H.sapiens]	15.4
	429324	AA488101	Hs.199245	inactivation escape 1	15.4
00	403766			predicted exon	15.4
20	413970	U59309	Hs.75653	fumarate hydratase	15.4
	456674	BE266120	Hs.269358	ESTs	15.4
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	15.4
	430125	U46418	Hs.233950	serine protease Inhibitor, Kunitz type 1	15.4
25	452154 422984	AW953265 W28614	Hs.271277 Hs.75984	hypothetical protein from EUROIMAGE 363668 chorlonic somatomammotropin hormone 2	15.4 15.4
23	408649	BE242232	Hs.26045	protein tyrosine phosphatase, receptor type, A	15.4
	417497	AW402482	Hs.82212	CD53 antigen	15.4
	404666			predicted exon	15.4
• •	456847	Al360456	Hs.37776	ESTs	15.4
30	426995	AA400646	Hs.221988	ESTs	15.4
	445350	AF052112	Hs.12540	lysophospholipase I	15.4
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	15.4
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HEMBB100	15.4
35	411660 442653	AW855718 BE269247	Hs.170226	gb:RC1-CT0279-070100-021-a06 CT0279 Homo saple Homo sapiens clone 23579 mRNA sequence	15.4 15.4
55	447552	Al394125	Hs.160413	ESTs	15.4
	448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, done LNG15735	15.4
	420180	AI004035	Hs.25191	ESTs	15.4
40	440099	AL080058	Hs.6909	DKFZP564G202 protein	15.4
40	427550	BE24281B	Hs.179606	nuclear RNA helicase, DECD variant of DEAD box fam	15.4
	432894	AW167668	Hs.279772	brain specific protein	15.3
	412113	AW161274	Hs.74427	p53-induced protein	15.3
	431614 445870	A1189827 AW410053	Hs.13406	gb:qd19d07.x1 Soares_placenta_8to9weeks_2NbHP8to syntaxin 18	15.3 15.3
45	424347	AA723883	Hs.145513	Homo sapiens mRNA; cDNA DKFZp434L0435 (from	15.3
	425132	AW250114		gb:2821134.5prime NIH_MGC_7 Homo sapiens cDNA	15.3
	439756	AL359651	Hs.283852	Homo sapiens mRNA full length insert cDNA clone EU	15.3
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	15.3
50	406130			predicted exon	15.3
50	453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxypeptidase-like p	15.3
	405491	A A 270507	Un E400	predicted exon	15.3 15.3
	436481 446826	AA379597 AK000626	Hs.5199 Hs.16230	HSPC150 protein similar to ubiquitin-conjugating enzy hypothetical protein FLJ20619	15.3
	441211	AW946155	Hs.7750	hypothetical protein AL133206	15.3
55	418711	AW247977	Hs.87595	translocase of inner mitochondrial membrane 22 (yeast)	15.3
	457301	AA469146		gb:nc67e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA c	15.3
	449999	Al679421	Hs.231098	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	15.3
	439090	H65724	Hs.271663	ESTs	15.3
60	416586	D44643	Hs.14144	secreted modular calcium-binding protein 1	15.3
UU	411940	AW876686 AW205369	Hs 252936	gb:CM4-PT0031-180200-507-e05 PT0031 Homo saple ESTs	15.3 15.3
	407639 458012	AI424899	Hs.188211	ESTs	15.3
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	15.3
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.3
65	437371	AK000868	Hs.5570	hypothetical protein FLJ10006	15.3
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) homolog	15.3
	441890	AI809547	Hs.128075	ESTs	15.3
	409442	AA310162	Hs.169248	cytochrome c	15.3
70	407078	Z26256	Un 10112E	gb:H.sapiens isoform 1 gene for L-type calcium channe	15.2 15.2
, 0	436553 443177	AW407157 BE268461	Hs.181125 Hs.202	immunoglobulin lambda locus benzodiazapine receptor (peripheral)	15.2
	448771	BE315511	Hs.296244	SNARE protein	15.2
	436837	A1968248	Hs.187869	ESTs	15.2
	423623	AB011117	Hs.129943	KIAA0545 protein	15.2
75	422651	NM_015670	Hs.118926	DKFZP586K0919 protein	15.2
	403221	AL134878	Hs.119500	karyopherin alpha 4 (importin alpha 3)	15.2
	431620	AA126109	Hs.264981	2'-5'oligoadenylate synthetase 2	15.2
	404794	NM_000078	Hs.89538 Hs.197143	cholesteryl ester transfer protein, plasma ESTs	15.2 15.2
80	412944 450817	AA384110 N71597	Hs.29698	ESTS	15.2
-	418666	AF001434	Hs.155119	EH domain containing 1	15.2
	451636		Hs.140444	ESTs	15.2
	426302	AA459085	Hs.275163	non-metastatic cells 2, protein (NM23B) expressed in	15.2
	454485	AW795322		gb:PM0-UM0018-120400-002-h01 UM0018 Homo sap	15.2

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440617 AA894880
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           human chromosome 22* Dunham, et al. (1999) Nature 402:489-495
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           Nt_position: Indicates nucleotide positions of predicted exons
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403286

8080320

Plus

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	403362	8571772	Plus	64099-64260
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	403695	3046276	Plus	168272-168514
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	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
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65	405333	3165399	Plus	149905-150215
	405411	3451356	Minus	17503-17778,18021-18290
	405423	4753276	Plus Plus	6162-6983
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70	405515	9454624	Plus	37329-37469
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75	405600	5923640	Plus	26662-27225
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	405783	5738434	Minus	27238-27885
80	405867	6758731	Minus	74553-75173
	406086	7107817	Plus	9418-9573
	406124	9149714	Minus	1331-1774
	406130	9161404	Minus	32394-32498 40997-50210
	406140	9168231	Minus	49887-50219
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	406160	7144945	Plus	55498-56268
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_	406268	6682695	Minus	6605-7072
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	406326	9212385	Plus	84508-84655
	406388	9256205	Plus	85153-85277
	406457	9755793	Plus	44966-45406
	406473	9795566	Minus	109669-109931
10	406537	7711478	Plus	32904-33017
	406571	7711622	Minus	65634-65912,66116-66596
	406580	7711838	Minus	96654-97640

15 TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indictive of extracellular localization.

TABLE 4A: ABOUT131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY Pkey: Primekey

Ex. Acon: Exemplar Accession

UG ID: UniGene ID

Title: Unigene Title

PFAM domains

Title: Versus a completions

20

25	ratio: turr	or vs. normal ov	ary	·		
23	Pkey	Ех. Ассп	UGID	Title	PFAM	ratio
	403077	CA ALGI	OGID	predicted exon	fn3	15.0
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
	403089	AUUTTUIZ	HS.200002	predicted exon	fn3	14.9
30	457148	AF091035	Hs.184627	KIAA0118 protein	arf;ras	14.8
50	431176	A1026984	Hs.293662	ESTs	taminin_EGF;taminin_B;	14.8
						14.8
	434293	NM_004445	Hs.3796	EphB6	fn3;pkinase;EPH_lbd	14.6
	408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1	14.5
35	428695	Al355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	
22	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxy	sugar_tr;MCT	14.3
	422125	NM_003459	Hs.111967	solute carrier family 30 (zinc transporte	Cation_efflux	14.2
	407483	NM_012368	11- 407040	(NONE)	7tm_1	14.2
40	446689	AW594695	Hs.167046	ESTs	7tm_1	14.1
40	410184	AW503667	Hs.59545	ring finger protein 15	zf-C3HC4;SPRY;zf-B_box	14.0 14.0
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermoly	fn3;vwa	14.0
	405448	Al015709	Hs.172089	Homo saplens mRNA; cDNA DKFZp5	trypsin:sushi;CUB	
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	ig	14.0
45	406692	L36607	11- 450007	gb:Homo sapiens (clone 22) pregnancy	ig	13.9
40	425549	U64863	Hs.158297	programmed cell death 1	ig	13.8
	452755	AW138937	Hs.213436	ESTs	cystatin	13.8 13.7
	427637 424591	AK000816	Hs.179986	flotilin 1	Band_7	13.7
	405024	R55704	Hs.150968	hypocretin (orexin) receptor 1	7tm_1	13.7
50	405024			predicted exon	TGF-beta;TGFb_propeptide	13.7
50	405265	AW402166	Hs.784	predicted exon	A2M;A2M_N	13.7
	420256	U84722	Hs.76206	Epstein-Barr virus Induced gene 2 (lym	7(m_1	13.6
	420256	AF052692	Hs.98485	cadherin 5, type 2, VE-cadherin (vascu	cadherin;Cadherin_C_term connexin	13.5
	448638	R17122	Hs.21639	gap junction protein, beta 4 (connexin 3 nuclear protein, marker for differentiat	ia	13.4
55	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	EGF:DSL	13.4
55	431117	AL133916	Hs.298998	ESTs	ig;pkinase;LRRNT;LRRCT	13.4
	424283	AA338246	Hs.301678	ESTs	E1-E2_ATPase;Hydrolase	13.3
	436233	Al742878	Hs.124116	ESTs	ig	13.3
	443859	NM_013409	Hs.9914	follistatin	kazal	13.2
60	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (IL8	13.2
UU	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologo	IL8	13.2
	400242	1414_002304	113.75705	predicted exon	Ephrin .	13.0
	429057	AF156557	Hs.194816	stomatin-like protein 1	Band_7;SCP2	12.9
	438294	Al693753	Hs.143004	ESTs	E1-E2_ATPase;Hydrolase	12.9
65	458493	AV649408	Hs.282418	ESTs	RYDR TPR	12.8
00	444181	AB033063	Hs.10491	KIAA1237 protein	fn3;ig;PH;RhoGEF	12.8
	422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
	409632	W74001	Hs.55279	serine (or cystelne) proteinase inhibitor	serpin	12.7
	407000	U12139	110.00210	gb:Human alpha1(XI) collagen (COL1	TSPN;Collagen;COLFI	12.6
70	417064	W02903	Hs.15440	ESTs Contract Contrac	lectin_c	12.6
, ,	439389	AA318940	Hs.56004	ESTs	hemopexin;Peptidase_M10	12.6
	407786	AA687538	Hs.38972	tetraspan 1	transmembrane4	12.5
	410498	AA355749	110.00012	gb:EST64459 Jurkat T-cells VI Homo	aa_permeases	12.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	vwd	12.5
75	422330	D30783	Hs.115263	epiregulin	EGF	12.5
. •	402425			predicted exon	ion_trans	12.4
	414875	H42679	Hs.77522	major histocompatibility complex, clas	lg	12.2
	424239	M67439	Hs.143526	dopamine receptor D5	7tm_1	12.2
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	EGF;ank;notch	12.2
80	405368			predicted exon	7tm_1	12.2
	402406			predicted exon	Gal-bind_lectin	12.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteoge	TGF-beta;TGFb_propeptide	12.1
	406811	U82979	Hs.67846	łeukocyte immunoglobulin-like recepto	ig	12.0
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo	ŠDF	12.0
				•		

	433221	AB040917	Hs.97860	KIAA1484 protein		fn3;lg;LRRCT		1.9
	442915	AA852875	Hs.8850	a disintegrin and metalloproteinase dom		disintegrin;Reprolysin;		1.9
	423613 411213	AF036035 AA676939	Hs.129910	hyaluronoglucosaminidase 3		ig;Sema;Acetyltransf		1.9
5	425483	AF231022	Hs.69285 Hs.301273	neuropilin 1 Homo sapiens protocadherin Fat.2 (FA		CUB;MAM;F5_F8_type_C EGF;cadherin;laminin_G		1.9 1.8
-	421258	AA286731	113.501210	gb:zs53d08.r1 NCI_CGAP_GCB1 Hom		7tm_3		1.8
	423795	AW849759		gb:lL3-CT0216-240200-077-C04 CT0		arf;ras		1.7
	422424	Al186431	Hs.116577	prostate differentiation factor		TGF-beta		1.7
10	443296	AI765286		gb:wi73b05.x1 NCI_CGAP_Kid12 Ho		ig		1.7
10	448999	AF179274	Hs.22791	transmembrane protein with EGF-like		kazal		1.7
	414878 429344	AA341040	Hs.77541	ADP-ribosylation factor 5		arf;ras		1:5 1.5
	429344	R94038	Hs.199538	inhibin, beta C predicted exon		TGF-beta laminin_EGF;laminin_G		1.5
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (IL8		1.5
15	430263	D12614	Hs.36	lyphotoxin alpha (TNF superfamily, m	•	TNF		1.4
	400464		•	predicted exon		Peptidase_S9		1.4
	456841	AA875863	Hs.152345	poliovirus receptor-related 1 (herpesvir		ig		1.4
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kal		laminin_EGF;laminin_B		1.4
20	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase re		fn3;ig;pkinase		1.3
20	426523 446051	S68616 BE048061	Hs.170222 Hs.153315	solute carrier family 9 (sodium/hydrog ESTs		Na_H_Exchanger Reprolysin;disintegrin		1.3 1.3
	439710	AF086543	TIS. 1300 10	gb:Homo sapiens full length insert cDN		Xink		1.3
	416602	NM_006159	Hs.79389	nel (chicken)-like 2		vwc;TSPN		1.3
	418299	AA279530	Hs.83968	Integrin, betà 2 (antigen CD18 (p95), ly		integrin_B		1.3
25	425721	AC002115	Hs.159309	uroplakin 1A.		transmembrane4;COX6B;Ets		1.2
	409757	NM_001898	Hs.123114	cystatin SN		cystatin		1.2
	430630	AW269920	Hs.2621	cystatin A (stefin A)		7tm_3;ANF_receptor		1.2
	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perleca		laminin_EGF;ig;Idl_recept_a SDF		1.1 11.1
30	427289 401248	A1097346 AB028989	Hs.174203 Hs.88500	solute carrier family 1 (glutamate/neutr mitogen-activated protein kinase 8 inte		vwa;vwd;TlL		11.1
50	412627	BE391959	Hs.74276	chloride intracellular channel 1		G-patch;lg;MutS_C		1.1
	420104	U09825	Hs.1287	zinc finger protein 173		zf-C3HC4;SPRY;zf-B_box		1.1
	405275	AB028989	Hs.88500	mitogen-activated protein kinase 8 inte		vwa;vwd;TlL		11.1
25	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily		7tm_1		11.1
35	446745	AW118189	Hs.156400	ESTs		vwa		11.1
	441834	AL138034	Hs.7979	KIAA0736 gene product Novel human gene mapping to chomos		sugar_tr PH;RhoGAP;Gal-bind_lectin		11.0 11.0
	450986 416118	BE241845 N52773	Hs.25744 Hs.167721	ESTs		hemopexin;Peptidase_M10		11.0
	443071	AL080021	Hs.8986	complement component 1, q subcompo		C1q;Collagen		10.9
40	431247	AL021578	Hs.278489	matritin 4		EGF;vwa		10.9
	431449	M55994	Hs.256278	tumor necrosis factor receptor superfam		TNFR_c6		10.9
	457044	S73899	Hs.2131	arginine vasopressin receptor 1A		7tm_1		10.9
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocyte		ig		8.01
45	402172	A F024004	Lla 142010	predicted exon		ig australia		10.7 10.6
45	424218 409208	AF031824 Y00093	Hs.143212 Hs.51077	cystatin F (leukocystatin) integrin, alpha X (antigen CD11C (p15		cystatin vwa		10.6
	426330	M77235	Hs.169331	sodium channel, voltage-gated, type V,		ion_trans;IQ		10.6
	439758	AA845235	Hs.124470	ESTs		transmembrane4		10.6
	412429	AV650262	Hs.75765	GRO2 oncogene		IL8	1	10.6
50	449987	AW079749	Hs.184719	ESTs, Weakly similar to AF116721 11		ABC_tran;ABC_membrane		10.6
	432408	N39127	Hs.76391	myxovirus (Influenza) resistance 1, hom		ion_trans;K_tetra		10.6
	406672	M26041	Hs.198253	major histocompatibility complex, clas		ig;MHC_II_alpha		10.5
	419749 419086	X73608 NM_000216	Hs.93029 Hs.89591	sparc/osteonectin, cwcv and kazal-like Kallmann syndrome 1 sequence		kazal;thyroglobulin_1 fn3:wap		10.5 10.5
55	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t		fn3;ig;Y_phosphatase;MAM		10.5
-	423869	BE409301	Hs.134012	C1g-related factor		GTP_EFTU;EFG_C		0.4
	430209	AF177941	Hs.235368	Pro-(alpha)3(V) collagen		Collagen; COLFI; TSPN	1	10.4
	400834			predicted exon		IRK		0.4
60	442941	AU076728	Hs.8867	cysteine-rich, angiogenic Inducer, 61		Cys_knot;tsp_1;vwc;IGFBP		10.4
60	403691	AJ011021	Hs.247905	predicted exon potassium voltage-gated channel, subfa		tsp_1;Reprotysin; ion_trans		10.4 10.3
	430776 432342	AL036128	Hs.274404	plasminogen activator, tissue		EGF;fn1;kringle;trypsin		10.3
	413731	BE243845	Hs.75511	connective tissue growth factor		Cys_knot;tsp_1;vwc		10.3
	423309	BE006775	Hs.126782	sushi-repeat protein		sushi;HYR		10.3
65	431728	NM_007351	Hs.268107	multimerin		EGF;C1q		10.3
	450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_HU		ig		10.2
	446983	AA157484	Hs.97199	complement component C1q receptor		EGF;Xlink		10.2
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		death;ank;ZU5		10.1
70	400253 406694	M94891	Hs.225932	predicted exon pregnancy specific beta-1-glycoprotein		7tm_1 ig		10.0 10.0
, ,	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1		ËGF		10.0
	410564	NM_006033	Hs.65370	lipase, endothelial		Ribosomat_L22		10.0
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo		pkinase;ig		10.0
75								
75	TABLE 48		ot idon!!!	ahor				
		ique Eos probes ber: Gene cluste		iuei				
		ber: Gene ciusti 1: Genbank acci						
	- ~~~	Companie acce						
80	Pkey	CAT Number	Accession					
	410498	120611_1	AA355749 A	A085520 AW966333 AA340319 BE170936				
	416441	159480_1		A182474 AA180369 BE275628 BE276131				
	421258	200725_1		A287621 AW188228 AW137774 W849758 T89549 AA331069				
	423795	232093_1	ntiotal 03 P	110-01-00 1 020-12 PENDO 1003				
					122			

47550_1 439710 AF086543 W96291 W96225 443296 56539_2 Al765286 AW297086 BE568658 TABLE 4C: 5 Pkey: Unique number corresponding to an Eos probeset Ref. Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495 Strand: Indicates DNA strand from which exons were predicted Nt_position: Indicates nucleotide positions of predicted exons 10 Strand Nt_position 400464 400834 9929670 Plus 22074-22214 121963-122288 8705192 Plus 402114 8318586 71578-71715 Plus 15 402172 8575911 143378-143671 Minus 402406 402425 3970929 Plus 10872-11123,12932-13048 Minus 50224-50395 9796347 8954241 146923-147222,147326-147628 403077 Plus 403089 8954241 Plus 171964-172239 20 403691 7387384 Minus 88280-88463 405024 7107727 Plus 88500-88697 55744-55903,57080-57170,61478-61560 405285 6139075 Minus 405368 2104517 46055-47188 Plus 25 TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary). TABLE 5A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY 30 Pkey: Primekey Ex. Accn: Exemplar Accession UG ID: UniGene ID Title: UniGene Title ratio: ration normal ovary vs tumor 35 Pkey Ex. Accn UGID 421013 M62397 Hs.1345 mutated in colorectal cancers 14.8 ESTs, Weakly similar to Z141_HUMAN ZINC FINGE 439360 AA448488 Hs.55346 12.B nuclear receptor subfamily 1, group D, member 2 D16815 12.6 407644 Hs.37288 40 Hs.119059 424851 AA676441 gb:RC1-CT0249-170200-025-h04 CT0249 Homo sapie 455056 420727 AW853057 11.5 Hs.99886 complement component 4-binding protein, beta H75701 11.3 Hs.168000 ESTs 451617 C01056 10.0 predicted exon ESTs 401308 9.9 45 AA911705 Hs.130229 9.7 AAN987 409725 T40760 Hs.90459 **EST** putative transmembrane protein BE314524 Hs.78776 9.7 415752 437690 AAB04362 Hs.180544 ESTs 9.6 AJ908263 9.5 9.2 437787 Hs 291625 **ESTs** 50 459054 AW798466 Hs.82396 2',5'-oligoadenylate synthetase 1 435330 R16769 Hs.185689 **ESTs** 9.2 AA724430 AL120800 9.1 9.1 436642 Hs.127960 **ESTs** gb:DKFZp762E152_r1 762 (synonym: hmel2) Homo sa 453752 Hs.207673 AI808964 451683 ESTs 55 401464 AF039241 Hs.9028 histone deacetylase 5 9.0 gb:til-H-BWO-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Hom gb:601062418F1 NIH_MGC_10 Homo saplens cDNA ESTs 436812 AW298067 8.7 8.7 410758 BE535988 412637 AA115097 Hs.261313 419166 AA234638 Hs.293584 8.3 60 8.1 8.1 423739 413813 AA398155 Hs.97600 **ESTs** M96956 Hs.75561 teratocarcinoma-derived growth factor 1 416211 R14625 gb:yg45c03.r1 Soares infant brain 1NIB Homo sapiens 443131 A1033833 Hs.132689 7.9 7.9 7.8 7.7 7.6 7.5 7.5 7.4 7.4 7.4 7.4 7.3 415866 T10115 Hs.92423 KIAA1566 protein 65 Al912097 Hs.163208 410130 **ESTs** Al131502 Hs.143135 ESTs, Weakly similar to FAFY_HUMAN PROBABLE 439426 408141 U69205 Hs.45152 ESTs, Moderately similar to neurogenic basic-helix-loop 419015 441573 T79262 BE563966 ESTs ESTs Hs:14463

gb:od17e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA

gb:RC2-BN0033-180200-015-g06 BN0033 Homo saple

ESTs, Weakly similar to neuronal thread protein AD7cgb:PM3-HT0344-071299-003-c08 HT0344 Homo sapie gb:601117374F1 NIH_MGC_16 Homo sapiens cDNA gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDN

gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien

ESTs, Weakly similar to similar to O-sialoglycoprotein

Hs.6529

Hs.143868

Hs.285097

Hs.144513

Hs.128051

Hs.114541

Hs.117183

Hs 201217

Hs.130558

ESTs

ESTs

ESTs

FSTs

predicted exon ESTs

70

75

80

419386

430562

434738

403283

415861

412732

441247

442865

409699

420352

421418 413597

454102

445487

457604

AA236867

AA836265

D78260

Z43123

N57659

AW993300

AW118681

BE154650

BE258835 AA806639

AW302885

AW752363

A1806287

AI004397

7.3 7.3 7.2 7.2

7.1

	400942			predicted exon	6.9
	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sa	6.9
	422046	AI638562		gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA c	6.9
5	441284	AA927676	Hs.196542	ESTs	6.9
,	446224 424943	AW450551	Hs.13308 Hs.153924	ESTs death-associated protein kinase 1	6.9 6.9
	453967	AU077260 AW009077	Hs.232947	ESTs	6.9
	448683	AA167642	Hs.14632	ESTs	6.8
	431877	AA521204	Hs.105507	ESTs	6.8
10	411337	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapie	6.8
	410596	AA374186		gb:EST86290 HSC172 cells I Homo sapiens cDNA 5' e	6.8
	417762	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937233) Homo	6.7
	406364			predicted exon	6.7
15	452238	F01811	Hs.187931	ESTs, Moderately similar to S22703 voltage-gated pota	6.7
15	415288	R15794	Hs.141027	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
	407437 439126	AF220264 AF085984		gb:Homo sapiens MOST-1 mRNA, complete cds. gb:Homo sapiens full length insert cDNA clone YT99F	6.7 6.6
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapiens cDNA	6.6
	431800	AW452768	Hs.162045	ESTs	6.5
20	426380	AI291267	Hs.149990	ESTs, Weakly similar to unnamed protein product [H.sa	6.5
	449529	AI990559	Hs.232033	ESTs	6.4
	437755	AW204256	Hs.291887	ESTs	6.4
	448307	A1480289	Hs.211026	ESTs	6.4
25	439586	AA922936	Hs.110039	ESTs	6.4
25	420051	N35696	Hs.44745	ESTs ESTs	6.4 6.4
	425806 433923	AI522299 AI823453	Hs.173369 Hs.146625	ESTs	6.4
	408159	H63977	Hs.118526	ESTs	6.3
	434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
30	430197	AA468888	Hs.187697	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
	440332	Al218517	Hs.188051	ESTs	6.3
	450061	Al797034	Hs.201115	ESTs ·	6.3
	454994	AW850176		gb:IL3-CT0219-271099-022-H04 CT0219 Homo sapien	6.3
25	402105	14/50003	11. 400405	predicted exon	6.3
35	409090	W56067	Hs.103105	ESTs predicted exon	6.2 6.2
	405752 408074	R20723	Hs.124764	ESTs	6.2
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	6.1
	416310	T81421	Hs.221396	ESTs	6.1
40	421976	AL138443	Hs.23450	mRNA for FLJ00023 protein	6.1
	429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
	448732	BE614063		gb:601503993F1 NIH_MGC_71 Homo sapiens cDNA	6.0
	453909	AW004045	Hs.203365	ESTs	6.0
45	431178	AA493884	Hs.218008	Homo sapiens cDNA: FLJ21440 fis, clone COL04389	6.0
43	449671	AW959755	Hs.288896	Homo saplens cDNA FLJ12977 fis, clone NT2RP20062	6.0 6.0
	421349 453282	W01715 AK000043	Hs.102958 Hs.32922	ESTs, Weakly similar to Lpg6p [S.cerevislae] hypothetical protein FLJ20036	5.9
	420618	AA278781	Hs.280698	ESTs	5.9
	412480	BE142364	1101200000	gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
50	449858	AW205979	Hs.196065	ESTs	5.9
	429884	AL049925	Hs.225984	DKFZP547G0910 protein	5.9
	416453	H5696B	Hs.114593	ESTs ·	5.9
	459497	AA825742	Hs.87517	ESTs	5.9
55	433773	AA759293	Hs.112692 Hs.8850	ESTs a disintegrin and metalloproteinase domain 12 (meltrin a	5.9 5.9
33	458942 436054	AA009647 A1076262	Hs.119813	ESTs	5.9
	410495	N95428	113.113010	gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF H	5.8
	403277	1100120		predicted exon	5.8
	444302	Al140115	Hs.225130	ESTs	5.8
60	439834	AI754576	Hs.124523	ESTs	5.8
	404020			predicted exon	5.8
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coll domains 1(cy	5.7
	430922	AW373747 N55394	Hs.183337 Hs.96398	ESTs 8-oxoguanine DNA glycosylase	5.7 5.7
65	420289 428498	AA429575	Hs.243032	ESTs	5.7 5.7
05	445597	H65649	113.240002	gb:yr72d10.r1 Soares fetal liver spleen 1NFLS Homo sa	5.7
	411543	AW851248		gb:lL3-CT0220-160200-066-F01 CT0220 Homo sapien	5.7
	408354	Al382803	Hs.159235	ESTs	5.7
70	444431	AW513324	Hs.42280	ESTs	5.7
70	406605			predicted exon	5.7
	405541	AF039241	Hs.9028	histone deacetylase 5	5.6 5.6
	458090 464629	A1282149 Z45439	Hs.56213 Hs.270425	ESTs, Highly similar to FXD3_HUMAN FORKHEAD ESTs	5.6 5.6
	454529 445832	Al261545	113.210423	gb:qz30a07.x1 NCI_CGAP_Kld11 Homo sapiens cDNA	5.6
75	441223	AI475067	Hs.132499	ESTs	5.6
. –	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
	443650	A1698330	Hs.151444	ESTs	5.6
	403714			predicted exon	5.6
00	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.6
80	458914	BE327696	Hs.280922	ESTs	5.6
	420620	AA278807	Hs.173343	ESTs ESTs Weakly similar to P28830 1 (U capiens)	5.5 5.5
	458228	AA934995	Hs.184846	ESTs, Weakly similar to R28830 1 [H.sapiens] src homology 3 domain-containing protein HIP-55	5.5 5.5
	448067 427000	R68568 Al187420	Hs.183373 Hs.145221	ESTs	5.5 5.5
	72.1000	711.07720	7022	,	5.5

	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W Homo sa	5.5
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen 1NFLS Homo sa	5.5
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.5
_	450938	AW753734	Hs.277215	ESTs	5.5
5	431888	H99557	Hs.2864	early endosome antigen 1, 162kD	5.4
	459418	W96550	Hs.26418	ESTs	5.4
	416718	R83017	Hs.204828	ESTs	5.4
	413236	H16442	Hs.127376	KIAA0266 gene product	5.4
	439063	AF085922	Hs.113968	ESTs	5.4
10	446361	AJ291234	Hs.282241	ESTs	5.4
	458253	AW296952	Hs.196802	ESTs ·	5.4 5.4
	433682	AA642418	Hs.17381	ESTs	5.4 5.4
	455790	BE090690	110.17001	gb:RC1-BT0720-280300-011-g02 BT0720 Homo sapie	
		AW294870	Un occeso		5.4
15	445755		Hs.223672	ESTs	5.3
IJ	436513	AJ278110	Hs.125507	DEAD-box protein	. 5.3
	416671	N94087	Hs.26073	ESTs, Moderately similar to HG14_HUMAN NONHIS	5.3
	440231	AW015420	Hs.163323	ESTs	5.3
	429866	AA460104	Hs.99540	ESTs	5.3
20	437779	AA345232	Hs.21227	ESTs	5.3
20	424029	AB014594	Hs.137579	KIAA0694 gene product	5.3
	425614	AI334963	Hs.156256	ESTs	5.3
	430653	AW902062	Hs.30280	ESTs	5.2
	408855	T83061	Hs.279604	desmin	5.2
	410454	AW749041		gb:RC3-BT0319-100100-012-c05 BT0319 Homo saple	5.2
25	438116	A1904105	Hs.122016	ESTs	5.2
	409138	W73159	Hs.58290	ESTs	5.2
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-specific)	5.2
	440212	AW300959	Hs.126216	ESTs, Weakly similar to good similarity to E. coli hypo	5.2
	404108		, _02.10	predicted exon	5.2
30	456253	T12198		gb:A588F Heart Homo saplens cDNA clone A588, mRN	5.2
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.1
	444013	T08531	Hs.44404	hypothetical protein PRO1488	5.1
	454071	AID41793	Hs.42502	ESTs	5.1
	419761			25.5	
35		M17373	Hs.93177	interferon, beta 1, fibroblast	5.1
33	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone NT2RM4000	5.1
	405290	****		predicted exon	5.1
	454487	AW796342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
	444131	A1806600	Hs.207119	EST, Weakly similar to Intrinsic factor-812 receptor pr	5.1
40	441679	BE502267	Hs.65996	ESTs	5.1
40	450077	AA523752	Hs.120855	ESTs	5.1
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
	445140	A1650599	Hs.197913	ESTs	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
	447037	Al357568	Hs.157612	ESTs	5.1
45	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapiens	5.0
	436196	AK001084		gb:Homo sapiens cDNA FLJ10222 fis, clone HEMBB1	5.0
	442772	AW503680	Hs.300513	ESTs, Weakly similar to T15B7.2 [C.elegans]	5.0
	444138	AI701572	Hs.151153	ESTs	5.0
	458589	AV654623	Hs.288141	Homo sapiens cDNA FLJ13016 fis, clone NT2RP30006	5.0
50	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chromos	5.0
	441318	AI078234	Hs.176130	ESTs	5.0
	407490	\$79281		gb:pancreatic ribonuclease [human, mRNA Recombinan	4.9
	438224	AA933999		gb:on91f04.s1 Soares_NFL_T_GBC_S1 Homo sapiens	4.9
	451638	AW798466	Hs.82396	2'.5'-oligoadenylate synthetase 1	4.9
55	457356	AA489621	Hs.191670	ESTs	4.9
	430679	R44428	Hs.22801	ESTs	4.9
	445747	A1820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9
	409036	T88693	Hs.226410	ESTs	4.9
	433382	T64293	Hs.291453	ESTs	4.9
60	401287	. 5 /200	1700	predicted exon	4.9
	424188	AW954552	Hs.142634	zinc finger protein	4.9
	404868		172007	predicted exon	4.9
	410152	AW593104	Hs.23681	ESTS	4.9
	444997	AVV595104 AI204451	Hs.146196	ESTs	4.9
65	444997 431075	BE267477	(15.140130	qb:601189542F2 NIH_MGC_7 Homo sapiens cDNA cl	4.9 4.8
03			11- 404750		
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolog 6	4.8
	414337	BE386606	11	gb:601273980F1 NIH_MGC_20 Homo sapiens cDNA	4.8
	410336	BE391510	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	4.8
70	445283	AW515763	Hs.246872	ESTs	4.8
70	434792	AA649253	Hs.132458	ESTs	4.8
	433403	AF040247		gb:Homo sapiens erythroid differentiation-related factor	. 4.8
	454940	AW846202		gb:QV0-CT0179-011299-061-f10 CT0179 Homo saple	4.8
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo sapi	4.8
75	416437	N48990	Hs.37204	ESTs	4.8
75	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sapiens cDNA	4.8
	434977	A1734233	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated receptor, alpha	4.8
	459218	AA812633	Hs.10845	ESTs	4.8
0.0	402109			predicted exon	4.8
80	444490	A1151080	Hs.146830	ESTs	4.8
	432632	AW973801	Hs.134656	ESTs	4.8
	438683	AA813982	Hs.291842	ESTs	4.8
	404044			predicted exon	4.8
	449862	A1672277	Hs.199475	ESTs	4.8

	419002	T78625	Hs.268594	ESTs	4.7
	425582	AL157686	Hs.293737	ESTs	4.7
	416086	H18252	Hs.227263	ESTs	4.7
_	441133	AA918191	Hs.194457	ESTs	4.7
-5	446323	AI288274	Hs.149868	ESTs	. 4.7
	440347	Al125590	Hs.142864	ESTs	4.7
	439481	AF086294	Hs.125844	ESTs	4.6
	456388	W28557		gb:48d8 Human retina cONA randomly primed sublibra	4.6
	441864	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SU	4.6
10	445910	R93483	Hs.260273	ESTs	4.6
~ 0	403531	100100	110.200210	predicted exon	4.6
	429773	Al332482	Hs.218791	proteoglycan 4, (megakaryocyte stimulating factor, artic	4.6
	422563	BE299342	Hs.19348	Homo sapiens cDNA FLJ13119 fis, clone NT2RP30026	4.6
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phospha	4.6
15	453663	AL048807			4.6
IJ			Hs.180714 Hs.164144	cytochrome c oxidase subunit VIa polypeptide 1	
	447839	N72050	Hs.13301	ESTs ESTs	4.5
	415612	F12893	MS. 1330 I		4.5
	433371	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3' simila	4.5
20	410667	AW936099		gb:QV0-DT0020-210100-095-d04 DT0020 Homo sapie	4.5
20	410890	AW809575		gb:MR4-ST0121-060200-002-a12 ST0121 Homo saple	4.5
	404451	41007050	=====	predicted exon	4.5
	441705	AI087052	Hs.55993	ESTs	4.5
	439597	W79579	Hs.58552	ESTs	4.5
25	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
25	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) ho	4.5
	456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [H.sapiens	4.5
	424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen 1NFLS Homo sa	4.5
	439542	AW297571	Hs.17646	ESTs	4.5
20	444433	AV649844	Hs.282436	ESTs	. 4.5
30	438831	BE263273	Hs.301128	ESTs	4.5
	410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo saplen	4.5
	453895	AA039843	Hs.61948	ESTs	4.5
	458250	A1807339	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGE	4.5
	423403	AA325483		gb:EST28475 Cerebellum II Homo sapiens cDNA 5' en	4.5
35	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo sapien	4.5
	445368	Al221631	Hs.166788	ESTs	4.5
	401004			predicted exan	4.5
	425837	AF007567	Hs.159609	insulin receptor substrate 4	4.5
	420497	AW206285	Hs.253548	ESTs	4.5
40	449438	AA927317	Hs.176719	ESTs	4.5
	429409	Al694817	Hs.155980	ESTs	4.5
	447959	Al452784	Hs.270270	ESTs	4.4
	407340	AA810168	Hs.232119	ESTs	4.4
	424326	NM_014479	Hs.145296	disIntegrin protease	4.4
45	443479	AF027219	Hs.9443	zinc finger protein 202	4.4
7.5	443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein [H.sapien	4.4
	414475	BE302955	Hs.119598	ribosomal protein L3	4.4
	432075	AW972934	113.113030	gb:EST385030 MAGE resequences, MAGM Homo sap	4.4
	417906	R24769	Hs.23725	ESTs	4.4
50	406518	W28077	Hs.79389	nel (chicken)-like 2	4.4
50	441460	Al962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU	4.4
	450549	T49427	Hs.181244	major histocompatibility complex, class I, A	4.4
	426528	AA380828	110.1012-71	gb:EST93827 Activated T-cells VII Homo saplens cDN	4.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo sapi	4.4
55	408479	BE047329	Hs.144483	ESTs	4.3
55	448636	Al557139	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PLACE10090	4.3
	411280		113.123173	gb:yy89h02.r1 Soares_multiple_sclerosis_2NbHMSP H	4.3
	440790	N50617 AW593050	Hs.128580	gu.yyosnoz.ri soaies_muupie_scielosis_znunmor n ESTs	4.3
			1 120300		4.3
60	458301	AF003834	He 202204	gb:AF003834 Clontech Hi1149x Homo sapiens cDNA	4.3 4.3
50	442277	AW448914	Hs.202391	ESTs ESTs	
	449463	Al657038 H69125	Hs.196109	ESTs ESTs	4.3 4.3
	433426		Hs.133525		
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT2RM4002	4.3
65	423040	AA320749	Hs.209464	KIAA1604 protein	4.3
65	432430	AW079984	Hs.262480	ESTs	4.3
	432072	N62937	Hs.269109	ESTs	4.3
	452213	AL1 10237	Hs.28425	Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3
	403635	41550000	U- 400404	predicted exan	4.3
70	441919	AI553802	Hs.128121	ESTs	4.3
70	416717	H79559	Hs.297726	ESTs	4.3
	430995	NM_005092	Hs.248197	tumor necrosis factor (ligand) superfamily, member 18	4.2
	429269	AA449013	Hs.99203	ESTs	4.2
	415840	R15955	Hs.21758	ESTs	4.2
75	451300	AA017066	Hs.237686	EST	4.2
75	445366	Al221511	Hs.298662	ESTs	4.2
	424194	BE245833	Hs.169854	hypothetical protein SP192	4.2
	459105	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	4.2
	455387	BE069037		gb:QV3-BT0379-161299-040-e12 BT0379 Homo sapie	4.2
00	410507	AA355288	Hs.271408	ESTs	4.2
80	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2) Homo	4.2
	450966	AA017245	Hs.32794	ESTs	4.2
	432694	AW991585	Hs.276755	ESTs, Weakly similar to F53B1.2 [C.elegans]	4.2
	455108	AW856866		gb:RC0-CT0299-291199-031-G02 CT0299 Homo sapie	4.2
	443609	AV650231	Hs.282941	ËSTs	4.2

	427469	AA403084	Hs.269347	ESTs	4.2
	417178	N51636		gb:yy87b01.s1 Soares_multiple_sclerosis_2NbHMSP H	4.2
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDNA clone EU	4.2
_	431982	AW419296	Hs.105754	ESTs	4.1
5	442641	AI890955	Hs.262983	ESTs	4.1
	422128	AW881145	11. 434000	gb:QV0-OT0033-010400-182-a07 OT0033 Homo sapie	4.1
	449156	AF103907	Hs.171353	prostate cancer antigen 3	4.1
	419668	AI033098	Hs.132777	ESTs	4.1
10	418236 432663	AW994005 AI984317	Hs.172572 Hs.122589	hypothetical protein FLJ20093 ESTs	4.1 4.1
10	448313	BE622486	Hs.121688	Homo sapiens cDNA FLJ13463 fis, clone PLACE10034	4.1
	411279	AW884776	18.121000	gb:QV4-OT0067-010300-121-d01 OT0067 Homo saple	4.1
	440652	AI216751	Hs.143977	ESTs	4.1
	416608	R11499	Hs.189716	ESTs	4.1
15	420405	AA743396	Hs.189023	ESTs	4.1
	405717			predicted exon	4.1
	435267	N23797	Hs.110114	ESTs	4.1
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr virus) recepto	4.1
	403560	Al929721	Hs.5120	dynein, cytoplasmic, light polypeptide	4.1
20	449162	AI632740	Hs.10476	ESTs	4.1
	459157	Al904385		gb:CM-BT054-080399-054 BT054 Homo sapiens cDN	4.1
	432474	AA584042		gb:nn65e09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA	4.1
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo saple	4.0
25	426456	AA580748	Hs.130658	ESTs	4.0
23	438597	AA811662	Hs.171497	ESTs small nuclear ribonucleoprotein polypeptide G	4.0
	437934 459385	AW880871 8E380047	Hs.77496	gb:601159362F2 NIH_MGC_53 Homo sapiens cDNA	4.0 4.0
	439385 436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, sequence 2	4.0
	457740	AW500458	110.101240	gb:UI-HF-BNO-akb-d-07-0-UI.r1 NIH_MGC_50 Homo	4.0
30	437385	AA757055	Hs.164060	ESTs ,	4.0
-	444530	AV650124	Hs.282435	ESTs	4.0
	408066	AA046914		gb:zf47h10.r1 Soares retina N2b4HR Homo sapiens cD	4.0
	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo sapie	4.0
~ =	433582	BE548749	Hs.148016	ESTs	4.0
35	438637 ·	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein [H.sapiens	4.0
	414571	BE410746	Hs.22868	protein tyrosine phosphatase, non-receptor type 11	4.0
	446190	Al279299	Hs.256564	ESTs	4.0
	443542	Al927065	Hs.146040	ESTs	4.0
40	430444	AW296421	Hs.121035	ESTS	4.0
70	454573 409846	BE146471 AW501748		gb:QV0-HT0216-011199-043-c09 HT0216 Homo sapie gb:UI-HF-BR0p-ajm-b-12-0-UI.r1 NIH_MGC_52 Hom	4.0 4.0
	. 456141	A1751357	Hs.288741	Homo saplens cDNA: FLJ22256 fis, clone HRC02860	4.0
	456140	AA169515	Hs.6006	ESTs	4.0
	441685	Al459261	Hs.144481	ESTs	4.0
45	416677	T83470		gb:yd46g06.r1 Soares fetal liver spleen 1NFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
	442594	AW272467	Hs.254655	Untitled	3.9
50	426294 411922	AA374185 AW876260		gb:EST86289 HSC172 cells I Homo sapiens cDNA 5' e gb:PM4-PT0019-131299-006-E04 PT0019 Homo sapie	3.9 3.9
50	452320	AA042873	Hs.160412	ESTs	3.9
	431644	AW972822	Hs.169248	cylochrome c	3.9
	409892	AW956113	110.1002-10	gb:EST368183 MAGE resequences, MAGD Homo sap	3.9
	418132	T92670	Hs.117421	ESTs	3.9
55	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (937208) Homo sap	3.9
	400196			predicted exon	3.9
	416900	M59964	Hs.1048	KIT ligand	3.9
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coil domains, bind	3.9
60	435957	N39015	Hs.190368	ESTs	3.9
JU	442299 419499	AW467791 AA808136	Hs.155561	ESTs	3.9 3.9
	438403	AA808136 AA806607	Hs.177698 Hs.292206	ESTs ESTs	3.9
	449386	AA001308	Hs.193213	ESTs	3.9
_0	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens cDNA	3.9
65	406481			predicted exon	3.9
_	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo sapiens cDN	3.9
	415558	AA885143	Hs.125719	ESTs	3.9
	416874	H98752	Hs.42568	ESTs	3.9
70	454885	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo sapie	3.9
70	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo saplens cDNA clon	3.9
	440962	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Secypa Compl	3.9
	419401 406562	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sap predicted exon	3.9 3.8
	405690	BE409855	Hs.808	heterogeneous nuclear ribonucleoprotein F	3.8
75	435282	AA677428	Hs.189731	ESTs	3.8
	402451			predicted exan	3.8
	451577	N69101	Hs.32703	ESTs	3.8
	457141	AA521410	Hs.41371	ESTs	3.8
00	407817	H92553	Hs.40400	ESTs	3.8
80	412613	AA653507	Hs.285711	Homo saptens cDNA FLJ13089 fis, done NT2RP30021	3.8
	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric, alpha polypep	3.8
	446357	AW161533	Hs.300866	ESTs	3.8
	407448 456383	AJ001865 Al148037		gb:Homo Sapiens mRNA, partial cDNA sequence for h gb:qg61e01.r1 Soares_testis_NHT Homo sapiens cDNA	3.8 3.8
	430303	~ (40W)		go:ggo:eori.ri soares_(esus_NH) Homo sapielis cDNA	3.0
				190	

	444651	W58469	Hs.103120	ESTs	3.8
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo saple	3.8
	442657	BE502631	Hs.130645	ESTs	3.8
	429142			ESTs	
5		AA835639	Hs.104972		3.8
5	429274	Al379772	Hs.99206	ESTs	3.8
	437774	AW978199	Hs.291648	ESTs	3.8
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME31P [H.s	3.8
	405671			predicted exon	3.8
	413627	BE182082	Hs.246973	ESTs	3.8
10					
10	438858	R37529	Hs.269924	ESTs	3.8
	416612	H70565		gb:yr97c04.r1 Soares fetal liver spleen 1NFLS Homo sa	3.8
	423045	AW967472	Hs.301511	ESTs, Highly similar to KPT2_HUMAN SERINE/THR	3.8
	453361	AA035197	Hs.107375	ESTs	3.7
	437243	AA747549	Hs.259122	ESTs	3.7
15	437987	AW450202	Hs.122963	ESTs	3.7
IJ					
	408781	BE148621	Hs.254602	ESTs	3.7
	455895	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo saple	3.7
	431492	AW612343		gb:hg97c10.x1 NCI_CGAP_Kid11 Homo sapiens cDN	3.7
	413247	AW963969		gb:EST376042 MAGE resequences, MAGH Homo sap	3.7
20	422866	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-g	3.7
		AA572994	110.12.1002		
	431828		11.00000	gb:nm33f12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	3.7
	438872	R64197	Hs.23589	ESTs	3.7
	438673	Al824717	Hs.123443	ESTs	3.7
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen 1NFLS Homo sa	3.7
25	401963			predicted exon	3.7
	402867			predicted exon	3.7
		A141470440			
	408315	AW179148		gb:MR4-ST0067-200899-002-B07 ST0067 Homo sapie	3.7
	418320	D86981	Hs.84084	amylold beta precursor protein (cytoplasmic tail)-bindin	3.7
	447199	A1939421	Hs.160900	ESTs	3.7
30	422590	AA312758	Hs.193945	Homo sapiens cDNA FLJ13962 fis, clone Y79AA10012	3.7
	451996	AW514021	Hs.245510	ESTs	3.7
		AW953444		laminin, alpha 4	3.7
	412463		Hs.78672		
	440928	AL046575	Hs.130198	ESTs	3.7
~ =	441951	W31002	Hs.128195	ESTs	3.7
35	440705	AA904244	Hs.153205	ESTs	3.7
	434231	AF119901	Hs.250568	hypothetical protein PRO2831	3.7
	411039	AL135674	Hs.163348	ESTs	3.7
		BE066915	113.100070	=	3.7
	413137		11. 57700	gb:PM0-BT0340-231199-001-b07 BT0340 Homo saple	
40	417970	AA309234	Hs.57760	Homo sapiens cDNA: FLJ23119 fis, clone LNG07978	3.7
40	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDNA clone EU	3.7
	459595	AL040421		gb:DKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
	443601	AI078554	Hs.15682	ESTs	3.7
	404041			predicted exon	3.6
	406122			predicted exon	3.6
45					
43	404582			predicted exon	3.6
	455786	BE090077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo sapie	3.6
	411899	AA370573		gb:EST82238 Prostate gland I Homo sapiens cDNA 5' e	3.6
	426758	AL036430	Hs.197772	ESTs	3.6
	421776	AW301994	Hs.108183	candidate tumor suppressor p33 ING1 homolog	3.6
50	430169	AA468531	Hs.189047	ESTs	3.6
50					3.6
	407695	A1808007	Hs.66450	ESTs	
	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapie	3.6
	425902	X52509	Hs.161640	tyrosine aminotransferase	3.6
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
55	429066	AA868555	Hs.178222	ESTs	3.6
	428690	Al948490	Hs.98765	ESTs	3.6
	437302	AA837146	Hs.180275	ESTs	3.6
	443973	AI580083	Hs.176154	ESTs	3.6
	453993	AW615224	Hs.252839	ESTs	3.6
60	413623	AA825721	Hs.246973	ESTs	3.6
	409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
	424916	AW867440	Hs.23096	ESTs	3.6
					3.6
	424769	H06469	Hs.142653	ret finger protein	
CF.	400080	*****		predicted exon	3.6
65	421521	A1638760	Hs.161795	ESTs	3.6
	405549			predicted exon	3.6
	446114	AI275715	Hs.145926	ESTs	3.6
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T	3.6
	424025	Al701852	Hs.301296	ESTs	3.5
70			16.501230	gb:PT1.3_03_G05.r tumor1 Homo sapiens cDNA 5, mR	3.5
70	448527	AI525606	11- 5103		
	437063	AA351109	Hs.5437	Tax1 (human T-cell leukemla virus type I) binding prot	3.5
	449880	A1673006	Hs.231948	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CL	3.5
	449311	A1657014	•	gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA c	3.5
_	442999	AW662889	Hs.132395	ESTs	3.5
75	416238	W90448		gb:zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.5
			Un incom		3.5
	423209	8E278528	Hs.106823	H.sapiens gene from PAC 42616, similar to syntaxin 7	
	409854	AW501833		gb:UI-HF-BR0p-ajo-d-01-0-UI.r1 NIH_MGC_52 Hom	3.5
	414941	C14865	Hs.182159	ESTs	3.5
		AW751661	Hs.65919	ESTs	3.5
	456337				
80	456337 415296			op:HSCU1AU11 normalized intant brain cuna Homo s	ა. ა
80	415296	F05086	Hs 127339	gb:HSC01A011 normalized infant brain cDNA Homo s KIAA0492 projein	3.5 3.5
80	415296 423338	F05086 AB007961	Hs.127338	KIAA0492 protein	3.5
80	415296 423338 415618	F05086	Hs.127338	KIAA0492 protein gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5 3.5
80	415296 423338 415618 405583	F05086 AB007961 F12954		KIAA0492 protein gb:HSC3GG091 normalized infant brain cDNA Horno s predicted exon	3.5 3.5 3.5
80	415296 423338 415618	F05086 AB007961	Hs.127338 Hs.283077	KIAA0492 protein gb:HSC3GG091 normalized infant brain cDNA Homo s	3.5 3.5

	450867	AA011454	Hs.245122	ESTs	3.5
	431339	AA506294	Hs.257266	ESTs	3.5
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.5
-	431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HEMBA100	3.5
5	434317	A1674095	Hs.116323	ESTs	3.5
	414741	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MAMMA10	3.5
	439707	AW297702	Hs.102915	ESTs	3.5
	443178	AI631241	Hs.47312	ESTs	3.5
	400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
10	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo sapie	3.5
	434362	W27081	Hs.295446	ESTs	3.5
	409211	AA078835	113.230110	gb:zm94h04.s1 Stratagene colon HT29 (937221) Homo	3.5
	414390	BE281040		gb:601156234F1 NIH_MGC_21 Homo sapiens cDNA	3.5
			Hs.290969	<u> </u>	3.5
15	457142	Al924353		EST	
1)	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
	453363	A1989776	Hs.232623	ESTs	3.5
	418913	BE046745	11	gb:hn39b06.x1 NCI_CGAP_RDF2 Homo saplens cDN	3.4
	440016	AW118114	Hs.137057	ESTs	3.4
20	405096			predicted exon	3.4
20	435072	AW592176	Hs.116932	ESTs	3.4
	438535	L09078		gb:Homo saplens mRNA fragment	3.4
	424001	W67883	Hs.137476	KIAA1051 protein	3.4
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.4
~ ~	410587	AA370706	Hs.11252	ESTs, Weakly similar to Weak similarity with the Ysy6	3.4
25	454543	AW806895		gb:QV4-ST0023-160400-172-c06 ST0023 Homo sapien	3.4
	419515	S81944	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
	410280	AA083558	Hs.261286	ESTs	3.4
	425714	AW963278		gb:EST375351 MAGE resequences, MAGH Homo sap	3.4
	416895	AW961600		gb:EST373672 MAGE resequences, MAGG Homo sap	3.4
30	427935	AW503687	Hs.119424	ESTs, Weakly similar to unnamed protein product [H.sa	3.4
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo sapien	3.4
	453339	AW992599	Hs.252797	ESTs	3.4
	424696	BE439547	Hs.151903	Homo sapiens clone 24706 mRNA sequence	3.4
	436242	AK002187		gb:Homo sapiens cDNA FLJ11325 fis, clone PLACE10	3.4
35	442837	AI022082	Hs.50492	ESTs	3.4
55	452807	AA028933	Hs.162434	ESTs	3.4
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fis, clone HRC01333	3.4
	433936	Al208072	Hs.123459	ESTs	3.4
	458177	Al744995	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4
40		A1144333	113.20/0/2	predicted exon	3.4
70	401896 406237	-		predicted exon	3.4
		A1 440457	11- 2042		3.4
	457688	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (from	
	456914	AW363582	Hs.75323	prohibitin	3.4
45	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone LNG08361	3.4
43	419321	N48146	Hs.269069	ESTs	3.4
	447876	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
	406197	4100=404	11- 000040	predicted exon	3.4
	443005	Al027184	Hs.200918	ESTs	3.4
50	450078	Al681743	11- 454500	gb:tx38g10.x1 NCI_CGAP_Lu24 Homo saplens cDNA	3.4
50	431301	AA502384	Hs.151529	ESTs	3.4 3.4
	430202	T85775	11- 07044	gb:yd60g02.r1 Soares fetal liver spleen 1NFLS Homo s	
	428559	H24338	Hs.27041	ESTS	3.4
	455731	BE072188		gb:QV4-BT0536-211299-055-b09 BT0536 Homo saple	3.4
55	420735	AW297440	Hs.88653	ESTs	3.4
55	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
	405836	A1000740	U- 407507	predicted exon	3.3
	449178	Al633748	Hs.197597	ESTs	3.3
	453265	U61232	Hs.32675	tubulin-specific chaperone e	3.3
60	430700	AA768902	Hs.247812	H2A histone family, member K, pseudogene	3.3
60	424496	A1733451	Hs.129212	ESTs	3.3
	446963	A1862668	Hs.176333	ESTs	3.3
	422879	Al241409	Hs.188092	ESTs	3.3
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65	406255			predicted exon	3.3
	412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo saple	3.3
	401350			predicted exon	3.3
	439098	AF085955		gb:Homo sapiens full length insert cDNA clone YR86G	3.3
	450589	Al701505	Hs.202526	ESTs	3.3
70	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral related oncogene, n	3.3
	430689	AI695595	Hs.293219	ESTs	3.3
	454753	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo saple	3.3
	444479	AA194980	Hs.30818	Homo sapiens cDNA FLJ13681 fis, clone PLACE20000	3.3
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo sapie	3.3
75	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens cDNA 5' end,	3.3
	457107	AA418246	Hs.185796	ESTs, Weakly similar to b34l8.1 [H.sapiens]	3.3
	421480	NM_016158	Hs.104671	erythrocyte transmembrane protein	3.3
	444289	BE267060	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	3.3
	417725	R25257	Hs.21503	ESTs	3.3
80	453631	AL046418		gb:DKFZp434N247_r1 434 (synonym: htes3) Homo sa	3.3
	450692	H50603	Hs.94037	hypothetical protein FLJ23053	3.3
	413357	W47611		gb:zc35e06.r1 Soares_senescent_fibroblasts_NbHSF H	3.3
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.3
	457569	AW970021	Hs.291120	. ESTs, Weakly similar to ALUS_HUMAN ALU SUBFA	· 3.3
	10,000				0.0

	448601	R61666	Hs.293690	ESTs	3.3
	436526	AW993633	Hs.287681	Homo sapiens cDNA: FLJ21685 fis, clone COL09372	3.3
	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from	3.3
_	418768	T39310	Hs.1139	cold shock domain protein A	3.3
5	426768	AW303337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.283818	Homo saplens TNF receptor homolog mRNA, partial cd	3.3
	433565	AA599763	Hs.112520	EST8	3.3
	424093	AA335025		gb:EST39621 Epididymus Homo sapiens cDNA 5' end,	3.3
10	449552	AA001742	Hs.83722	ESTs	3.3
10	431892	AA521315	Hs.194424	ESTs	3.3
	405512			predicted exon	3.3
	446990	Al354717	Hs.223908	ESTs	3.3
	457729	AI821863	Hs.293467	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.2
1.	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.2
15	456420	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
	403497			predicted exon	3.2
	427145	R52635	Hs.25935	ESTs	3.2
	406454			predicted exon	3.2
20	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens cDNA	3.2
20	408444	AW661839	Hs.253204	ESTs	3.2
	434739	AA804487	Hs.144130	ESTs	3.2
	437060	AA745591	Hs.292063	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
0.5	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
25	443362	AI053464	Hs.166505	ESTs -,	3.2
	437500	AL390150		gb:Homo sapiens mRNA; cDNA DKFZp547L156 (from	3.2
	425458	H89317	Hs.182889	ESTs	3.2
	439171	AA831133	Hs.294128	ESTs	3.2
20	407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo saple	3.2
30	435608	AW183971	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTS	3.2
	457525	AW973800		gb:EST385901 MAGE resequences, MAGM Homo sap	3.2
	413800	Al129238	Hs.192235	ESTs	3.2
25	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens cDNA	3.2
35	455565	BE000537		gb:RC3-BN0072-240200-011-d07 BN0072 Homo sapie	3.2
	410061	T91029	Hs.15069	ESTs	3.2
	450666	T99968	Hs.18799	ESTs	3.2
	458529	AV652120	Hs.213232	ESTs .	3.2
40	424751	AA769482	Hs.296320	ESTs	3.2
40	442225	Al306597	Hs.129192	ESTs	3.2
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	435644	AA700867	Hs.269659	ESTs	3.2
	405347	.1000440	11 400000	predicted exon	3.2
45	441202	Al632143	Hs.135853	ESTs	3.2 3.2
43	446694	AV659942	Hs.258132	ESTS	3.2
	454652	AW812088	Un 07400	gb:RC4-ST0173-191099-032-a07 ST0173 Homo sapien	3.2
	418985	A1042330	Hs.87128	ESTs, Weakly similar to similar to YBS4 YEAST [C.el	3.2
	430118	Al377255	Hs.183287	ESTs ESTs	3.2
50	430691	C14187	Hs.103538	ESTs, Weakly similar to ALUB_HUMAN IIII ALU CL	3.2
50	416313	H47206	Hs.194109	ESTs	3.2
	446122	AI362790	Hs.181801	gb:48c5 Human retina cDNA randomly primed sublibra	3.2
	453725	W28543 AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	3.2
	453954 428166	AA423849	Hs.79530	M5-14 protein	3.2
55	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone CAS05917	3.2
33	401871	KIOIIO	113.23000	predicted exon	3.2
	442160	Al337127	Hs.156325	ESTs	3.2
	404708	AUDOI 121	113.100020	predicted exon	3.1
	412588	AW993055	Hs.44024	ESTs	3.1
60	431976	AA719001	Hs.291065	ESTs	3.1
55	408884	AW891024	Hs.281172	ESTs	3.1
	433811	AW975015	Hs.123138	ESTs	3.1
	431691	Al208511	Hs.292510	ESTs	3.1
	418719	AW975590	Hs.161707	ESTs	3.1
65	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PRO1777 [H	3.1
	435699	AI911488	Hs.213724	ESTs	3.1
	459344	AW499533	Hs.257976	ESTs	3.1
	431729	AW004714	Hs.162033	ESTs	3.1
~~	436771	AW975687	Hs.292979	ESTs	3.1
70	434480	AW956268	Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
	459547	A1400579	Hs.225186	EST	3.1
	427962	AA946582	Hs.133546	Homo sapiens cDNA: FLJ21120 fis, clone CAS05691	3.1
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~~	413560	BE148411		gb:MR0-HT0241-131299-002-f04 HT0241 Homo sapie	3.1
75	454372	H96643	Hs.283565	FOS-like antigen-1	3.1
	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	3.1
	428839	AI767756	Hs.82302	ESTs	3.1
	407110	AA018042	Hs.95078	ESTs	3.1
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	446877	A1559472	Hs.270720	ESTs	3.1
	429053	AA443967	Hs.194114	ESTs	3.1
	425189	H16622		. gb:ym26c07.r1 Soares Infant brain 1NIB Homo sapiens	3.1
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	404434			andiated aven	3.1		
	404134 441404	A1638880	Hs.126895	predicted exon ESTs	3.1		
	400076	MIDSODOU	NS. 120033	predicted exon	3.1		
	411876	AW961336	Hs.69705	ESTs, Weakly similar to KIAA0443 [H.sapiens]	3.1		
5	451048	AA013349	Hs.60602	ESTs	3.1		
5	447021	Al356564	Hs.161406	ESTs	3.1		
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	415833	H05175	Hs.107510	ESTs	3.0		
	402142	1.55175	110.101010	predicted exon	3.0		
10	415820	R53720	Hs.189745	ESTs	3.0		
	441140	AW016534	Hs.226994	ESTs	3.0		
	449376	AA001278	Hs.59905	ESTs	3.0		
	457593	Al738815	Hs.117323	ESTs .	3.0		
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	449561	Al022240	Hs.17924	ESTs	3.0		
	406241			predicted exon	3.0		
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20	413161	BE068130		gb:CM2-BT0368-171299-056-a01 BT0368 Homo sapie	3.0		
20	448221	BE622615 Z45684		gb:601440775T1 NIH_MGC_72 Homo saplens cDNA gb:HSCZRD121 normalized Infant brain cDNA Homo	3.0		
	415920 459135	AI902802		gb:RC-BT015-311298-026 BT015 Homo sapiens cDNA	3.0		
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	454724	AA091228	•	gb:cchn2152.seq.F Human fetal heart, Lambda ZAP Ex	3.0		
25	429395	AK002071	Hs.201624	hypothetical protein FLJ11209	3.0 ·		
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	443598	AW499970	Hs.14822	ESTs	3.0		
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30	426763	ALD42262	Hs.172101	Human DNA sequence from clone RP1-202121 on chro	3.0		
	403473			predicted exon	3.0		
	427501	Al369280	Hs.131743	ESTs	3.0		
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35	404587	M99587	Hs.104134	homeo box (H6 family) 1	3.0		
33	433964	AW241987 AL037925	Hs.197025	ESTs gb:DKFZp564M037_r1 564 (synonym: hfbr2) Homo sa	3.0		
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	425626	AI537536	Hs.173519	ESTs	3.0		
40	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, noncatalytic acc	3.0		
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	431899	AA521381	Hs.187726	ESTs	3.0		
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AW298067 AA731645 AA810101 AW194180 Al690673 AW978773
AL390150 AW959182 AA358923
AA772920 D9870 D61151 Al591331
             436242
                          41641_1
                          427323_1
43772_1
             436812
55
             437500
             437948
                          445966_1
                                                AA933999 AA781181
L09078 L03145 L09094 L09098 L03165 L09102
AF085955 H69158 H69081
             438224
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439098
                          45946_1
                          46859_1
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                           46887_1
                                                AF085984 H95905 H95906
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            .441033
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56492 -1
                                                BE562555
BE568610
                                                H65649 AW753545 Al244270
             445597
                          644513_1
                                                AI261545 N59134 AW875371 AW875247
             445832
                          651925_1
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                                                BE622615
             448221
448527
                          75534_-1
766707_1
                                                A1525606 BE549857
                          77773_-1
                                                BE614063
             448732
                                                Al657014 AW594035 Al657036 Al638390
AA001793 AA001871
Al681743 AW897287 AW897205 AW897284
             449311
                           804513_1
                          81018_1
823882_1
             449570
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             450078
             452351
                           91233_1
                                                AA025647 R45716 AW753786
                                                Al902519 Al902518 Al902516
AL037925 AL037931 AL037957
             452453
                           918300_1
                          968371_1
97021_1
975024_1
             453472
                                                AW021633 AA036730 Al866854
             453530
75
             453631
                                                AL046418 N52738 R33840
                                                W28543 AL119531
AL120800 BE378580
AL137967 BE064160 BE064186
                           978760_1
             453725
                          979899_1
982526_1
             453752
             453823
                           1011603_1
                                                AW752363 BE147120 N22640
             454102
80
                                                AW796342 AW796356 BE161430
AW806895 AW866476 AW866465 AW866535 AW866623
              454487
                           1216101_1
                           1223775_1
1224407_1
              454543
                                                AW807573 AW807566 AW807572
              454564
                                                BE146471 AW833743 AW833609 AW821469 AW821488 AW821541 AW821531 AW821513 AW821549 AW821384 AW821625 AW821577
                           1225624_1
              454573
                                                 AW821547 AW834577
```

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454679
                                    1228071_1
1228929_1
                                                                 AW812088 AW812105 AW812082
AW813110 AW813113
                 454724
                                                                  AA091228 H71860 H71073
                                    123128 1
                                                                  AW819212 AW819170 BE 158474 AW819172 AW819213 AW819200 AW819256 AW819254 AW819178 AW819214 AW819215 AW819233
                 454753
                                    1233576 1
   5
                                                                 AW836922 AW876719 AW876688 AW836919 AW836997 AW836908 AW836912 AW836993
                 454885
                                    1238874 1
                                                                 AW840503-ZZ AW80707 IS AW0709000 AW830919 AW830997 AW830908 AW8305912 AW8305933 AW846533 AW846532 AW846181 AW846458 AW846206 AW8464532 AW846553 AW846553 AW846533 AW846530 AW846530 AW846530 AW84659 AW84659 AW846530 AW846500 AW846530 AW846
                 454940
                                    1245640_1
10
                                    1248637_1
1250934_1
                 454994
                                                                  AW853057 AW853039 AW853042 AW853050 AW853114 AW853105 AW853102 AW853111 AW853121 AW853109 AW853126
                 455056
                 455067
                                    1252050_1
                                                                  AW854538 AW854418 AW854412
                 455108
                                    1253916_1
                                                                  AW856866 AW856858 AW856856
                                                                 BE069037 AW936025 BE069178 AW936034
AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
                 455387
                                    1287871_1
15
                                    1287904_1
1322942_1
                 455388
                                                                  AW991925 AW991919
                 455534
                 455565
                                    1329591_1
                                                                  BE000537 BE180584 BE180540 BE180542 BE180546
                                                                  BE072188 BE072299 BE072269 BE072317 BE072238
BE090077 BE090079
                  455731
                                     1353872_1
                  455786
                                     1365510_1
20
                                                                  BE090690 BE090688 BE090681 BE090693 BE090675
                                    1365950_1
                  455790
                                                                  BE154173 BE154098 BE154096
                  455887
                                     1380836_1
                                                                  BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899 T12198 T19584 T11583 R15526 R15585 R45876 R15562 Al148037 AA287178 AA236756
                  455895
                                     1381386_1
                  456253
                                     1699178_1
                  456383
                                     184252 1
                                                                  AV38037 AA237178 AA238788
W28557
AW973800 AA557589 AA559886
AW500458 AW160900 AF161362 AF150327 AW578393 AW360921 AW360920 AW360902 AW360890 AW732529
AF003834 W36292
25
                  456388
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                  457525
                                     351732_1
                  457740
                                    39528_1
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                  458301
                                                                   A1902802 A1902783 A1902800
                                     918516_1
                  459135
30
                  459157
                                     919804_2
                                                                   A1904385 A1904382
                  TABLE SC:
                  Project 30. Thique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
35
                  human chromosome 22* Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
                  Nt_position: Indicates nucleotide positions of predicted exons
                                       Ref
7656749
                                                                                   Nt_position
91593-91757,92720-92843,93962-94079,94824-94997
                  Pkey
400942
                                                              Strand
40
                                                              Minus
                  401004
                                        7229982
                                                              Pius
                                                                                   62580-62772
                  401287
                                                                                   42287-42431
169019-169649
                                        9801612
                                                              Minus
                  401308
401350
                                       9212516
9931226
                                                              Plus
                                                                                    14471-14623
                                                              Plus
45
                  401740
                                        2982169
                                                                                    148357-148484,148591-148690
                                                              Plus
                                                                                   58158-59585
115129-115294
                  401871
                                        8079355
                                                              Minus
                  401896
                                        8569194
                                                              Plus
                                        3126783
                                                                                   51382-51521
                  401963
                                                              Plus
                                        8131588
                                                                                    22856-24055
                  402105
                                                              Minus
 50
                  402109
                                        8131678
                                                              Minus
                                                                                    171722-171859,173197-173303
                  402142
402451
                                        7704985
9796677
                                                                                    29932-30698
                                                              Minus
                                                                                    48137-48343
                                                              Minus
                                                                                    52806-53106,53500-53818
                   402867
                                        5596716
                                                              Plus
                   403277
                                        8072597
                                                              Minus
                                                                                   27494-27642
71124-71996
 55
                   403283
                                        8076905
                                                              Minus
                                        9255944
                                                                                    92554-92795
                   403375
                                                              Minus
                                                                                   54241-54437
7221-7441
75903-76134
                   403473
                                        9945095
                                                              Minus
                                        6067111
8076842
                   403497
                                                              Plus
                   403531
                                                              Minus
 60
                                                                                    157028-157145,161725-161900
                   403635
                                        6862664
                                                              Minus
                                         7210030
                                                                                    145556-145873
                   403714
                                                              Minus
                                        7652003
8655966
                                                                                    136463-136646 174449-174663
                    403743
                                                              Minus
                   404020
                                                              Minus
                                                                                     1334-1503,2483-2585,5230-5337,19656-19804
                    404041
                                         8886967
                                                               Minus
 65
                    404044
                                         9558573
                                                              Minus
                                                                                    225757-225939
                                                                                    16650-17082
                    404083
                                        9944029
8247074
                                                              Minus
                   404108
404134
                                                                                    63603-64942
                                                              Minus
                                         6981900
                                                              Minus
                                                                                     40633-40911
                                                                                    93110-93259
153339-153481,155099-155294
105191-105622
                    404227
                                         7838233
                                                               Minus
 70
                   404418
404451
                                        7382420
7638438
                                                               Minus
                                                              Minus
                    404582
                                                                                    53230-53424
                                         9739220
                                                               Plus
                                                                                    77522-77658
39954-40430
                    404708
                                         9800828
                                        9454593
8072599
                    404868
                                                              Plus
  75
                                                                                     140844-140897,148510-148581
                   405096
                                                              Plus
                    405290
                                         3900849
                                                                                     79582-79765
                                                               Minus
                    405347
                                         2979602
                                                                                     977-1116
                                                               Minus
                                                                                     17802-17966,18573-18697
10878-11048
                                         9454624
1552494
                    405512
                                                              Plus
                    405549
                                                              Plus
  80
                    405583
                                                                                     56211-56353
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4512287

2565031

9588573

9212305

5686282

405671

405717

405752

405836

Plus

Plus

Plus

25805-26923 11275-11973

91392-91528

5031-5217

	406122	9144087	Minus	30940-31386	
	406197	7289992	Minus	47520-47961	
	406237	7417725	Plus	30032-30501	
	406241	7417725	Minus	34951-35752	
5 ·	406255	7417729	Plus	2959-3200	
	406364	9256114	Minus	50715-50833	
	406454	9588380	Minus	91746-91958	
	406481	9864741	Minus	91439-91579	
	406562	7711584	Plus	37316-37426	
10	406605	8272666	Minus	23275-23493,23723-23903	

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey
Ex. Accn: Exemplar Accession

UG ID: UniGene ID
Title: UniGene Title

ratio: ration of normal ovary vs. tumor

25	Pkey	Ex. Acon	UGID	Title	ratio
20	424851	AA676441	Hs.119059	ESTs	7.9
	437690	AA804362	Hs.180544	ESTs	4.7
	433682	AA642418	Hs.17381	ESTs	4.1
	407437	AF220264		gb:Homo sagiens MOST-1 mRNA, complete cds.	4.1
30	437787	AI908263	Hs.291625	ESTs	4.0
-	453282	AK000043	Hs.32922	hypothelical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	A1033833	Hs.132689	ESTs	3.8
	431075	BE267477	110.102000	gb:601189542F2 NIH_MGC_7 Homo sapiens cDNA clo	3.6
35	412637	AA115097	Hs.261313	ESTs	3.6
23	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.5
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	3.5
	430653	AW902062	Hs.30280	ESTs	3.4
	401308	**********	1,0,000,00	predicted exon	3.4
40	410758	BE535988		gb:601062418F1 NIH_MGC_10 Homo sapiens cDNA c	3.4
	421418	AAB06639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.4
	450061	A1797034	Hs.201115	ESTs	3.3
	409725	T40760	Hs.90459	EST	3.3
	434738	AA836265		gb:od17e02.s1 NCI_CGAP_GCB1 Homo saplens cDNA	3.3
45	431644	AW972822	Hs.169248	cytochrome c	3.3
	450938	AW753734	Hs.277215	ESTs	3.2
	420497	AW206285	Hs.253548	ESTs	3.2
	439426	Al131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE C	3.2
	407596	R86913		gb:yq30f05.r1 Soares fetal liver spleen 1NFLS Homo sap	3.2
50	448683	AA167642	Hs.14632	ESTs	3.2
	431982	AW419296	Hs.105754	ESTs	3.1
	452320	AA042873	Hs.160412	ESTs	3.1
	419401	AW804663		gb:QV4-UM0094-160300-135-d06 UM0094 Homo sapim	3.1
E E	402105			predicted exon	3.1
55	444997	Al204451	Hş.146196	ESTs	3.1
	403283			predicted exon	3.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo sapie	3.0
	428559	H24338	Hs.27041	ESTs	2.9
60	419002	T78625	Hs.268594	ESTs	2.9 2.9
OU	404868	WECOCZ.	15-402405	predicted exon	2.9
	409090	W56067	Hs.103105	ESTs	29
	406605 441202	Al632143	Hs.135853	predicted exan ESTs	2.8
	422046	AI632143 AI638562	NS. 133033	gb:ts50a10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA cl	2.8
65	442865	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-N	2.8
05	444431	AW513324	Hs.42280	ESTs	2.8
	426294	AA374185	NS.42200	gb:EST86289,HSC172 cells I Homo sapiens cDNA 5' en	2.8
	412480	BE142364		gb:CM0-HT0143-270999-062-d12 HT0143 Homo sapie	2.8
	449858	AW205979	Hs.196065	ESTs	2.8
70	401464	AF039241	Hs.9028	histone deacetylase 5	2.7
, 0	439126	AF085984	113.3020	gb:Homo sapiens full length insert cDNA clone YT99F0	2.7
	403277	A1-003304		predicted exon	2.7
	450078	AI681743		gb:bx38g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	2.7
	458090	Al282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD D	2.7
75	420620	AA278807	Hs.173343	ESTs	2.7
	459054	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	2.6
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cyt	2.6
	454529	Z45439	Hs.270425	ESTs	2.6
80	446877	AI559472	Hs.270720	ESTs	2.6
	412588	AW993055	Hs.44024	ESTs	2.6
	449862	A1672277	Hs.199475	ESTs	2.6
	446694	AV659942	Hs.258132	ESTs	2.6
	424029	AB014594	Hs.137579	KIAA0694 gene product	2.6

454102

```
gb:RC0-CT0201-270999-011-f03 CT0201 Homo sapien
                             AW752363
                                                                                                                                                             2.6
2.6
2.5
2.5
2.5
2.5
2.5
2.5
             430922
                                                Hs.183337
                             AW373747
                                                                   ESTs
              420289
                             N55394
                                                                  8-oxoguanine DNA glycosylase
gb:zb80d09.s1 Soares_senescent_fibroblasts_NbHSF Ho
                                                Hs.96398
              410495
                             N95428
  5
             412319
                             AW936903
                                                                   gb:RC1-DT0029-030200-012-d02 DT0029 Homo sapien
                                                                  gb:PM3-HT0344-071299-003-c08 HT0344 Homo sapien gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA
             409699
                             BE154650
             445832
                             AJ261545
                             NM_001364
                                                                   discs, large (Drosophila) homolog 2 (chapsyn-110)
              429755
                                                Hs.215839
              445755
                             AW294870
                                                Hs.223672
10
             TABLE 6B:
             Pkey: Unique Eos probeset identifier number
             CAT number: Gene cluster number
             Accession: Genbank accession numbers
15
             Pkey
                             CAT Number
                                                    Accession
              407596
                              1003489_1
                                                    R86913 R86901 H25352 R01370 H43764 AW044451 W21298
                                                    BE154650 BE154785 AW468343 BE154816 BE154667
N95428 W24040 AW751366 H81987
BE535988 AW801777
              409699
                             1149033_1
             410495
                             1205826_1
                             1219899_1
1288602_1
20
             410758
              412319
                                                    AW936903 AW936907 AW936908 AW936914
                                                   AW930930 AW930907 AW930906 AW930916
BE142364 BE142341 AA112025
AW804663 AW805017 AA236969
AA806639 AA291008 AA836274 AW978806
AI638562 T16929 H13401 F07773 R55836
             412480
419401
                              129929_1
                             184454_1
                             202288_1
             421418
25
              422046
                             210744_1
                                                    AA374185 AW956180 H38344
BE267477 AA491488 AW836723
AA836265 AA648266 AW974440
              426294
                             263994_1
                             327638_1
             431075
              434738
                             392562_1
              439126
                              46887_1
                                                    AF085984 H95905 H95906
30
                                                    Al261645 N59134 AW875371 AW875247
Al681743 AW897287 AW897205 AW897284
AW752363 BE147120 N22640
              445832
                             651925_1
              450078
                             823882 1
                             1011603_1
              454102
                              1287904_1
                                                    AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
              455388
35
             TABLE 6C:
             PRey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA"
             sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons
40
             401308
402105
                                                              169019-169649
22856-24055
27494-27642
                             9212516
                                              Plus
                             8131588
                                              Minus
             403277
                             8072597
                                              Minus
45
              403283
                             8076905
                                              Minus
                                                              71124-71996
              404868
                             9454593
                                                              39954-40430
                                              Plus
             406605
                             8272666
                                              Minus
                                                              23275-23493.23723-23903
50
             Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01
             GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove
             gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the
             denominator before the ratio was evaluated.
55
              TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
             Pkey: Primekey
Ex. Accn: Exemplar Accession
             UG ID: UniGene ID
60
              Title: UniGene Title
             ratio: ration tumor vs. normal tissues
              Pkey
                                              UG ID
                                                                  Title
                                                                                                                                            ratio
                           Ex. Accn
              109680
                           F09255
                                                                                                                                            23.2
                                              Hs.4993
65
              119743
                           W70242
AA283006
                                              Hs.58086
                                                                   ESTs
                                                                                                                                            22.0
              132528
                                              Hs.50758
                                                                   chromosome-associated polypeptide C
                                                                                                                                            22.0
                                                                                                                                            20.0
```

				•	
	105298	AA233459	Hs.26369	ESTs	9.7
	108857	AA133250	Hs.62180	ESTs	9.1
	113168	T53592 ·	Hs.161586	EST .	9.0
_	115892	AA435946	Hs.50831	ESTs	8.9
5	125666	AA199856	Hs.118811	ESTs	8.9
	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
	108055	AA043562	Hs.62637	ESTs	8.6
	132572	AA448297	Hs.237825	signal recognition particle 72kD	8.6
	115909	AA436666	Hs.59761	ESTs	8.5
10	109166	AA179845	Hs.73625	RAB6 Interacting; kinesin-like (rabkinesin6)	8.3
	121779	AA422036	Hs.98367	ESTs	8.3
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	8.0
	105317	AA233926	Hs.23635	ESTs	7.8
	125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	7.8
15	126960	AA317900	Hs.161756	ESTs	7.8
	122969	AA478539	Hs.104336	ESTs	7.7
	130376	R40873	Hs.155174	KIAA0432 gene product	7.7
	123339	AA504253	Hs.101515	ESTs	7.7
	134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
20	111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi	7.5
	123689	AA609556	Hs.256562	ESTs	7.5
	123494	AA599786	Hs.112110	ESTs	7.4
	131985	AA434329	Hs.36563	ESTs	7.4
	106738	AA470145	Hs.25130	ESTs	7.4
25	108768	AA127741	Hs.61345	ESTs -,	7.3
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	7.2
	123308	AA496211	Hs.103538	ESTs	7.2
	106124	AA423987	Hs.7567	ESTs	7.2
20	111345	N89820	Hs.14559	ESTs	7.1
30	105200	AA195399	Hs.24641	ESTs	7.1
	116416	AA609219	Hs.39982	ESTs	7.1
	118846	N80567	Hs.50895	ESTs	7.1
	133434	AA278852	Hs.250786	ESTs	7.1
25	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [6.9
35	115291	AA279943	Hs.122579	ESTs	6.9
	111185	N67551	Hs.12844	EGF-like-domain; multiple 6	6.9
	108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	6.9
	132939	U76189	Hs.61152	exostoses (multiple)-like 2	6.9
40	134520	N21407	Hs.257325	ESTS	6.9
40	114724	AA131701	Hs.256287	ESTS; Highly similar to SPERM SURFACE PROTEIN	6.8 6.8
	116296 102136	AA489033 U15552	Hs.62601 Hs.85769	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c acidic 82 kDa protein mRNA	6.7
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7 (35kD	6.5
	109648	F04600	Hs.7154	ESTs	6.4
45	116401	AA599963	Hs.59698	ESTs	6.4
10	127563	Al367707	Hs.150587	ESTs	6.4
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to L1CAM	6.4
	120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	6.2
	131978	D80008	Hs.36232	KIAA0186 gene product	6.2
50	134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2
	120571	AA280738	Hs.128679	ESTs	6.2
	102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
	100661	HG2874-HT30		Ribosomal Protein L39 Homolog	6.1
	118204	N59859	Hs.48443	ESTs	6.0
55	131386	AA096412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0
	129097	S50223		HKR-T1=Kruppel-like zinc finger protein [huma	5.9
	131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (bamacan)	5.9
	106369	AA443828	Hs.25324	ESTs	5.9
C C	108255	AA063157	Hs.172608	ESTs	5.8
60	125370	AA256743	Hs.151791	KIAA0092 gene product	5.8
	130010	N52966	Hs.142838	ESTs	5.8
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37kD)	5.7
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.7
CE	102221	U24576		LIM domain only 4	5.6
65	130757	R00641	Hs.18925	ESTs; Weakly similar to cDNA EST yk339a7.5 co	5.6
	131278	U81523	Hs.25195	endometrial bleeding associated factor (left-	5.6
	101383	M14113	Hs.79345	coagulation factor VIIIc; procoagulant compon	5.5
	131836	AA610086 U26727	Hs.32990	DKFZP566F084 protein	5.5 5.5
70	129628		Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	5.5
10	106523 111772	AA453441 R28287	Hs.31511 Hs.237146	ESTS ESTS	5.5
	101255	L34600	Hs.149894	mitochondrial translational initiation factor	5.5
	106895	AA489665	Hs.25245	ESTs	5.5
	104943	AA065217	Hs.169674	ESTs	5.5
75	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	5.4
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	5.4
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	5.4
	112305	R54822	Hs.26244	ESTs	5.3
	123972	C14782	Hs.70337	immunoglobulin superfamily; member 4	5.3
80	102676	U72514	Hs.12045	putative protein	5.3
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	5.2
	107865	AA025104	Hs.61252	ESTs	5.2
	121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein S	5.2
	127162	N76398	Hs.21187 .	ESTs	5.2

	131646	AA171895	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA seque	5.2
	121770	AA421714	Hs.11469	KIAA0896 protein	5.2
	122512 105870	AA449311	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	5.1
5	100341	AA399623 D63506	Hs.23505 Hs.8813	ESTs	5.1 5.1
9	116848	H65187	Hs.39001	syntaxin binding protein 3 ESTs	5.1
	120821	AA347419	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	5.1
	130690	AA084286	Hs.139033	palemally expressed gene 3	5.1
	122661	AA454936	Hs.245541	ESTs	5.1
10	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [5.1
	108810	AA130596	Hs.71331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
	120619	AA284372	Hs.111471	ESTs	5.0
1.5	122792	AA460225	Hs.99519	ESTs	5.0
15	129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen (H.s	5.0
	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	129890 101084	M13699 L05425	Hs.111461	ceruloplasmin (ferroxidase)	4.9 4.9
	134859	D87716	Hs.90315	Homo sapiens autoantigen mRNA; complete cds KIAA0007 protein	4.9
20	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	4.9
	105516	AA257971	Hs.21214	ESTs	4.9
	114932	AA242751	Hs.16218	KIAA0903 protein	4.9
	106672	AA461300	Hs.30643	ESTs	4.8
	106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR [M.musculus]	4.8
25	110695	H93463	Hs.124777	ESTs	4.8
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; nonpo	4.8
	133282	U52960	Hs.250855	SRB7 (suppressor of RNA polymerase B; yeast)	4.8
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	4.7
30	120695	AA291468	11- 402425	ESTs	4.7
50	128651 103152	AA446990 X66533	Hs.103135	ESTs guanylate cyclase 1; soluble; beta 3	4.7 4.7
	108699	AA121514	Hs.77890 Hs.70832	ESTs	4.7
	115094	AA255921	Hs.88095	ESTs	4.7
	121429	AA406293	Hs.193498	ESTs	4.7
35	123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
	126802	AA947601	Hs.97056	ESTs	4.7
	130527	C17384	Hs.184227	F-box protein 21	4.7
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.7
40	100449	D87470	Hs.75400	KIAA0280 protein	4.7
40	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	4.7
	115901	AA436403	Hs.86909	ESTs; Moderately similar to Frizzled-6 [H.sap	4.7
	109799	F10770	Hs.180378	Homo saplens clone 669 unknown mRNA; complete ESTs	4.6 4.6
	116195 132122	AA465148 U65092	Hs.72402 Hs.40403	Cbp/p300-interacting transactivator, with Glu	4.6
45	108990	AA152296	Hs.72045	ESTs	4.6
-1.5	109055	AA160529	Hs.48524	ESTs	4.6
	115937	AA443269	Hs.30991	KIAA0957 protein	4.6
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	4.6
	131200	AA609427	Hs.210706	ESTs: Moderately similar to !!!! ALU SUBFAMIL	4.6
50	121369	AA405657	Hs.128791	Human DNA sequence from clone 967N21 on chrom	4.5
	132880	AA444369	Hs.177537	ESTs	4.5
	127386	Al457411	Hs.106728	ESTs	4.5
	120067	W93592	Hs.47343	ESTs	4.5
55	122986 135286	AA479063 AA401269	Hs.102947 Hs.97849	ESTs ESTs	4.5 4.5
55	130155	L33404	Hs.151254	kaliikrein 7 (chymotryptic; stratum comeum)	4.5
	106103	AA421104	Hs.12094	ESTs	4.5
	102654	U68494	Hs.24385	Human hbc647 mRNA sequence	4.4
	107876	AA025315	Hs.61184	Novel human gene mapping to chomosome X	4.4
60	109454	AA232255	Hs.46912	ESTs	4.4
	125960	D63307	Hs.145968	ESTs	4.4
	126892	AI160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.4
	100269	D38550	Hs.1189	E2F transcription factor 3	4.4
65	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	4.3
65	100502	HG1496-HT1		Adrenal-Specific Protein Pg2	4.3
	105542	AA261858	Hs.8241	ESTs; Weakly similar to heat shock protein hs	4.3 4.3
	109787 110759	F10610	Hs.34853	inhibitor of DNA binding 4; dominant negative	4.3
	129970	N21671 AA478975	Hs.19025 Hs.200434	ESTs ESTs	4.3
70	134666	AA482319	Hs.8752	putative type II membrane protein	4.3
, 0	117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h12.5 c	4.3
	111008	N53388	Hs.7222	ESTs	4.3
	120977	AA398155	Hs.97600	ESTs	4.2
	105808	AA393808	Hs.21490	KIAA0438 gene product	4.2
75	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [4.2
	100893	HG4557-HT		Small Nuclear Ribonucleoprotein U1, 1snrp	4.2
	107176	AA621762	Hs.7576	ESTs	4.2
	118976	N93629	Hs.93391	ESTs	4.2
oΛ	130703	N63295	Hs.18103	ESTs	4.2
80	106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
	119367	T78324	Hs.90905	ESTs	4.2
	133633	D21262	Hs.75337 Hs.33085	nucleolar phosphoprotein p130 WD repeat domain 3	4.2 4.2
	105520 114264	AA258068 Z40074	Hs.27595	ESTs	4.2
	HVAFIL		,,	,	701

	131046	X02530	Hs.2248	IP10; 'small inducible cytokine subfamily 8 (4.1
	105220	AA210695	Hs.17212 ·	ESTs	4.1
	103111 125640	X63187 R37700	Hs.2719 Hs.208261	epididymis-specific; whey-acidic protein type ESTs	4.1 4.1
5	110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CONJUGATING	4.1
	118092	N54915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.1
	134891	F03517	Hs.90787	ESTS	4.1 4.1
	112364 120699	R59312 AA291716	Hs.197642 "Hs.97258	ESTs; Weakly similar to DNA-DIRECTED RNA POLY ESTs	4.1
10	106272	AA432074	Hs.32538	ESTs	4.1
	112041	R43300	Hs.22929	ESTs	4.1
	131689 116134	AA599653 AA460246	Hs.30696 Hs.50441	transcription factor-like 5 (basic helix-toop ESTs; Highly similar to CGI-04 protein [H.sap	4.1 4.1
	107638	AA00952B	Hs.42743	ESTs; Weakly similar to predicted using Genef	4.0
15	131941	D62657	Hs.35086	ubiquitin-specific protease 1	4.0
	106154	AA425304	Hs.6994	ESTs	4.0
	105546	AA262032 AA436606	Hs.26089 Hs.7392	ESTs; Weakly similar to 62D9.a [D.melanogaste ESTs; Weakly similar to Gu protein [H.sapiens	4.0 4.0
	106319 121816	AA424814	Hs.187509	ESTs	4.0
20	122851	AA463627	Hs.99598	ESTs	4.0
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi	4.0
	128643 129011	N40212 S72869	Hs.102958 Hs.107932	ESTs DNA segment; single copy; probe pH4 (transfor	4.0 4.0
	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transpor	4.0
25	132323	AA436102	Hs.256559	ESTs	4.0
	134255	J05032	Hs.80758	aspartyl-tRNA synthetase	4.0
	102827 102123	U91327 U14518	Hs.6456 Hs.1594	chaperonin containing TCP1; subunit 2 (beta) centromere protein A (17kD)	4.0 4.0
	102813	U90651	Hs.151461	embryonic ectoderm development protein	3.9
30	113970	W86748	Hs.8109	ESTs	3.9
	107145	AA621108	Hs.173001	ESTs	3.9
	114212	Z39338 AA458934	Hs.21201 Hs.179912	DKFZP566B0846 protein ESTs	3.9 3.9
-	106614 132742	AA490862	Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	3.9
35	120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago nashi	3.9
	129337	R63542	Hs.110488	KIAA0990 protein	3.9
	103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9 3.9
	133330 133928	U42360 N34096	Hs.71119 Hs.7766	Putative prostate cancer tumor suppressor ubiquitin-conjugating enzyme E2E 1 (homologou	3.9
40	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	3.9
	133350	AA135468	Hs.71573	ESTs	3.9
	115623	AA401475 \$82597	Hs.39733 Hs.80120	postsynaptic protein CRIPT UDP-N-acetyl-alpha-D-galactosamine:polypeptid	3.9 3.9
	101973 102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.9
45	134248	AA292677	Hs.80624	ESTs	3.9
	102380	U40434	Hs.155981	mesothelin	3.9 3.8
	116157 106691	AA461063 AA463453	Hs.44298 Hs.23259	ESTs; Highly similar to HSPC011 [H.saplens] ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8
	115844	AA430124	Hs.234607	ESTs	3.8
50	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.cerevi	3.8
	106498	AA452141	Hs.7171	ESTs	3.8
	134405 106260	J04177 AA431448	Hs.82772 Hs.5250	collagen; type XI; alpha 1 ESTs; Weakly similar to BACR37P7.g [D.melanog	3.8 3.8
	109864	H02554	Hs.30323	ESTs	3.8
55	124648	N91948	Hs.125034	ESTs	3.8
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8 3.8
	113702 128639	T97307 N91246	Hs.161720 Hs.102897	ESTs; Moderately similar to IIII ALU SUBFAMIL ESTs	3.8
	111299	N73808	Hs.24936	ESTs	3.7
60	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	3.7
	119741	W70205	Hs.43670	kinesin family member 3A	3.7 3.7
	105012 128734	AA116036 AA343629	Hs.9329 Hs.104570	chromosome 20 open reading frame 1 kallikrein 8 (neuropsin/ovasin)	3.7
	130567	L07493	Hs.1608	replication protein A3 (14kD)	3.7
65	114253	Z39909	Hs.14831	ESTs	3.7
	103169	X68560	Hs.44450 Hs.18885	Sp3 transcription factor ESTs; Highly similar to CGI-116 protein [H.sa	3.7 3.7
	111269 112876	N70711 T03488	Hs.4842	ESTs	3.7
	118261	N62780	Hs.94122	ESTs	3.7
70	130385	AA126474	Hs.155223	stanniocalcin 2	3.7
	129300 134388	C20976 M15841	Hs.110165 Hs.82575	ESTs; Highly similar to ribosomal protein L26 small nuclear ribonucleoprotein polypeptide B	3.7 3.7
	106968	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
~-	100906	HG4716-HT	5158	Guanosine 5'-Monophosphate Synthase	3.7
75	100418	D86978	Hs.84790	KIAA0225 protein	3.7
	101484 102547	M24594 U57911	Hs.20315 Hs.46638	interferon-induced protein 56 chromosome 11 open reading frame 8	3.7 3.7
	102547	Z29083	Hs.82128	5T4 oncofetal trophobiast glycoprotein	3.7
00	130600	AA478601	Hs.258737	ESTs	3.7
80	128733	AA328993	Hs.104558	ESTs	3.7
	134375 134098	AA412720 X06323	Hs.82389 Hs.79086	ESTs; Highly similar to CGI-118 protein [H.sa ribosomal protein; mitochondrial; L3	3.7 3.6
	101188	L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.6
	132149	T10822	Hs.4095	ESTs	3.6

	116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.saplens]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	128609	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
_	101078	L04510	Hs.792	ADP-ribosylation factor domain protein 1; 64k	3.6
5	108693	AA121289	Hs.49597	ESTs; Highly similar to retinoic acid-induced	3.6
	109139	AA176121	Hs.59757	zinc finger protein 281	3.6
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical protein	3.6
	113848	W60080	Hs.27099	DKFZP564J0863 protein	3.6
	127947	AI432475	Hs.146327	ESTs	3.6
10	128056	Al379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
	129914	U22377	Hs.13321	rearranged L-myc fusion sequence	3.6
	132148	AA283988	Hs.4094	ESTs	3.6
	134644	S83308	Hs.87224	SRY (sex-determining region Y)-box 5	3.6
	115047	AA252627	Hs.22554	homeo box 85	3.6
15	102398	U42359		Human N33 protein form 1 (N33) gene, exon 1 a	3.6
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	3.6
	105545	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit [3.6
	101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6
20	105709	AA291268	Hs.26761	DKFZP586L0724 protein	3.6
20	122636	AA454103	Hs.110031	ESTs	3.6
	124792	R44357	Hs.132784	ESTs: Weakly similar to cDNA EST EMBL:T01421	3.6
	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypeptid	3.5
	105427	AA251330	Hs.28248	ESTs	3.5
25	121553	AA412488	Hs.48820 Hs.43728	ESTs .	3.5 3.5
23	115167	AA258421		hypothetical protein	3.5
	134570 110787	U66615 N24716	Hs.172280 Hs.12244	SWI/SNF related; matrix associated; actin dep ESTs; Weakly similar to C44B9.1 [C.elegans]	3.5
	131621	U77665	Hs.139120	ribonuclease P (30kD)	3.5
	132813	N72116	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
30	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
	131965	W90146	Hs.35962	ESTs	3.5
	115221	AA262942	Hs.79741	ESTs	3.5
	116093	AA456020	Hs.50848	ESTs; Weakly similar to KIAA0862 protein (H.s	3.5
	123507	AA600176	Hs.112345	ESTs	3.5
35	129801	F11087	Hs.239666	ESTs	3.5
	115084	AA255566	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	3.5
	123442	AA598803	Hs.111496	ESTs	3.5
	115061	AA253217	Hs.41271	ESTs	3.5
40	100146	D13645	Hs.2471	KIAA0020 gene product	3.5
40	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
	115360	AA281950	Hs.5057	carboxypeptidase D	3.5
	130261	D83767	Hs.153678	reproduction 8	3.4
	100824	HG4058-HT4		Oncogene Aml1-Evi-1, Fusion Activated	3.4
45	102287	U31814	Hs.3352	histone deacetylase 2	3.4 3.4
43	102788	U86602	Hs.74407 Hs.50854	nucleolar protein p40 ESTs	3.4
	118836 102423	N79820 U44754	Hs.179312	small nuclear RNA activating complex; polypep	3.4
	106300	AA435840	Hs.19114	high-mobility group (nonhistone chromosomal)	3.4
	106156	AA425354	Hs.4210	ESTs	3.4
50	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
•	107868	AA025234	Hs.61260	ESTs	3.4
	108187	AA056538	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	3.4
	116123	AA459282	Hs.43756	ESTs	3.4
	119501	W37721	Hs.151363	ESTs	3.4
55	129121	AA127459	Hs.108788	ESTs; Weakly similar to zeste [D.melanogaster	3.4
	131638	D87120	Hs.29882	predicted osteoblast protein	3.4
	132962	N34893	Hs.6153	ESTs; Highly similar to CGI-48 protein [H.sap	3.4
	133767	D63875	Hs.173288	KIAA0155 gene product	3.4
60	111823	R35253	Hs.24944	ESTs	3.4 3.4
UU	134372	D63877	Hs.82324	KIAA0157 protein ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4 3.4
	130938	AA013250	Hs.21398		3.4
	115169 123978	AA258427 C20653	Hs.58427 Hs.170278	ESTs ESTs	3.4
	108807	AA129968	Hs.49376	ESTs; Weakly similar to PROTEIN PHOSPHATASE P	3.4
65	132581	R42266	Hs.52256	ESTs; Weakly similar to bela-TrCP protein E3R	3.4
0.5	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [S.cerevi	3.4
	105730	AA292701	Hs.5364	DKFZP564I052 protein	3.4
	111295	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjugating	3.3
	102009	U02680	Hs.82643	protein tyrosine kinase 9	3.3
70	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s	3.3
	130604	X03635	Hs.1657	estrogen receptor 1	3.3
	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	3.3
	121748	AA421171	Hs.234545	ESTs	3.3
75	106698	AA463745	Hs.29403	ESTs: Weakly similar to PROBABLE ATP-DEPENDEN	3.3
75	134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3
	134154	AA211320	Hs.79404	neuron-specific protein	3.3
	133142	F03321	Hs.65874	ESTs	3.3
	124461	N50641	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from c	3.3
80	104903	AA055534	Hs.124134	ESTs ESTs: Weakly similar to protein phosphatase.1	3.3
UU	106772	AA478106 F09687	Hs.12692 Hs.12876	ESTs; Weakly similar to protein phosphatase-1 ESTs	3.3 3.3
	109704 111131	N64267	Hs.12070	ESTS	3.3
	115019	AA251906	Hs.48473	ESTs	3.3
	116019	AA450312	Hs.237480	Homo sapiens mRNA; cDNA DKFZp434E102 (from cl	3.3

	118528	N67889	Hs.49397	ESTs	3.3
	124027	F03625	Hs.107537	ESTs	3.3
	131699	R68657	Hs.90421	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.3
_	111044	N55443	Hs.23625	ESTs	3.3
5	103768	AA089997	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
	131882	N49091	Hs.3385	ESTs; Highly similar to CGI-134 protein [H.sa	3.3
	123673 132936	AA609471 AB002305	Hs.112712 Hs.6111	ESTs KIAA0307 gene product	3.3 3.3
•	103023	X53793	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
10	120572	AA280794	Hs.258787	ESTs	3.3
	132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	3.3
	105658	AA282914	Hs.10176	ESTs	3.2
	105086	AA147719	Hs.159441	ESTs	3.2
15	118695 112092	N71781	Hs.50081 Hs.140889	Homo sapiens mRNA full length insert cDNA clo ESTs	3.2 3.2
IJ	125154	R44538 W38419	Hs.24936	ESTs.	3.2
	108040	AA041551	Hs.48644	ESTs	3.2
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
••	124006	D60302	Hs.108977	ESTs	3.2
20	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT	3.2
	106753	AA476944	Hs.7331	ESTs	3.2
	102621 103330	U66075 X85373	Hs.50924 Hs.77496	GATA-binding protein 6 small nuclear ribonucleoprotein polypeptide G	3.2 3.2
•	128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [H.s	3.2
25	101167	L15309	Hs.193677	zinc finger-protein 141 (clone pHZ-44)	3.2
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sap	3.2
	112917	T10196	Hs.4263	ESTs; Weakly similar to Iprediction	3.2
	120358	AA213459	Hs.100932	transcription factor 17	3.2
30	121857 122124	AA426017 AA434257	Hs.62694 Hs.186679	ESTs; Highly similar to DNA-REPAIR PROTEIN CO ESTs; Moderately similar to !!!! ALU SUBFAMIL	3.2 3.2
50	132231	H99131	Hs.42635	ESTs	3.2
	134272	X76040	Hs.223014	protease; serine; 15	3.2
	115860	AA431719	Hs.61809	ESTS	3.2
25	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melano	3.2
35	134125	R38102	Hs.50421	KIAA0203 gene product	3.2
	129160 121710	AA131252 AA419011	Hs.109007 Hs.96744	ESTs DKFZP586D0823 protein	3.2 3.2
	102242	U27185	Hs.32943	retinoic acid receptor responder (tazarotene	3.2
	104956	AA074880	Hs.120975	ESTs: Weakly similar to hypothetical protein	3.2
40	113047	T25867	Hs.7549	ESTs	3.2
	115017	AA251880	Hs.179982	tumor protein p53-binding protein	3.2
	133780	M14219	Hs.76152	decorin	3.1
	129453 130353	AA421213 X86018	Hs.111632 Hs.172210	Lsm3 protein MUF1 protein	3.1 3.1
45	106036	AA412505	Hs.10653	EST8	3.1
	102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
	106133	AA424346	Hs.107573	sialyltransferase	3.1
	116803	H47357	Un 6670	ESTs; Moderately similar to weak similarity t	3.1
50	106721 107115	AA465194 AA610108	Hs.6670 Hs.27693	ESTs ESTs; Highly similar to CGI-124 protein [H.sa	3.1 3.1
50	133228	N90029	Hs.6831	Homo sapiens cione 1400 unknown protein mRNA;	3.1
	104733	AA019498	Hs.23071	ESTs	3.1
	103879	AA228148	Hs.50252	ESTs; Weakly similar to putative [C.elegans]	3.1
55	103038	X54941	Hs.77550	CDC28 protein kinase 1	3.1
23	135154 114860	AA126433 AA235112	Hs.173242 Hs.106227	sorting nexin 4 ESTs; Moderately similar to similar to murine	3.1 3.1
	102437	U46569	Hs.221986	aquaporin 5	3.1
	100352	D64159	110.00	Homo sapiens mRNA for 3-7 gene product, parti	3.1
	103631	Z48570		H.saplens Sp17 gene	3.1
60	104238	AB002364	Hs.27916	a disintegrin-like and metalloprotease (repro	3.1
	108613	AA100967	Hs.69165	ESTs	3.1
	115915 120640	AA436884 AA286945	Hs.48926 Hs.163933	ESTs ESTs	3.1 3.1
	124068	H03099	Hs.101619	ESTs	3.1
65	130375	U91931	Hs.155172	adaptor-related protein complex 3; beta 1 sub	3.1
	131632	AA443671	Hs.29826	ESTs	3.1
	131523	H88801	Hs.201676	M phase phosphoprotein 10 (U3 small nucleolar	3.1
	115827	AA427890	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
70	108828 112198	AA131584 R49483	Hs.71435 Hs.22159	DKFZP56400463 protein ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1 3.1
, 0	123960	AA621785	Hs.170008	methylmalonate-semialdehyde dehydrogenase	3.1
	131538	Z29331	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous	3.1
	105616	AA280670	Hs.24968	ESTs	3.1
75	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (zeta	3.1
75	100280	D42085	Hs.155314	KIAA0095 gene product	3.1
	132744 103105	X54326 X61970	Hs.55921 Hs.76913	glutamyl-prolyl-IRNA synthetase proteasome (prosome; macropain) subunit; alph	3.1 3.1
	106984	AA521201	Hs.7129	ESTs	3.1
0.0	105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity t	3.1
80	102302	U33052	Hs.69171	protein kinase C-like 2	3.1
	117708	N45114	Hs.46476	ESTs H.sapiens novel gene from PAC 117P20; chromos	3.1 3.0
	111314 132902	N74574 AA490969	Hs.33922 Hs.168147	ESTs	3.0
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0

	400400				
	128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens] ESTs	3.0
	108746 127236	AA126974 Al341818	Hs.43388 Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	3.0 3.0
	114208	Z39301	Hs.7859	ESTs	3.0
5	107071	AA609053	Hs.35198	ESTs	3.0
_	104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c [S.cerevi	3.0
	124073	H05394	Hs.127376	KIAA0266 gene product	3.0
	130869	AA128100	Hs.2057	undine monophosphate synthetase (orotate pho	3.0
10	101232	L28997	Hs.242894	ADP-ribosylation factor-like 1	3.0
10	104276 126160	C02193 N90960	Hs.85222 Hs.247277	ESTs; Weakly similar to R27090_2 [H.sapiens]	3.0 3.0
	128584	M11433	Hs.101850	ESTs; Weakly similar to transformation-relate retinol-binding protein 1; cellular	3.0
	100405	D86425	Hs.82733	nidogen 2	3.0
	101335	L49054		Homo sapiens t(3;5)(q25.1;p34) fusion gene NP	3.0
15	108761	AA127514	Hs.61603	ESTs	3.0
	111346	N89829	Hs.13259	ESTs	3.0
	114988	AA251089	Hs.94576	ESTs; Weakly similar to phosducin; retinal [H	3.0
	116008	AA449338	Hs.48589	ESTs; Weakly similar to finger protein HZF6;	3.0 3.0
20	116545 117873	D20313 N49967	Hs.74899 Hs.46624	ESTs ESTs	3.0
20	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 protein [H.s	3.0
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	3.0
	131185	M25753	Hs.23960	cyclin B1	3.0
0.5	134380	D38073	Hs.179565	minichromosome maintenance deficient (S. cere	3.0
25	105740	AA293206	Hs.10852	ESTs -,	3.0
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	3.0 3.0
	134423 104896	W96151 AA054228	Hs.83006 Hs.23165	ESTs; Highly similar to CGI-139 protein [H.sa ESTs	3.0
	134407	X72964	Hs.82794	caltractin (20kD calcium-binding protein)	3.0
30	106378	AA445994	Hs.21331	ESTs	3.0
	112283	R53545	Hs.20952	Homo sapiens clona 24411 mRNA sequence	3.0
	109018	AA156960	Hs.114992	ESTs	3.0
	114239	Z39742	Hs.222478	ESTs	3.0 3.0
35	114969 116408	AA250775 AA608752	Hs.87747 Hs.71969	ESTs Homo sapiens mRNA; cDNA DKFZp564P0823 (from c	3.0
33	115286	AA279803	Hs.82204	ESTs	2.9
	105809	AA393827	Hs.20104	ESTs	2.9
	113811	W44928	Hs.4878	ESTs	2.9
40	107248	D59894	Hs.34782	ESTs	2.9
40	134489	U09284	Hs.112378	LIM and senescent cell antigen-like domains 1 KIAA0244 protein	2.9 2.9
	134064 127370	D87685 Al024352	Hs.78893 Hs.70337	immunoglobulin superfamily; member 4	2.9
	113277	T65797	Hs.11774	protein (peptidyl-prolyl cis/trans isomerase)	2.9
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.9
45	109010	AA156460	Hs.44229	dual specificity phosphatase 12	2.9
	130095	F01831	Hs.14838	ESTs	2.9 2.9
	106618 103427	AA459249 X97303	Hs.8715	ESTs; Weakly similar to Similarity with snail H.sapiens mRNA for Ptg-12 protein	2.9
	133980	D00760	Hs.181309	proteasome (prosome; macropain) subunit; alph	2.9
50	111353	N90430	Hs.6616	ESTs	29
	105344	AA235303	Hs.8645	ESTs	2.9
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	2.9
	117910	N50828	Hs.12940	zinc-fingers and homeoboxes 1	29 29
55	118903 121713	N90774 AA419198	Hs.132207 Hs.105577	ESTs; Moderately similar to IIII ALU SUBFAMIL ESTs	29
	129080	H19307	Hs.108507	ESTs	29
	129404	AA172056	Hs.111128	ESTs	2,9
	129457	X55330	Hs.207776	aspartylglucosaminidase	2.9
60	130352	D87450	Hs.154978	KIAA0261 protein	2.9 2.9
	133415 120649	X69699 AA287115	Hs.73149 Hs.99697	paired box gene 8 ESTs	2.9
	131257	AA256042	Hs.24908	ESTs	2.9
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
~~	116734	F13789	Hs.93796	DKFZP586D2223 protein	2.9
65	105028	AA126719	Hs.25282	ESTs	2.9
	114986	AA251010	Hs.87807	ESTs ESTs	2.9 2.9
	105651 1017:14	AA282481 M68874	Hs.18439	Human phosphatidylcholine 2-acylhydrolase (cP	2.9
	123398	AA521265	Hs.105514	ESTs	2.9
70	106007	AA411462	Hs.11042	ESTs; Weakly similar to veli 1 [H.sapiens]	2.9
	109450	AA232183	Hs.173042	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.9
	104685	AA010530	Hs.9599	Human BAC clone GS025M02 from 7q21-q22	2.9
	108677 116028	AA115629	Hs.118531	ESTs thioredoxin-like	2.9 2.9
75	105404	AA452112 AA243303	Hs.42644 Hs.21187	ESTs	2.9
15	132365	AA598694	Hs.46541	Homo sapiens PAC clone DJ0894A10 from 7q32-q3	2.9
	119638	W52480	Hs.56148	ESTs; Moderately similar to NY-REN-58 antigen	2.9
	124637	N80716	Hs.75798	Human DNA sequence from clone 1183/21 on chro	2.9
00	130588	AA287735	Hs.16411	Human DNA sequence from clone 1189B24 on chro	2.9
80	105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s	2.9 2.9
	131818 119298	Z39297 T23820	Hs.3281 Hs.155478	neuronal pentraxin II cyclin T2	2.9
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	2.9
	115089	AA255876	Hs.86919	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.9

	100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1;6) fucosyltran	2.8
	132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide	2.8
	113490	T88700	Hs.173374	ESTs	2.8
5	133451	Y00764	Hs.73818	ubiquinol-cytochrome c reductase hinge protei	2.8 2.8
,	128770 129122	H98645 N62515	Hs.143460 Hs.108790	prolein kinase C; nu ESTs	2.8
	104827	AA035630	Hs.8551	PRP4/STK/WD splicing factor	2.8
	111348	N90041	Hs.9585	ESTs	2.8
	130987	R45698	Hs.21893	ESTs; Weakly similar to cAMP inducible 2 prot	2.8
10	102139	U15932	Hs.2128	dual specificity phosphatase 5	2.8
	114902	AA236359	Hs.39504	ESTs	2.8
	106094	AA419461	Hs.18127	ESTs	2.8
	126438	N93125	Hs.137300	ESTs	2.8
1.5	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	2.8
15	104491	N71513	Hs.39328	ESTs	2.8
	105043	AA132239	Hs.11810	ESTs; Weakly similar to CD4.2 [C.elegans]	2.8
	106855	AA486182	Hs.17975	ESTs	2.8 ·
	109695	F09530	Hs.180591	ESTs; Weakly similar to R06F6.5b [C.elegans]	2.8
20	120455	AA251083	Hs.104347	ESTs	2.8
20	130861	N23393	Hs.20509	ESTs	2.8
	131649	AA481254	Hs.30120	ESTs	2.8 2.8
	128517	AA280617 HG1112-HT1	Hs.100861	ESTs; Weakly similar to p60 katanîn [H.saplen Ras-Like Protein Tc4	2.8
	100486 116729	F13700	Hs.115823	ribonuclease P; 40kO subunit	2.8
25	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor 2)	2.8
23	115465	AA286941	Hs.43691	ESTs	2.8
	100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (theta)	2.8
	125837	H05323	Hs.146401	endothetial monocyte-activating polypeptide	2.8
	131562	U90551	Hs.28777	H2A histone family; member L	2.8
30	129445	AA306121	Hs.111515	ESTs; Weakly similar to predicted using Genef	2.8
	129239	D31544	Hs.109701	ESTs; Moderately similar to weak similarity t	2.8
	106507	AA452584	Hs.91585	protein phosphatase 1; regulatory (inhibitor)	2.8
	101664	M60752	Hs.121017	H2A histone family; member A	2.B
~~	129426	AA412087	Hs.168272	EST; Highly similar to protein inhibitor of a	2.8
35	103437	X98260	Hs.82254	M-phase phosphoprotein 11	2.8
	129821	F11019	Hs.12696	cortactin SH3 domain-binding protein	2.8
	130160	Z39228	Hs.151344	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransfe	2.8
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated	2.8 2.8
40	116204	AA465701 AA262925	Hs.108646 Hs.180034	ESTs cleavage stimulation factor; 3' pre-RNA; subu	2.8
40	125914 131510	AA202323 AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly	2.8
	106291	AA435551	Hs.30824	ESTs	2.8
	122761	AA459296	Hs.105039	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.8
•	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-inducing f	2.8
45	108535	AA084505	Hs.226440	Homo sapiens clone 24881 mRNA sequence	2.8
	116226	AA478729	Hs.76450	ESTs	2.8
	120266	AA173939	Hs.193902	ESTs; Weakly similar to Inner centromere prot	2.8
	128654	H20689	Hs.103180	actin-like 6	2.8
50	116726	F13681	Hs.42309	ESTs	2.7
50	132640	U33821	N= covco	Tax1 (human T-cell leukemia virus type I) bin	2.7 2.7
	133273	AA147725	Hs.69469 Hs.44155	dendritic cell protein DKFZP586G1517 protein	2.7
	108846 105621	AA132983 AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (from c	2.7
	129164	AA282183	Hs.109045	ESTs	2.7
55	133618	U78524	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding prot	2.7
-	120521	AA258785	Hs.107476	ATP synthase; H+ transporting; mitochondrial	2.7
	116429	AA609710	Hs.82837	Human chromosome 3p21.1 gene sequence	2.7
	110984	N52006	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	2.7
	100372	D79997	Hs.184339	KIAA0175 gene product	2.7
60	125134	W19228	Hs.100748	ESTs	2.7
	129254	AA453624	Hs.1098	deoxynucleotidyltransferase; terminal	2.7
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	2.7 2.7
	106589	AA456646	Hs.28661	ESTs	2.7
65	119118	R44122	Hs.42743	ESTs; Weakly similar to predicted using Genef	2.7
05	105973	AA406320	Hs.21201	DKFZP566B0846 protein ESTs	2.7
	106317 115551	AA436568 AA365527	Hs.172140 Hs.177861	ESTs; Highly similar to CGI-110 protein [H.sa	27
	103789	AA096178	Hs.70337	immunoglobulin superfamily; member 4	27
	105079	AA143190	Hs.12677	ESTs; Highly similar to CGI-147 protein [H.sa	2.7
70	109299	AA205649	Hs.86371	zinc finger protein 254	2.7
. •	122089	AA432136	Hs.98682	ESTs	2.7
	129108	L20321	Hs.1087	serine/threonine kinase 2	2.7
	129385	D82675	Hs.110950	Homo sapiens done 25007 mRNA sequence	2.7
	131412	U34044	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	2.7
75	104052	AA393164	Hs.97644	mammaglobin 2	2.7
	116254	AA481146	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PRO	2.7
	106878	AA488872	Hs.12314	Home sapiens mRNA; cDNA DKFZp586C1019 (from c	2.7
	114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED SPLICI	2.7 2.7
80	106831	AA482014 M21259	Hs.29463 Hs.1066	centrin; EF-hand protein; 3 (CDC31 yeast homo small nuclear ribonucleoprotein polypeptide E	2.7
00	101445 124428	M21239 N36881	Hs. 1000 Hs. 82202	ribosomal protein L17	2.7
	114471	AA028074	Hs.103387	ESTs	2.7
	102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	2.7
	106916	AA490814	Hs.24170	ESTs; Weakly similar to ribosomal S1 protein	2.7

	116142	AÁ460649	Un 20457	ESTs	2.7
	116142 109912	H05509	Hs.39457 Hs.24639	ESTS	2.7
	103193	X70476	Hs.75724	coatomer protein complex; subunit beta 2 (bet	2.7
_	102046	U07151	Hs.182215	ADP-ribosylation factor-like 3	2.7
5	104567	R64534	Hs.101469	ESTs	2.7
	112996	T23539	Hs.7165	zinc finger protein 259	2.7
	118138 123095	N57773 AA485724	Hs.93560	ESTs; Weakly similar to trg [R.norvegicus] ESTs	2.7 2.7
	123095	H94892	Hs.192119 Hs.6906	v-ral simian leukemia viral oncogene homolog	2.7
10	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (from cl	2.7
	132834	H77546	Hs.57898	ESTs; Highly similar to NY-REN-49 antigen [H.	2.7
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	2.7
	130648	AA075427	Hs.17296	ESTs; Weakly similar to /prediction	2.7
1.5	106685	AA461551	Hs.16251	ESTs; Highly similar to 73 kDA subunit of cle	2.6
15	133848	AA093287	Hs.76728	ESTs ·	2.6
	134880 128871	AA092376 AA400271	Hs.90606 Hs.106778	15 kDa selenoprotein Homo sapiens mRNA for putative Ca2+-transport	2.6 2.6
	106846	AA485223	Hs.34892	ESTs	2.6
	119892	W84548	Hs.94896	ESTs	2.6
20	132309	AA460917	Hs.2780	jun D proto-oncogene	2.6
	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	2.6
	114365	Z41688	Hs.18653	ESTs	2.6
	114162	Z38909	Hs.22265	ESTs	2.6
25	133370 106818	AA156897 AA480890	Hs.72157 Hs.3542	DKFZP56411922 protein ESTs -4	2.6 2.6
23	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6
	100530	HG1869-HT1		Male Enhanced Antigen	2.6
	130553	AA430032	Hs.252587	pituitary tumor-transforming 1	2.6
	108917	AA137078	Hs.173648	ESTs	2.6
30	122249	AA436679	Hs.258543	ESTs; Highly similar to CGI-07 protein [H.sap	2.6
	119598	W45531	Hs.94642	ESTs	2.6
	119902	W84865	Hs.40094	Human DNA sequence from clone 167A19 on chrom	2.6 2.6
	133272 132575	AA465016 AA045365	Hs.69423 Hs.5188	katlikrein 10 ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.6
35	130459	AA460264	Hs.155983	KIAA0677 gene product	2.6
-	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	2.6
	131130	T19399	Hs.23255	nucleoporin 155kD	2.6
	112043	R43317	Hs.26312	glioma amplified on chromosome 1 protein (leu	2.6
40	116146	AA460701	Hs.193200	ESTs	2.6
40	122378	AA446100	Hs.103617 Hs.2839	ESTs Norrie disease (pseudoglioma)	2.6 2.6
	103134 133395	X65724 AA491296	Hs.72805	ESTs	2.6
	115652	AA405098	Hs.38178	ESTs	26
	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.6
45	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	2.6
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	2.6
	100092	AF000231	Hs.75618	RAB11A; member RAS oncogene family	2.6
	102635	U66838	Hs.79378	cyclin A1	2.6 2.6
50	104490 106813	N71503 AA479922	Hs.43087 Hs.181022	ESTs; Weakly similar to dysferlin [H.saptens] ESTs	2.6
50	106872	AA487907	Hs.18282	ESTs; Highly similar to unknown [H.sapiens]	2.6
	107022	AA599041	Hs.28866	programmed cell death 10	2.6
	107113	AA610073	Hs.23900	ESTs; Weakly similar to oligophrenin-1 like p	2.6
55	113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2.6
22	115586	AA399218 AA424183	Hs.92423 Hs.70945	ESTs ESTs	2.6 2.6
	115779 122895	AA469946	Hs.105325	ESTS	2.6
	124726	R15740	Hs.104576	carbohydrate (keratan sulfate Gal-6) sulfotra	2.6
	129775	R94659	Hs.12420	ESTs	2.6
60	131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6
	132518	D57975	Hs,5064	ESTs	2.6
	134612	AA451712	Hs.171581 Hs.154320	ESTs; Highly similar to ubiquitin C-terminal ubiquitin-activating enzyme E1C (homologous t	2.6 2.6
	130313 131971	AA620323 R70167	Hs.3611	ESTs	2.6
65	133175	AA134767	Hs.66666	ESTs	2.6
	102083	U10323	Hs.75117	Interleukin enhancer blnding factor 2; 45kD	2.6
	125670	A1432621	Hs.82685	CD47 antigen (Rh-related antigen; Integrin-as	2.6
	121822	AA425107	Hs.97016	ESTs; Moderately similar to SH3 domain-bindin	2.6
70	106719	AA465171	Hs.236844	ESTs	2.6 2.6
70	130029 124328	AA236412 H97781	Hs.236510 Hs.14415	ESTs; Moderately similar to PFT27 [M.musculus ESTs; Highly similar to CGI-108 protein [H.sa	2.6
	105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.6
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alph	2.6
	116294	AA489000	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	2.6
75	135339	D59269	Hs.127842	Homo saplens mRNA full length insert cDNA clo	2.6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2.6
	102504	U52077	Hs.247948	Human mariner1 transposase gene; complete con	2.6 2.6
	131076 114096	H44386 Z38342	Hs.22666 Hs.27007	ESTs chromosome condensation 1-like	2.6 2.6
80	120402	AA234339	Hs.50282	GTP-binding protein ragB	2.6
	102125	U14550	Hs.107573	sialyltransferase	2.6
	134653	AA452818	Hs.87385	ESŤs	2.6
•	101959	S80343	Hs.180832	arginyHRNA synthetase	2.6
	116766	H13260	Hs.95097	. ESTs	2.6
				4 - 4	

	104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
	108771	AA127924	Hs.71034	ESTs	2.5
	116439	AA610068	Hs.43913	PIBF1 gene product	2.5
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	2.5
5	132792	AA401903		hemoglobin; gamma G	2.5
			Hs.242985		
	129620	AA010686	Hs.239720	ESTs; Weakly similar to KIAA0691 protein [H.s	2.5
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s	2.5
	115615	AA401186	Hs.48617	ESTs	2.5
	102983	X17620	Hs.118638		2.5
10				non-metastatic cells 1; protein (NM23A) expre	
10	106288	AA435536	Hs.24336	ESTs	2.5
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5
	104525	R16007	Hs.75355		2.5
				ubiquitin-conjugating enzyme E2N (homologous	
	128917	AA204876	Hs.206097	oncogene TC21	2.5
	102299	U32907	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.5
15	115363	AA282071	Hs.152759	activator of S phase kinase	2.5
13					
	130399	AA449417	Hs.155356	Homo sapiens mRNA for putative glucosyltransf	2.5
	130752	D50927 ·	Hs.18895	tousled-like kinase 1	2.5
	132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
					2.5
20	106743	AA476352	Hs.21938	ESTs; Weakly similar to KIAA0704 protein [H.s	
20	128949	AA190993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
	125685	AI040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
•	105826	AA398243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
	110841	N31610	Hs.18645	ESTs; Weakly similar to partial CDS [C.elegan	2.5
	111987	R42036	Hs.6763	KIAA0942 protein	2.5
25	132669	AA188378	Hs.54602	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.5
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mis5; S	. 25
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subunit [2.5
	114481	AA033562	Hs.151572	ESTs	2.5
	113404	T82323	Hs.70337	Immunoglobulin superfamily; member 4	2.5
20					
30	100260	D38491	Hs.174135	KIAA0117 protein	2.5
	103563	Z22534	Hs.150402	activin A receptor; type I	2.5
	104573	R68952	Hs.29780	ESTs	2.5
					2.5
	105025	AA126336	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	
	105524	AA258158	Hs.22153	ESTs; Wealdy similar to KIAA0352 [H.saplens]	2.5
35	106157	AA425367	Hs.32094	ESTs	2.5
	107243	D59489	Hs.34727	ESTs	2.5
	109920	H05733	Hs.30558	ESTs .	2.5
	109981	H09552	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	2.5
	114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	2.5
40					
40	114768	AA149007	Hs.182339	Ets homologous factor	2.5
	118906	N91000	Hs.94433	ESTs	2.5
	119025	N98926	Hs.55209	ESTs; Weakly similar to DMR-N9 PROTEIN [H.sap	2.5
					2.5
	131712	N29502	Hs.30991	KIAA0957 protein	
4	132233	X04706	Hs.93574	homeo box D3	2.5
45	132740	AA227751	Hs.55896	ESTs	2.5
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the beta t	2.5
	128820	F10338	Hs.105309	Friend of GATA2	2.5
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5
	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypeptide F	2.5
50					2.5
50	121361	AA405494	Hs.183052	ESTs	
	134133	X93920	Hs.180383	dual specificity phosphatase 6	2.5
	102502	U51678	Hs.78050	small acidic protein	2.5
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
ے ہے	132874	AA425776	Hs.58609	ESTs	2.5
55	109646	F04543	Hs.5028	DKFZP564O0423 protein	2.5
	111197	N68093	Hs.22909	ESTs	2.5
			Hs.154672		2.5
	102968	X16396		methylene tetrahydrofolate dehydrogenase (NAD	
	124911	R88992	Hs.123645	ESTs .	2.5
	106628	AA459657	Hs.12311	Homo sapiens clone 23570 mRNA sequence	2.5
60	116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens	2.5
00			11- 2205		2.5
	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (
	133578	X78627	Hs.75066	translin	2.5
	100420	D86983	Hs.118893	p53-responsive gene 2	2.5
		W87710	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	2.5
<i>C</i> E	130743				
65	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein (H.sap	2.5
	115117	AA256492	Hs.49007	poly(A) polymerase	2.5
	124582	N68477	Hs.108408	ESTs; Highly similar to CGI-78 protein [H.sap	2.5
	104771	AA025911	Hs.24994	ESTs; Highly similar to CGI-53 protein [H.sap	2.5
	108059	AA043944	Hs.62663	ESTs	2.5
70	105628	AA281251	Hs.35696	ESTs: Weakly similar to putative zinc finger	2.5
					2.5
	109261	AA195255	Hs.61779	ESTs	
	119789	W73140	Hs.50915	kallikrein 5	2.5
	130512	AA045304	Hs.181271	ESTs; Highly similar to CGI-120 protein (H.sa	2.5
		U25165	Hs.82712	fracile X mental retardation; autosomal homol	2.5
75	134402				
75	104769	AA025887	Hs.114774	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	2.5
	125787	. AA744748	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	2,5
	131775	AA459555	Hs.31921	KIAA0648 protein	2.5
•					
	TADLEZ	п.			

TABLE 7B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

PCT/US02/19297 WO 02/102235

	5 4	04741	
	Pkey 101335	CAT Number 46413_1	Accession L49054 N87447 AA248791 AA452193 AI015525 AI762070 AA781526 AW183498 AA625682 AI268713 AA400391 AI193725 AW590304 W56360 AA936067 AI990398 AA406183 AA628888 AA844206 AA621117 AI141092 AI808150 BE379750 AJ351482 AA093527 AA405119 AA400562 AW368723 AA463811 AW242927 R50034 W56334 F21257 AA164314 BE074125 AA470924 AI307439 W16738 AA026647
5	100906	4312_1	T35999 T19178 AA164313 AI744010 AI015466 AI014921 AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 AI795876 AA644165 T36030 AW392852 AA446421 AW881866 AI469428 BE548103 T96204 R94457 N78225 AI564549 AW004984 AW780423 AW675448 AW087890 AA971454
10			AA305698 AA879433 AA535069 AI394371 AA928053 AI378367 N59764 AI364000 AI431265 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 AI202011 R00723 AI753769 AI460161 AW079585 AW275744 AI873729 D25791 BE537646 T81139 R00722
	102221	3861_1	NM_006769 U24576 AW161961 AW160473 AW160465 AW160472 AW161069 AI824831 AW162635 AI990356 AW162477 AW162571 AI520836 AW162352 AW162351 AW162752 AI962216 AI537346 AA853902 H17667 BE045346 BE559802 BE255391 AA985217 AA235051 AI129757 AW366451 T34489 D56106 D56351 AI936579 AW023219 AW889335 AW889120 AW889232 AW889175 BE093702 AW889349
15			AA147546 AI952998 AA912579 A1143356 AW902211 R64717 AW157236 AI815242 D45274 AW263991 AA442920 AA129965 AL035713 AI923255 AI949082 AI142826 AI684160 AI701987 AI678954 AI827349 BE463635 AW628092 AW302281 AA493203 BE348856 BE536419 AW193969 AW673561 AW592609 AI224044 H43943 AA091912 R49532 R48353 AI568409 R48256 Al198046 H27986 H43899 AI678759 AI680310 AI624220 H17052 AA156410 N56062 AI699430 AA664529 T09406 T10459 AA627506 AI379584 N3831 N88633 AW022651 AA971281 AA248036 AI039197 AI914689 AA973825 AL047305 AA129966 AI798369 AW264348 AI445879 AI658759 N67924 AI933507
20			AI216121 AI333174 T10972 AI375028 AI186756 AI273778 AA610487 AI797946 AA853903 AA903939 AI338587 AI278494 AW627595 AA904019
_0	101714	30725_1	M68874 AL022147 M72393 AL049797 BE439441 T27650 Al766240 AW150345 AW778943 Al627464 BE439479 AA587049 Al277900 Al984983 Al630935
_0	116803 116988	55078_4 185904_1	H47357 W33034 H55976 H55975 R67830 AA527091 F24482 AW841585 R66514 AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
25	132640	179_1	AW162087 AA224538 AA471218 AA088655 AA375275 BE440052 AF090891 AA324435 AF063549 AI110675 AA322223 AW953306 AA233590 AW949864 AW949859 AA388721 AA081878 U33821 NM_006024 AA350900 AA081588 AI148087 AF268075 AA088185 AI142478 AA081824 AI887930 AA070570 BE185248 AI459825 BE257794 AA420459 AA420859 AA777997 AA081219 AW815721 AW854758 AA157932 BE018208 AW378974 AL041212 AI247554 AW551897 AI002897 BEE43242 AIB11690 AW852076 AW852270
30			AA360969 AA094943 AA090680 AW601554 AA099673 AA662226 AA356814 AA330174 AA187544 C02751 AA315460 BE168358 AW080447 AI813764 AI624222 AW156901 AI954032 AW473780 AI861975 AA173643 AW511541 AI951492 BE301686 AA669760 BE182212 AA081009 T69431 AI186207 AA604124 AA707346 AA173953 AI016700 AI125916 AA356962 AI673719 T90593 T90497 T10776 AW513002 AW304292 AA724885 AW474759 AI811621 AW068925 AA666305 AI8680161 AI128023 AW471151 AA534849 AA666358 AI078833 AI139223 AI244874 AI381658 AW763441 AI32440 AW802882 N66401 AA224251 AI167469 AI141060 AA099214 AI537130
			AL120428 AA948655 D53110 AA076099 AA938617 AA826543 Al357914 AA565098 AA807994 Al288812 AA632832 AA157933 AA639802
35		,	AA634268 AA282337 AA651431 AA557374 AA256923 AA872943 AA009665 H89626 AA810386 T92925 T36145 AA632190 AA130436 AI686635 AA130437 AW392904 AW392839 AW392848 AW392836 AA729737 AA070450 AW392890 W04825 AA771848 AA084634 AA481985 AI263840 AI801006 AA235380 AI954229 AI559330 AI208724 AA887638 T25894 AA041269 W44443 AI581770 W46171
			AAB78485 W46535 AA197336 AA894945 AA394224 A1766834 A1582590 A1033007 AA481889 AW190598 AW392855 R27279 AA398137 A1248407 A1241386 A1991753 A1826585 AA865699 A1096806 A1833030 AA041279 AW888745 A1703279 N70572 A1912553 BE549931
40			Al240422 AW376187 AW591692 AA975905 AW614967 AA009666 W44332 AA664659 T06561 BE468150 Al650695 AA587920 Al473310
			Al032991 AA256499 AW104241 BE163782 Al984973 BE163613 Al263906 AA628191 AA282072 BE163769 BE163775 Al492939 Al473315 D56907 AA587930 H89480 Al362373 AA598483 D56595 Al167590 C16223 Al935415 D62555 D62884 D63130 Al760286 Al650286 AW173598 Al499145 Al122566 AW903408 Al810569 AA854936 BE049510 D62065 D61900 D62101 R27475 Al469835 Al669086 N80399
45	400407	40000 4	N48922 N48746 AA481381 R22858 H13912 AC004549 AW602500 AW768788
43	103427 103631	43892_1 152_34	BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000192 BE562219 BE266655 BE264970 R64730 AF214731 T19173 BE258318 AF161446 BE542228 BE383856 BE206748 BE543260 AA640735 AA788907 BE251313 BE221852
			AW855357 AA224407 AW855346 BE150454 AW070651 BE326867 AW051698 AI829278 AI470927 AW855345 AI804942 AI971004 BE046620 AI863664 AA808492 AI915971 BE046949 AW590711 AI468066 BE409685 AA332653 BE385394 AA852623 BE255591
50			BE254968 AA211871 BE255493 BE257727 BE255389 BE257491 BE262528 BE261296 BE313277 BE261714 BE314316 Z28434 AA315545 BE008562 BE012093 BE161393 T31969 AA305848 AW955238 BE619156 AI191748 AA323396 AW361760 AA216118 BE264939 AA325954 AW580281 AA302597 AW888908 AW888893 BE312970 AA134402 H52679 AA478191 T34090 AW961505 Z24771 AA179552 R57244
			BE315207 AW503121 AI372747 T33143 AW377460 T33141 R14922 AW352414 H93249 AW405576 T33102 R89545 N46625 H08434
55			BE165062 AW367891 H93121 H47325 T30931 AW402852 H47410 Z20368 T18928 T30758 H93254 AW389725 R96628 Al372407 R88995 AI815980 AW157278 AW607664 AW163288 AA133492 AA099328 AA157348 Al816063 AW449556 AA157252 AW608980 H66576
23			ANI 13980 AW 187276 AW 105266 AW 105266 AM 153492 AW 29526 AM 154 ANI 13066 ANI 13056 AW 2449350 AW 24526 AW 26566 ANI 13046 AW 24526 AW 2
60			BE547161 BE082634 AA642471 BE619719 BE082719 W28879 AW794944 C01685 Al291127 AW166099 Al936102 Al476929 R70284 AA872914 W31065 N54216 Al568741 H56262 NM_017425 Z48570 Al831777 T75007 AA354867 AA427988 Al922844 AA733170 AW821145 BE081547 AW881571 AW881573 AW055249 AA204724 Al417415 Al127303 Al355013 Al039527 AW593259 AA576745
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03			AA854796 AA427863 AA224345 AA889899 AI347782 AA931056 AI076059 AI360841 AI797975 AI362268 AI200968 BE350785 R97433 N98499 AA134403 AA035355 AW263162 AI369607 D80144 AI376627 AI520801 AA365942 AI707705 AI123495 T33101 H08716 AA804238
			AA922201 AA723522 AW183592 AI445884 F34614 AW022342 AA363998 AA568793 AA152475 D31233 AA852622 AA099862 AI129147 AA922699 AA782664 T33142 T30009 T32913 AI676138 AI914657 N34899 AI372746 AI265911 AI352444 AA443158 AA910603 AI420273
70			AABEB050 ALZ77700 C14224 AVIO82087 R41447 Z38385 AI911845 AI961888 R91976 F04560 AA661955 AI857675 AA369666 AA424207 N79953 AA382958 AA894626 AI884964 AA846989 AA215454 AI742580 AI339437 AI806879 AI091373 AA782558 AI026868 AW590904
			AW204599 BE348235 AI819318 AA122324 AA939221 AW139711 AA131608 AW613548 AA122286 AI309179 AA437247 AW339322
	129097	25953_1	AIG71305 AW439848 AA131701 AI078075 N64624 AA812881 AI140547 BE243933 AA355449 T29766 F08396 N83324 NM_006963 S50223 AI207648 AA258092 AA113952 AI311718 AI128612 AW607449 M77172
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80			AW104611 Al338576 R21507 Al367623 BE244484 Al269308 AA031667 Al884346 AA731989 AA988943 AA235951 AA807887 AA642645 Al246489 N29739 Al216718 Al383349 Al038618 Al351476 AA806031 Al914178 H10711 Al095573 H89220 AW470854 AA729015 R83353 AA782239 R34295 H87165 AW419059 Al653689 Z40349 H89114 AW074506 AA397785 AA888377 Al911228 F03193 Al468783 AA702615
	120695	9683_3	AI830829 AA748323 R37224 AA424915 AA731647 H47183 AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201
			A1633384 AA425910 A1017004 A1241295 AA402816 AA291468 156
			130

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	100352	37786_1	AL133887 D64159 AF112218 AJ766533 AL039303 AL133888 BE620604 AW976259 AW262792 AW591383 AJ365413 N36652 AA807027 AJ472041 BE620065
	101084	13883_1	AW409934 AW245855 AU077157 AW163245 AW161434 AW250083 AA316055 BE621134 AA171883 BE272494 L05425 BE250310
_	•		NM_013285 BE311494 AAB58436 AA308223 AW362598 AA373618 BE394454 AA126101 AA581348 AA303227 AA058438 AA126544
5			AL135350 AW996947 AA403201 AA446682 W79685 AW246249 AW577783 AW002316 AA320025 AW753913 Al798554 AW070650 BE250413 AW250835 BE076336 Al925558 Al907634 AW804193 AW804270 AA902387 AW804232 AW804255 AW607751 Al909114
	_		AW157242 AA9334590 AI628921 A1470650 AW409935 AW172793 AA401208 AW162279 AA888018 BE206452 AI826742 AA857353
			AA483614 AA126418 AA722289 AA780182 AW768894 AW183614 AW156969 Al244063 AA863491 Al376281 AA582490 AA846248
10			AI474094 AW246802 AA446557 AA126000 AI699045 AI702310 AI253092 AA171554 AA831455 AW118384 AI954511 AI760439 AI867001
10	100502	26409_1	AA493881 W81287 AA515590 AA659297 AA635139 AA659293 AA766044 AA196109 N32569 AI907635 U15979 X17544 W52755 NM_003836 Z12172 AW370136 BE262564 T49116 AA333753 BE262238 BE313737 H38153 AW583056 R28890
	100502	20409_1	BE259532 D16897 AA885610 AA911293 AA319627 R94472 R29022 AA443405 R96397 W04904 W01746 W01204 N74203 N58621
			AA701996 AW418723 N53220 AA602813 AA576129 AA593786 AA911577 AA575957 A1149135 AW573058 AA772985 A1188918 A1372065
1.5			AA575838 W60010 Al004576 Al131265 AA319845 T50070 Al335742 AA235245 W32706 AA447372 R96355 N59573 AA904616 Al291224
15			BE467454 T49117 Al268620 AA928248 AA449494 AA318817 T49929 R94473 H38154 Al076649 AW935307 AW605112 AW935433 AW935342 AW935310 AW935345 Al298308 AW935395 AW935384 Al184857 AA319871 T29465 C21134 Z19785 AA329107 T52079
			AW353346 C06234 AI951555 T49928 AA371745 AA369296 AA346673 R82547 T50006
	102398	entrez_U42359	U42359
20			
20	Table 84 lists	s about 64 agges up	regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01
			to of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to

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enerunp array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 8A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene Title
ratio: ration turnor vs. normal tissues

30

0.0	Pkey	Ex. Accn	UGID	Title	ratio
35	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	12.1
	101249	L33881	Hs.1904	protein kinase C; iota	11.8
	132528	AA283006	Hs.50758	chromosome-associated polypeptide C	11.5
	102610	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.0
	115536	AA347193	Hs.62180	ESTs	10.0
40	· 129571	X51630	Hs.1145	Wilms tumor 1	9.3
	105298	AA233459	Hs.26369	ESTs	7.8
	121779	AA422036	Hs.98367	ESTs	7.3
	104301	D45332	Hs.6783	ESTs	6.9
	132191	AA449431	Hs.158688	KIAA0741 gene product	6.7
45	102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.6
	101804	M86699	Hs.169840	TTK protein kinase	6.5
	132572	AA448297	Hs.237825	signal recognition particle 72kD	5.9
	106738	AA470145	Hs.25130	ESTs	5.8
	108857	AA133250	Hs.62180	ESTs	5.8
50	115291	AA279943	Hs.122579	ESTs	5.8
	132632	N59764	Hs.5398	guanine-monophosphale synthetase	5.8
	116401	AA599963	Hs.59698	ESTs	5.7
	132725	L41887	Hs.184167	splicing factor, arginine/serine-rich 7 (35kD	5.7
	129097	S50223		HKR-T1=Kruppel-like zinc finger protein (huma	5.6
55	134520	N21407	Hs.257325	ESTs	5.5
	108778	AA128548	Hs.90847	general transcription factor IIIC; polypeptid	5.4
	131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (barnacan)	5.2
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	5.2
	108055	AA043562	Hs.62637	ESTs	5.1
60	132939	U76189	Hs.61152	exostoses (multiple)-like 2	5.1
	115909	AA436666	Hs.59761	ESTs	5.0
	120438	AA243441	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.0
	123494	AA599786	Hs.112110	ESTs	5.0
	109648	F04600	Hs.7154	ESTs	4.9
65	132624	AA164819	Hs.53631	ESTs	4.9
	111234	N69287	Hs.21943	ESTs; Weakly similar to ORF YGL221c [S.cerevi	4.9
	135242	M74093	Hs.9700	cyclin E1	4.9
	123005	AA479726	Hs.105577	ESTs .	4.8
	116296	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (from c	4.7
70	100661	HG2874-HT3	3018	Ribosomal Protein L39 Homolog	4.6
	111345	N89820	Hs.14559	ESTs	4.6
	102627	U66561	Hs.158174	zinc finger protein 184 (Kruppel-like)	4.5
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.5
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)-like	4.5
75	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	4.5
	130376	R40873	Hs.155174	KIAA0432 gene product	4.4
	120619	AA284372	Hs.111471	ESTs	4.4
	122802	AA460530	Hs.256579	ESTs	4.4
	116416	AA609219	Hs.39982	ESTs	4.3
80	115094	AA255921	Hs.88095	ESTs	4.2
	126802	AA947601	Hs.97056	ESTs	4.2
	126892	Al160190	Hs.76127	hect (homologous to the E6-AP (UBE3A) carboxy	4.2
	105516	AA257971	Hs.21214	ESTs	4.1
	131985	AA434329	Hs.36563	. ESTs	4.1
				4	

	444000			507	4.0	
e	114965 120821 134621 134161	AA250737 AA347419 L02547 U97188	Hs.72472 Hs.96870 Hs.172865 Hs.79440	ESTs Homo sapiens mRNA full length insert cDNA clo cleavage stimulation factor; 3' pre-RNA; subu IGF-II mRNA-binding protein 3	4.0 4.0 4.0 4.0	÷
5	TABLE 8B					
	Pkey: Unit	que Eos probese er: Gene cluster : Genbank acces	number			
10	Pkey	CAT Numb	er Accession			
	101249	2520_1	L18964 N AW08751 AW95029	M_002740 l33881 aa095249 be080871 aW605320 M85; 4 ai480090 ai873147 t57875 ai217404 aa827196 ai279; 14 ai032193 ai953696 ai630583 aa062633 be541355 aa;	471 AA969093 AA815168 AA988896 AI754 180493 AW015748 AA255651	
15	100661 116401	23182_1 95855_1	AW89394 Z21891 A	1 L05096 AA383604 AW966416 N53295 AA460213 AW57 IO AW978851 AA034240 A1686323 A1767653 AA829515 A A835700 AA599963 T20152 AA533167	A053933 AA737691 W92607 AW261869 A	
	116416	373989_1		'6 R11789 AW001886 AA609219 AW780420 Al860557 Al2 142970 R63752	280331 Al334300 Al288870 AA669343 N29	918 BE537790 AA934687
20	132191	54683_4	AA50757 A1189144 A1743979 A1380330	6 A1610269 A1380079 R40309 A1203932 A1342128 A13425 A1016691 W45515 AA551452 AA449431 T10046 AA4240 A1283341 AW340338 AA774643 AW104778 A1078020 N2 A1247787 AA770467 A1200154 A1089863 A1089890 A1698 4 AA907692 N21250 AW994736 A1909337 A3887772 AW	159 NG2822 AW197701 AA465242 Al41898 21487 H97562 AA970063 BE327945 F0388 5738 W88524 Al471010 AA700191 AA7789	9 Al942433 Al891115 BE302316 10 F03885 AA970699 Al298468 137 BE440182 R79225 AA338236
25			AA46559	8 AA321185 AW130492 AI824479 AI682992		
	130941	2774_1	AW24890	369 D49394 BE252349 AW249320 AW249140 AW250535 D3 AA731733 AA804169 AA703169 AI435492 AI076288 AJ	A912176 AW248713 AA743457 R08170 C0	6167 R02351
	115909	47548_1	AA97533	27 AA453863 AA442475 AF086541 AA365801 Al692575 A 17 AA365503 Al632902 AA659686 AA665087 C00396 AA9	88869	
30 35	108778	18565_1	AA42930 Al126654 AW29514 AA42823	3 NM_012086 AA128292 S81493 AL137453 BE614053 AA 6 R13465 R56236 AW994182 W00838 AW994417 AW994 1 AA626457 AA291327 H67983 H66271 H67976 AW27095 43 Al433661 AW608361 AA873402 Al217453 Al953358 AA 8 Al001932 Al735550 Al951370 AA766807 S81492 AA918 3 Al635824 Al186039 AA741312 Al040184 H67656 AA258	1404 AW994426 AW994321 AA516147 AA: 15 AA758221 A1023487 A1921811 A1953370 A262143 AA928495 A1475268 A1167211 AV 1976 A1040967 R70939 AA469065 T70340	345603 AW953009 BE315104) AF085850 R70992 N25129 N385961 AA259045 AI762630 AA477615 AA478070 AI017743
33	102136	17647_1	AI206773 AA30057	3 A1879827 R64193 6 U15552 NM 014597 AA223318 AA171806 BE269461 A'	W578439 AW604388 AW953513 AA77281	6 AW604383 AW577851
40			AW0022 AI95341	2 AW117711 AW366303 AW366302 AW366308 AW36630 56 BE064947 BE064722 T10372 AW838681 AI811119 AW 3 AU64798 AI420425 AA191324 BE503222 AI632721 AA1	/262098 AA588547 Al916666 Al440083 Al0 80035 AA558329 W44843 T10610 W38442)78150 F24260 AA512919 2 BE542869 AI125024 BE279566
	108857	61_1	AK00148	36 AI589491 AA559096 AI090265 AA548959 AA223220 A 8 AA190315 AA374980 AW961179 AA307782 AA315295	AA347194 AW953073 AW368190 AW3681	92 AA280772 AA251247 N85676
45			A147516	2 A1216389 N87835 R12261 R57094 A1660045 AA347193 5 AA300756 R40626 A1122827 AA133250 A1952488 AA970 3 A1872789 A1919056 A1611216 AK001472 BE568761 AA5	0372 AA889845 AW069517 A1524385 AA19	00167 Al341261 Al818674 D20285 90314 Al673359 AA971105
73	102305	18424_1	AL04320 AA20720	2 U33286 NM_ 001316 AF053641 ALD48769 N99830 AA28 87 AA315560 AA113938 AW386317 AW386316 L44546 AV 84 AW993922 BE003403 AA251521 AA382754 AA339152	63091 AW408174 N90467 R84306 AA3178 N386335 AA243317 AA713588 AA192541 A	AA649035 BE300737 AW752491
50			BE07573	12 AA471242 H17790 F11801 T84903 R78076 BE614356 F	R16380 R16395 AA876127 W95535 AA164	1768 A1279876 H02142 C18698
50			AA8373 AA23699 A\75406	6 AW954410 Al539769 T39128 AL121103 AA192466 AA2 11 AA075484 AA075621 AA778294 AA587266 T69722 AA- 17 AA459274 Al150191 AA165156 Al198839 AA789258 AI 2 A1753243 AA934719 AW439362 H02038 C17463 Al4009 BE094097 Al826398 H58956 T17222 AW139044 Al27134	446118 x85624 ai334209 ai587101 ai2812 139373 aa236574 ai127770 aa678954 ai 951 aa227539 n66040 r89384 aa872668 a	280 AA568602 AA946837 C75603 140786 AA113939 AI187231 Al344110 W95420 AA164700
55			Al86871 Al27840 BE39793 AA45950	1 AA582354 AA524392 R01549 R01641 Z21083 AA52846 6 AW609291 AA137749 AA142866 AA639198 AW609271 11 AW609285 T66602 T99684 T97378 AW609366 T85647 33 N95643 AW821210 AW813461 AW582064 AW609293 V 56 AW582079 AW609276 AW609280 AW609290 AW55	3 T39127 AA989472 F09450 AA084485 BE AW149760 Al025112 AA236620 AA937248 AI572235 T99083 AA199583 AW303874 T AW609320 AW609270 AW582085 AW5820	2004378 AW974353 AA137250 B U90736 AW005487 AW674427 C35523 AA586445 Z39669 D71 AW609318 AW813451
60			F06655 . AA9126	AW605343 AA446426 BE090595 AW969578 T79852 Al08 24 D60376 T10180 AA705847 Al018123 AA493197 T6708: 53 H77483 H68082 R42337 H58601 T97267	2505 N63239 A1973168 A1086182 AA84671	11 AI874213 AA730605 AI927257
	109648 132528	708849_1 11027_8		A1362549 A1671064 T23526 F03426 F04694 F04600 A163! AA284422 AA283006	5856 Z38715 F02039 AW022635	
65	101804	26587_1	M86699	NM_003318 AL133475 AA122377 Z21415 R57092 AA806	.569 AA811904 BE538323 R41558 AA4216	20 Al337292 AA470077
	132572	31281_1	AI92965 BE2519	71 ÄA543024 A1677941 A1472200 A1215042 AA732384 A4 9 AA227827 AF069765 AW408768 NM_006947 AF077015 81 AA355433 AA481126 AW403053 BE542282 A1929818 90 W93905 W96519 A1863832 AA443177 AA730942 T995	9 AA220974 H07969 C14621 D52294 BE51 AL120605 AW753079 AW391834 BE01860	2960 BE614138 BE258539 33 BE395262 W21406 AW663259
70			AW0818 A192140 N74716 T90801	19 Aa714970 A122630 W04887 AW662427 Aa602680 W 4 Aa143770 Aa587675 BE302192 Aa813080 Al493386 A' AW969249 Aa468581 Aa516399 Al274726 A1131244 Al51 A1383246 A1740957 T86758 Al471248 A1864233 Aa91059	/93645 AA582946 AW008812 AA311187 A W327435 AW340871 Al143616 AA687231 72604 Al929236 AW327971 R65637 N9030 0 Al079094 AW805781 AA709025 AW1967	A463631 A1421918 A1400518 AA218961 A1362249 A1378345 D9 H07877 W96486 A1358806 707 AW327436 A1903790
75			AW7692 AF0861: R35393	6 T99348 A1924643 AW103910 A1802993 A1080390 T9905 95 W32639 AA363094 N89012 W39751 A1291329 A12913 31 AA373679 AA165043 AA355705 A1243507 A1027796 A AA448435 AA334659 AW879356 AA436527 AW972044 W 2 N50381 AA736938 A1089112 AA863053 A1359793 AA96	771 AA829411 A1985219 A1422775 AA9189 A573461 AA757260 A1370979 AA574149 A V25165 AA521219 A1094141 A1302096 AW	40 AA363108 AA192633 A558276 N70650 A1478948 578551 AW578534 AW390535
80	131985	113870_1	AA5030 AA4343	46 AA342341 AA355159 T85701 BE162893 T99703 20 A1858190 A1686571 AW615203 AW073686 AW172459 29 AA171844 A1684143 AA953518 AW470108 A1870700 A		
	132624	42095_1	AA3261	AA404225 AA075632 AA172293 H51911 08 W74020 AW612698 A1750909 AA487800 AJ270695 AA AA525338 AA526640 H84308 AA278942 AA164818 AA84		

			AA961206 N41430 N41439 AW630477 W37595 BE394538 AA365256 N47771 N34873 AA988105 A1242138 AW148523 A1978761 N50882 AA527448 AW086200 A1750910 N50868 AA709437 N51946 A1222179 AA732883 H96732 AW615360 N53720 W37490 R87362 AA613273 H98999 A1459022 A1368442 A1460122 N20486 N24087 AA164819 N24878 AW471270 AW590458 R68240 AA594434 N20400 A1419626 AW500664 A1033658 AA593215 AA907408 AA713508 A1422627 H85551 AA923571 D2680 AW627456 H96206 AA016289 AA485896 N25691
5	132632	4312_1	AU076916 BE298110 AW239395 AW672700 NM_003875 U10860 AW651755 BE297958 C03806 Al795876 AA644165 T36030 AW392852 AA446421 AW881866 A469428 BE548103 T96204 R94457 N78225 Al564549 AW004984 AW760423 AW675448 AW087890 AA971454 AA305698 AA879433 AA535069 Al394371 AA928053 Al378367 N59764 Al364000 A431285 T81090 AW674657 AW674987 AA897396 AW673412 BE063175 AW674408 Al202011 R00723 Al753769 Al460161 AW079585 AW275744 AB73729 D25791 BE537646 T81139 R00722
10	102610	9336_1	U65011 NM_006115 AW182053 BE383930 BE407839 BE409930 BE408826 AW370292 AA312859 AA136204 AW365852 AW365735 BE622732 AW939295 AA781195 Al017284 AW375329 AW375366 AW178038 AW178333 AW178424 AW365726 AF025440 AW172852 AL570998 AW117792 Al885499 BE465516 BE207427 AW130942 AW513316 AW770892 BE207426 AW173563 AW168292 AW173565 AW16101 AV744983 Al861974 BE207404 AV74982 AL613210 AW591505 AW169285 AL521444 AV745044 AL627904 AL690634 AL289305 AA861253 AL612799 BE207425 Al149694 AA902662 AL082468 AL014752 AA613844 AA725693 AA136089 AL290092 AA565489 AL689083
15	102627	25245_1	AI859014 AW051225 AA665758 AA496991 AA564738 T19428 AI567170 AW166726 AW084200 AW188723 AA617626 AI918664 AW381473 AW391543 AA598817 AW088942 AW050423 AI562502 AI680308 AI687500 BE327836 D20455 BE410282 BE254766 BE256014 AA357423 BE618208 AA489577 AW182114 BE379147 AL021918 AA160639 U66561 AA321623 U52098 AL119453 AA455712 N80080 N46550 W07223 N75923 W05057 AI811577 AA455657
20	132725	29101_1	Al275409 Al139121 Al927568 Al927562 Al139471 AA160473 N78795 Al719983 Al718928 AA723097 Al335776 N39140 N59184 Al587600 Al864812 AA732097 N74667 AA832398 H89600 D19825 Al554833 NM_006276 NM_006276 L41887 L22253 BE379909 BE567870 BE274265 BE539518 AW239523 AW239271 Al093618 BE504485 AA580279
20		25101_1	AAA94481 BE4A0161 AW780428 BE543960 D55986 AA852399 Al630020 W77996 AA278193 R10505 Al963201 Al739336 BE174301 AA662222 AA664912 AA244152 AW611553 BE503285 AA211023 AA383016 Al698174 AW195381 AA948229 Al768495 Al690437 N30025 AI718952 Al953572 BE464509 AA777315 Al337221 AW070910 Al953848 AW674561 H54177 AW510890 AW078699 Al436178 AA630759
25			BE502074 AA278769 Al499038 AW469072 AA778071 AW236753 Al933033 Al690458 Al276691 AW768235 Al952118 AA425156 AA610579 W73953 AA244153 W86034 Al948872 Al952678 AW0087811 Al333591 Al869883 Al926911 W48865 AL048024 AA214485 Al972522 A151368 W48738 AA214467 AA334640 Al678170 AA927525 AA581588 W96283 AA365470 Al471919 AW611488 AA211834 Al365198 Al698365 AW002238 AA507624 W96150 AA446490 AL048025 AA852400 AA362221 Al338376 R35083 AA290812 R10397 AA975988 AW236462 Z43032 H16969 F13487 D19858 AA452207 BE035942 AA344396 AW949533 AA279472 AW902406 AW070440 BE395195 H00835 AA300750
30			AA729303 AA420591 AA385025 AA420542 R69155 AA420592 AA281747 N88502 AI458206 AI700996 AW418607 AW341202 AI825892 W00640 AA214405 AA044744 AI950617 BE467493 AW474113 AA446310 BE328705 AI911573 AW243968 AI628622 AW173020 AW079958 AI140387 AW051969 AW299438 AI127170 AW769164 AI422435 AI307116 BE549519 AI371116 AA281748 AA701073 AA679948 BE551197 N50345 AW338776 BE326601 AI142892 AW470587 AI989568 AA911241 AW294822 AI174414 AA804366 AI004725 AW271994 AI559313 AI270102 AI351542 AW768904 AA765964 AI961708 AI149231 AA995907 AI094280 AI185753 H01219 AW768846 AA747500 AA970106 AI601238 AA513452 AW612802 BE075163 R39171 AI565328 AI375559 F10356 AA284625 BE241509 AI702889 AW193010 AA649847
35	111234	83711_2	AW439150 AA721407 AA810333 AA706384 AI049887 BE569015 BE562280 BE566618 AW957342 R69269 AA902656 A1185915 R43705 H15150 H09794 AA832464 AI697438 AI354538 AI436354 AA948272 AA928143 AI091263 R41658 AI352580 AI902656 A1185915 R43705 H15150 H09794 AA832464 AI697438 AI354538 AI436354 AA948272 AA928143 AI091263 R41658 AI352580 AI122948 AA946670 AI340088 AI275007 N70255 AA721176 AI934162 AA827098 AA935934 AA827088 AI081207 AA992399 AW130757 AI805667 AA035556 AI379266 AI093901 AI098234 AA909079 AA516079 AI572357 AA205969 AI432383 AA905290 AW628920 AW182996
40			Al266084 N49879 AW024457 Al246246 Al934031 Al369270 Al003836 AA010063 AA494361 Al284151 Al919536 N34884 N69287 AW510465 Al358609 AW081421 AA706205 Al085317 Al140633 Al347104 AA602547 Al686707 AA872686 AA694028 Al094546 Z40832 Al382838 AA510132 AA501433 H84120 Al140722 AW674839 BE5038022 AW663895 BE327472 AW393494 Al340087 W04189 AW393499 H56506 BE089878 BE301950 Al025475 AA724446 BE275324 H15210 AW957667
45	134161	16074_1	AA634543 AI682259 AF117108 BE396917 NM_006547 U97188 U76705 BE560799 BE396918 BE269531 BE560268 BE560346 AA836048 AL023775 BE545535 AA427803 C18804 D58801 AA303353 U46218 BE539704 AA187966 AA52545 AA261821 D63197 AI824109 A1086047 AI424833 AI807368 AI250857 AA741476 AI146832 AA169615 AI690821 AI274288 AW136704 AI206172 AA917039 AA243584 AI808611 AW674709 AA935733 AW450092 AA905172 AA917132 AA471196 AA302256 AW673348 AI352044 AW511295 AA247134 W81035 AA722962 AW662471 R6432 AW044616 AI086619 AW628546 AW043682 AA425750 AI743038 AI368723 AA187143 AI376987 AI803976 AI275537 AW471358 AW104877 AA195464 W81072 AW197351 AA932674 AI393420 AI434998 R63822 AW085083 AI240272 W87006 AA011347 H58428 AI497895 R23223
50	132939	11857_1	AB009284 AF000416 AA022636 BE082610 AW367997 AA491410 AA337477 AA336421 W38526 AA625283 AA773685 AA490078 T66134 AA847838 AA022647 AW054726 AI918001 AA431966 AI263596 AI804298 AW469314 U76189 AA779001 AA625945 AL042357 AI674730 AA410350 AK001450 AV664353 AA058443 DB1618 AA653665 W31930 AA334445 AW956767 N47777 AA883784 AA428916 AI652062 AA329703 AI417923 AI435031 AA708791 AI989636 AI220345 AI239913 AI220102 AI435875 AI076731 AI377049 AI039173 AW972638 N90076 AW263652 BE440048 BE440013 AA577463 AI039774 AW204992 AA846580 AA501952 AA342058 AA508525 D61670 W31725 AI689499
55	111345	6692_1	AI955969 AA526628 AI282717 T66198 AW263155 AA314512 AW408152 AA360413 BE206274 AK001402 AA307665 AW954678 W39078 AW369236 AW369115 AW369096 AW753235 AW369072 AW361194 AW369125 AW364187 H94225 T79502 AA131908 BE071359 AW368503 AW801517 AW801322 AI674163 AAB61077 AI738568 AI830199 AW118577 AI478895 AI688497 H92996 AW083479 AW970625 AW613124 AI632234 AI654210 AI696847
60	104301	145380_1	A1923423 AA131909 AA806630 AA806158 AW592520 R96509 AA813923 AA502823 AW467889 AA960972 AA994566 A1280346 AA884588 AA653563 A1200023 NB9820 AW768792 C00145 R96554 T79416 AA768491 AA476251 AA809748 A1862628 AA621244 A1379029 BE550341 AA651915 A1216376 A1215585 A1471780 AA7772159 AW181980 A1151169 AA758270 A1675769 A1018776 AA757335 AA148511 A1138378 AA504167 A1420617 AW261930 AW872797 N51759 AW614403 A1860533 AW573108 N64830 A1693732 A1436159 BE501089 A1436163 AA971485 A1269364 A1935358 A1222050 AW303978 AW573247
65	134520	13358_3	AIB71154 T16758 AI765893 AW969016 AA744720 BE094085 AA743769 AI476407 AA156619 AI768535 R81435 D45332 N75682 N51177 AW207406 AA425184 R20997 AA504168 Z43298 BE091005 BE641579 AW387738 AW366083 H13769 AW377820 AW369180 AW753239 AW672695 BE379572 AW021732 AW891450 AW891416 BE091358 N50375 BE091354 BE091365 BE091361 BE091363 BE091350 AA353863 AA845510 N21407 AW770981 AI361577
70	135242	5782_1	AA526557 AA525443 AW893622 AA630898 Al418983 BE172016 AA550754 AA664574 C16147 AA355902 AW958586 N51590 C20995 BE544186 Al337578 AA090549 Al807274 AW450654 BE067578 AA446781 AA447058 T10807 AA457082 Al267703 Al880220 BE568979 AW380506 BE150744 AW380468 AW380546 BE150713 D60029 H88099 BE546301 BE150731 AW368467 BE091348 AW380518 AW380512 AW339829 M74093 BE252510 BE252518 BE536901 U40788 W95578 BE018493 BE544205 N83637 Al671049 AW439693 AW300786 AW374970 AA592950 Al215885 Al215884 BE302101 Al186210 AW771831 T54213 AW452924 AA834019 W95471 AA628312
75	134621	27351_1	AW304866 AA570076 Al559873 T54121 AA037145 L02547 NM_001324 AW411516 AA314711 AA143605 BE394455 AA325731 AA093227 AA083307 BE299438 BE295669 AA370886 AA338272 AA166862 BE304837 BE298306 R60507 AW238966 N72750 AW505406 AW994153 AA309742 AA309929 BE090721 AW904189 AW904214 AA363564 R94127 AA362101 R28249 AA206337 AW577208 AA385473 AA355463 AA400696 AA075587 W72815 AA554033
80			AA075530 AA620555 AA554034 T27804 AW950014 AI570740 AI268538 AA704423 AW411517 AI278646 AW339924 AI668917 AI796034 AA994601 R94082 AW027137 AA400652 AW299746 W72816 AA988494 AA146582 AW087489 AA992763 AW516454 AA992759 AW270444 AA227188 AI208929 AA167720 AI052527 AA86560 AA569368 AI888464 AI670003 AA827620 AA507543 AI888385 R88418 AW959083 AI3341077 AI825719 BE552285 AA738076 AW085903 R28242
-0	126802	116467_4	AW805510 AW805503 AW805500 AW805819 AW517040 AW473670 AW516701 T30141 AA894497 EE349504 AI272007 AI985274 BE501962 AW102975 AI801727 AW197918 T24046 AA947601 AW900958
	126892	38252_1	AF121856 BE242657 U83194 AA226732 A1160190 AA948725 A1079958 AW513369 W39443 AW408479 W06854 AA094683 A1985095 AA316647 H95313 N78438 R81582 H95034 R79674 AA488552 W25292 W31697 W19918 T30640 R08686 H78637 AA165100 Z41909

5	105298	8689_1	AA165080 R34212 AA150886 T82168 N77082 W56864 R19848 AA888217 AA314539 AW750293 N62714 R58039 AA845453 N63268 W03474 N41923 AI264123 AI808533 AA824288 AW198143 N99916 AA902465 AA775397 AA772387 AI567675 AA227473 AI082614 R58334 N78878 R34329 AW438902 AA164685 AA558790 AI590102 AA863422 BE002625 AA934039 AI298102 W15351 H93997 AA725326.BE180993 W05350 AI510771 W06941 AA488414 R79863 N91264 R76884 AA312948 T71267 AW9595659 AI086695 N90421 AIZ780998 AA164588 AI300271 AA854381 R81331 AA700449 N06174 AW518427 AA876634 AA150778 N32393 H78585 T85364 BE002808 AW663196 N90337 BE252097 T71401 H06438 N40268 N31015 R77046 T99588 T85462 W25298 T59815 H09416 T85403 W32150 N79109 R78812 BE387790 BE276849 BE246825 BE246900 AA380487 AA332996 AW408727 AK000294 AI636887 AW197272 AW590657 AW594006 AI768979 AI751632 AA580098 AA313261 AA300475 AA133237 AA233499 BE242126 BE2422597 BE242254 AA314374 AW961210 AW939345 AA173535
10			AA305779 R99373 AA128304 AA447246 AA476365 T34973 BE264878 N25149 Z24939 BE263038 AA128317 Z46082 H23504 AW378551 AA088533 AA442625 H15235 H79172 AA344697 AA344742 AL040280 BE173256 BE173129 T59749 AA088410 BE242311 AA173576 AA455337 AA129715 AA582953 AW612637 AA917038 AW340019 AW006315 AW593024 H05915 AW294592 Al14684 AW195659 AW440271 Al209090 Al288689 H98630 H15174 Al214454 Al569471 AA085808 AW188361 AI751631 AW440477 AW300860 AA516088 Al365108 Al305805 Al264064 Al246276 AA442611 AA807059 AA233459 AA875987 Al374653 AA972665 AA947515 AA436867 Al216423 Al657181 Al680306 AA436854 Al537153 AA883723 Z28659 AA705973 Z40741 AA463884 Al216025 Al564986 AA476316 Al432566 Al571662 AA447126
15	120438	166102_1	AW293675 AI675617 AW009004 H23498 AW015242 AA831493 AI292346 AI076966 AI191561 AA243441 AI183309 AA252613 AI038422 AI306531 AW051480 AI348605 AA195119 AI817119 AI091896 AA738440 AA195013 AA976687 AA459659 AI246250 BE219252 AI703457 AA243291 AA243401 AA989100 AA931640 AA459782
20	105516	9334_1	AK001269 AL354613 AA147472 AA490803 BE207628 AW816113 AA085574 AW503392 AA299910 AW750305 BE079539 BE079484 BE512838 AK001593 AW968772 AW967440 AW206280 AA251270 Al627886 AA303599 AA147473 BE205616 AA490611 AA715039 AW590866 AW590447 AI864512 AA204731 AA894490 BE001136 AA612785 AA237035 AA149960 Z44257 R12986 AA448446 Al734041 AA422167 BE220551 R66041 R32927 R32942 AA258773 AW386142 R53730 N54624 AW80296 AA253485 AW954441 H98989 AW614348 AI654838 AA779793 AW237213 N66635 AI186812 AA947479 BE158011 AI859480 AW805579 N52010 AA806305 Al628445 AW270990 AA778165 AA149949 Al650728 AA749108 AA687257 Al261661 AA747442 AA481351 AA206339 AA903407 AW473306 Al688930 AA262281
25	129097	25953_1	AA448310 AA748820 Al347430 BE465692 R32839 AW510564 AA436408 AA257971 AA253362 AA938330 AA513150 AA976840 AA687117 Al281547 AA046243 R32825 Al631554 AW139818 Al244536 R52946 AW235443 R40183 AA299909 AA811958 Al302918 Z40213 BE158047 BE158060 AA767245 AW748159 AW500735 AA094074 BE243933 AA355449 T29766 F08396 N83324 NM_006963 S50223 Al207648 AA258092 AA113952 Al311718 Al128612 AW607449 M77172
30	123037	2000_1	A1951311 X52346 AA903307 A1569810 N55421 W77876 R37223 R83788 AA031666 H47092 AA133451 AA311095 AA906963 H87667 N56058 AA393593 W24864 H10710 F06925 F07239 AW386140 AA325018 AA235950 AW373176 N57158 AA258093 N39467 R21609 BE089979 R34173 AW889005 AA745644 A1693852 AA424914 AA744771 W72632 A1291213 AA524318 A1472134 A1911230 AA528418 AA115745 AA775720 A1671134 AA975044 AW298117 AA321015 N26288 AW952194 A1743379 A1204233 A1801026 AA830690 A1146980 AW104611 A1338576 R21507 A1367623 BE244484 A1269308 AA031667 A1884346 AA731989 AA988943 AA235951 AA807887 AA642645 A1246489 N29739 A1216718 A1383349 A1038618 A1361476 AA806031 A1914178 H10711 A1095573 H69220 AW470854 AA729015 R83353 AA782239
35	120619	169895_1	R34295 H87165 AW419059 Al653689 Z40349 H89114 AW074506 AA397785 AA888377 Al911228 F03193 Al468783 AA702615 Al830829 AA748323 R37224 AA424915 AA731647 H47183 AW965339 AL045632 AA333229 Al806195 AA284372 AA206108 AA682533 AW449514 AA804785 Al215473 Al357263 Al651208 Al651753
40	129229	20927_1	AF013758 NM_006451 Al538709 AA209236 AA300293 AA367274 AA126598 AA324825 AW955225 F11436 AW374740 AW374714 AW374774 AW751514 W73780 Al909015 AW997079 AW997087 AW379344 AW363397 W38589 AA043823 BE169280 Al909016 AW994851 Al740638 AW148560 AW368339 Al658333 AA314718 AW954872 AW468734 Al681980 AW519045 AW58171 AA579286 AW069164 AW615004 AA345052 Al446735 Al142106 AA662683 AW002813 Al418280 AW613203 Al613333 Al354480 Al929755 Al146977 W74674 AW799610 Al798529 Al589422 AA043957 Al223043 AA157016 Al446759 D56729 Al587471 F30716 AA812125 Al537301 AA653347 D11966 Al434383 AA598533 Al287254 AW139140 AW051033 AA601911 Al702506 AA737460 T30221 Al122081 N90213 AA805225 Al798518 BE001071 T10841
45	120821	19274_2	W20199 AW664594 AW195667 D60123 D61496 AW468018 AI720097 N90553 AA829375 AW513266 H92758 AA585324 C14767 AI922391 D60124 D60666 AW071558 BED44120 AA728821 AA211941 Y19062 NM_014393 AW296801 AK001576 AL079288 W16667 Z45664 AI768561 AL079286 R12736 AW080147 AW136530 AI202958 AW241579 R21013 AA347419 AI929333 AW198689 AI040867 F13437 AA918240 AI869798 AI365176 AW440030 AW440072 N80892 AW242030 Z44807 R12417 AA436784 AA442041 AA046503 AL157526 AI929265 AA055542 AA045462 AA683542 N51374 AW193508
50	106459	3897_1	A1873524 AW473151 AW004719 A1810504 A1581093 AA493977 Z40600 F04553 R46130 F09321 A789081 AW408328 NM_006530 U61384 AA449641 AW138216 AA448598 AJ245746 A1385301 N44728 AA255743 AA360783 BE550380 AW593925 A1962309 AA322097 AW964625 A1695988 AW672827 BE543256 AK001413 AW603395 AA651700 AA449053 AA465540 AW083185 T62128 Z78373 AW673713 AW468061 BE360755 AW673958 AW675504 AA995709 AW574841 AA835883 A1248439 AA548364 T62072 N33193 AA814046 A1376210 A1340020 AA449766 AA703407 AA427613 A1470108 A1298757 AA507602 A1658941 AA449478
55	115094 129571	190995_1 1726_1	AA633165 AA449741 AA831821 AA903673 AA682588 AW673075 AA255920 AIB17197 AA255921 AI612925 AW874669 AA493440 X51630 M80232 X61631 S75264 AA172249 AA134066 AA130278 AA130187 AA130291 AA031554 AI246677 Z21455 AI745434 AW273544 AW088613 AW471307 AI745483 AI399854 AI683952 AA031555 AA298075 AI935945 T29809 AA172099 AA366120
60	121779 106738	287665_1 174703_1	AW513143 AA422036 AI821669 AW514232 AA477828 AW772009 AW439799 AW089884 AW149266 R49246 AW237401 AA938113 AW665871 AI969698 AI950812 AW874276 AI571939 AA741222 AI869822 AW104061 AI569994 AW972559 AA506012 AI553704 AA470145 AI332421 AA218990 AW131361 AI709076 AW392488 AW392477 AI970981 AW392476 D61949
	123005	75629_1	H44981 BE172698 AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 AI480343 AA044582 AW956159 AA373451 AA127965
65	108055	100690_1	AL134913 AW994956 BE622314 BE006298 BE006312 BE006305 BE006317 BE006303 AA043906 AA234175 AA479726 AL3404672 AL3289819 AW976000 AA043561 AW450885 AW452879 AA043562 AA788832 AI564338 AI564330 AI368875 AA643607 AA994375 AA810342 AI367704
03	115291	22325_1	BE545072 Al540751 AA301103 Al916675 N85422 BE563965 AA327978 Al816094 AK001515 BE501319 AA279943 BE138895 AA343765 AW963051 AW082308 Al823992 Al653752 Al589007 Al816135 Al566535 BE501307 AW272765 AW242239 AA766315 Al014927 AA578848 Al354483 Al476548 Al038579 AA973322 AA992180 AW472921 BE504789 Al392988 AA506076 AA769228 Al370562 AL137710 BE005656
70	130376 115536	248274 61_1	AW965920 R40873 AK001468 AA190315 AA374980 AW961179 AA307782 AA315295 AA347194 AW953073 AW368190 AW368192 AA280772 AA251247 N85676 Al215522 Al216389 N87835 R12261 R57094 Al660045 AA347193 R16712 AW119006 N55905 N87768 AW900167 Al341261 Al818674 D20285 Al475165 AA300756 R40626 Al122827 AA133250 Al952488 AA970372 AA889845 AW069517 AL524385 AA190314 Al673359 AA971105 Al351088 AI872789 Al919056 Al611216 AK001472 BE568761 AA581004
75	114965 131228	153955_1 8262_1	A1733881 AA165164 A1826437 A1972791 AA165165 BEZ19575 A1732586 A1821571 AA250737 AW136875 A1984273 A1249271 AW207469 AL079814 AA364361 AF020043 AW291396 BE550484 NM, 005445 BE046917 AW594249 A1651554 A1631515 AW771344 A1
80	٠		AW022653 AA114219 AJ005015 AL046587 AA878141 AW271896 AW085287 AA150465 BE536295 AA463412 BE093222 AA213739 AA485586 AJ825913 AA706307 AJ337348 R31995 AJ819641 R32095 AW976653 AA742375 AA142957 AJ808214 AW468303 AJ205987 AJ206347 AJ769095 BE501640 AA113866 AJ093931 AJ752855 AA612743 AA463411 AA279157 AJ123791 AA213570 AJ207305 AW627814 R31945 R32040
	116238	10772_1	AV660717 NM_015437 AL050285 R95774 Al867094 AA443833 Al367670 AA609046 Al440298 Al613139 Al291826 AW028954 Al123242 Al824715 AW079750 AA479362 AW150151 Al952267 AA814094 Al168431 Al566595 Al521422 Al920793 AW051241 N70051 Al689429

	122802	287993_1	A1783813 A1769315 A1743691 A1915645 AA479473 C21435 N50944 N50902 AW978102 H23837 BE087538 AA316516 A1687303 AW571681 A1554465 A1684252 A1581056 AA604098 A1628160 A1859843 AA424021 AA460530 BE042778 AW273200 AW273223 AW167288 AW083347 A1654306 AW517496 AW104706 AW273214 BE139512 AW189487 AW130822 AW167419 A1289485 AW150010
5	123494	21202 1	H88004 AI743745 AW088710 AW179019 AW179011 AF135160 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW179007 AA345114 BE619758
,	123434	21202_1	BE619209 W25509 AA314339 AA336674 AA337956 AW954843 AW390412 N46796 AA316235 AA314286 R15686 BE535633 N57134 N46483
			AW368462 AA923517 AA665223 AI418513 AA837523 AI359320 AI309273 AI522278 N40939 AA904977 AA938272 N30240 AA887965 AI671972 AI028109 AA094652 AA883262 AA887781 AI744447 AW592944 AI077790 AW860883 AW148667 N89861 AA557195 AI191824
			AIG/1972 AIU28 IOS AAUS4052 AA065262 AA067761 AIT 44447 AVISS2944 AIU77790 AVISOUOS5 AVI 14007 NOSCOT AA057195 AIT 1624 AI433166 AI719760 AA453089 AA630656 AA300976 AA639620 AW675033 AA284393 AW886987 AI476335 AI332939 BE301513 AA452920
10			AW674302 AI925483 AW170412 AI698717 AI375985 BE220535 AI688151 AW514809 AW062346 AA599786 BE350848 AI560848 AI023075 AA864875 AA166871 AI807947 AW514579 AI978602 AI860340 AA830886 AI374788 AI283592 AA683152 AA743159 AI379932 AI432056
			AA604815 AA100011 A1001941 AWS 14519 A1910002 A1000340 AA650000 A1514100 A1265392 AA665152 AA145139 A1518952 A452050 A1128904 AW150433 N38909
	116296	11967_2	AW149502 Z43342 AW002826 AL049382 AA442545 AW971471 BE220243 AW968952 AA043607 AW299245 AA659892 Al038768 H26330
15			BE463534 AI628252 AA836139 AI277291 AA489033 AA741239 AI209064 AI300253 AI275761 Z39417 C01835

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY Primekey

25 Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs. normal tissues

20

30	Pkey	Ex. Accn	UGID	Title	ratio
	134454	L33930	Hs.173996	CD24 antigen (small cell lung carcinoma clust	86.2
	102927	X12876	Hs.65114	keratin 18	84.7
	115909	AA436666	Hs.59761	ESTs	72.3
	123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [66.8
35	115674	AA406542	Hs.71520	ESTs	65.4
	102193	U2075B	Hs.313	secreted phosphoprotein 1 (osteopontin; bone	63.1
	101839	M93036	Hs.692	membrane component; chromosomal 4; surface ma	56.8
	115221	AA262942	Hs.79741	ESTs	56.1
	108059	AA043944	Hs.62663	ESTs	52.3
40	121853	AA425887	Hs.98502	ESTs	47.8
-10	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	47.0
	103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	46.5
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin 1-lik	45.5
	102979	X17042	Hs.1908	proteoglycan 1; secretory granule	44.6
45	130967	AA134138	Hs.182579	Homo sapiens leucine aminopeptidase mRNA; com	44.5
73	102009	U02680	Hs.82643	protein tyrosine kinase 9	40.4
			Hs.161756	ESTs	39.6
	126960	AA317900			39.1
	103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	39.0
50	133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	38.9
30	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapiens]	38.8
	102803	U89916	Hs.26126	claudin 10	38.7
	104943	AA065217	Hs.169674	ESTs	
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (from cl	38.4
55	120655	AA287347	Hs.238205	ESTs	38.1
55	102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
	104052	AA393164	Hs.97644	mammaglobin 2	36.0
	109166	AA179845	Hs.73625	RAB6 Interacting; kinesin-like (rabkinesin6)	35.9
	101332	L47276		Homo sapiens (cell line HL-6) alpha topolsome	35.0
<i>c</i> 0	106167	AA425906	Hs.7956	ESTs	34.5
60	101042	J05428	Hs.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from c	33.7
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin; uteri	32.3
	126410	R51912	Hs.12409	somatostatin	32.1
~	134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	32.0
65	125739	AA428557	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
	132254	L20826	Hs.430	plastin 1 (I isoform)	31.4
	112610	R79392	Hs.23643	ESTs	30.9
	101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin	30.6
	116345	AA496981	Hs.199067	HER3 receptor tyrosine kinase (c-erb83; ERBB3	30.1
70	108860	AA133334	Hs.129911	ESTs	29.8
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	29.2
	107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	28.9
	106210	AA428239	Hs.10338	ESTs	28.9
	134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chronic g	28.0
75	125769	Al382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	27.5
	107222	D51235	Hs.82689	turnor rejection antigen (gp96) 1	27.4
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; importin a	26.9
	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	26.8
	105588	AA279215	Hs.10867	ESTs	26.3
80	130718	N70196	Hs.18376	ESTs	26.3
- - .	111185	N67551	Hs.12844	EGF-like-domain; multiple 6	25.6
	131965	W90146	Hs.35962	ESTs	25.6
	132903	AA235404	Hs.5985	Homo sapiens cione 25186 mRNA sequence	25.6
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride chann	25.5
				1.0	

	101185	L19872	Hs.170087	aryl hydrocarbon receptor	25.2
	128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alph	25.1
	116724	F13665	Hs.65641	ESTs	24.9
5	111929	R40057	Hs.112360	prominin (mouse)-like 1	24.9
3	102915 131210	X07820 AA430047	Hs.2258 Hs.24248	matrix metalloproteinase 10 (stromelysin 2) ESTs	24.8 24.7
	101714	M68874	H5.24240	Human phosphatidylcholine 2-acylhydrolase (cP	24.6
	100154	D14657	Hs.81892	KIAA0101 gene product	24.6
10	134656	X14787	Hs.87409	thrombospondin 1	24.3
10	100294	D49396	Hs.75454	antioxidant protein 1	23.9
	104080	AA402971	Hs.57771 Hs.18720	kallikrein 11 programmed cell death 8 (apoptosis-inducing f	23.7 23.7
	107056 115697	AA600310 AA411502	Hs.63325	ESTs; Weakly similar to airway trypsin-like p	23.7
	130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
15	105870	AA399623	Hs.23505	ESTs	23.6
	118528	N67889	Hs.49397	ESTS	23.4 23.2
	105309 109680	AA233790 F09255	Hs.4104 Hs.4993	ESTs; Weakly similar to cDNA EST yk386g7.5 co ESTs	23.2
	131501	AA121127	Hs.181307	H3 histone; family 3A	23.2
20	100824	HG4058-HT4		Oncogene Amil1-Evi-1, Fusion Activated	23.1
	111890	R38678	Hs.12365	ESTs	23.0
	101543	M31 166	Hs.2050	pentaxin-related gene; rapidly induced by IL-	22.8
	102095	U11313	Hs.75760 Hs.94576	sterol carrier protein 2 ESTs; Weakly similar to phosducin; retinal [H	22.8 22.8
25	114988 120695	AA251089 AA291468	N3.34370	ESTS -4	22.8
	130941	D49394	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	22.8
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine aminotr	22.7
	109141	AA176428	Hs.193380	ESTs	22.6 22.6
30	102345 115652	U37283 AA405098	Hs.58882 Hs.38178	Microfibril-associated glycoprotein-2 ESTs	22.6 22.4
50	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase polype	22.3
	105463	AA253370	Hs.32646	ESTs	22.2
	132624	AA164819	Hs.53631	ESTs	22.2
35	119743	W70242	Hs.58086	ESTs	22.0 22.0
33	132528 107174	AA283006 AA621714	Hs.50758 Hs.25338	chromosome-associated polypeptide C ESTs	21.8
	134495	D63477	Hs.84087	KIAA0143 protein	21.8
	131985	AA434329	Hs.36563	ESTs	21.5
40	105832	AA398346	Hs.21898	ESTs	21.2
40	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-relate ESTs .	21.2 20.9
	114846 109703	AA234929 F09684	Hs.44343 Hs.24792	ESTs; Weakly similar to ORF YOR283w [S.cerevi	20.9
	135154	AA126433	Hs.173242	sorting nexin 4	20.8
4.5	131185	M25753	Hs.23960	cyclin B1	20.7
45	105616	AA280670	Hs.24968	ESTs	20.5 20.2
	131148 129337	C00038 R63542	Hs.23579 Hs.110488	ESTs . KIAA0990 protein	20.2
	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
50	133711	J04130	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
	131818	Z39297	Hs.3281 Hs.107295	neuronal pentraxin II ESTs	19.7 19.6
	125303 109112	Z39821 AA169379	Hs.72865	ESTS	19.5
	105376	AA236559	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	19.2
55	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
	100661	HG2874-HT		Ribosomal Protein L39 Homolog	19.1 19.0
	129571 115239	X51630 AA278650	Hs.1145 Hs.73291	Wilms tumor 1 ESTs; Weakly similar to similar to the beta t	18.9
	131562	U90551	Hs.28777	H2A histone family; member L	18.9
60	131272	AA423884	Hs.139033	paternally expressed gene 3	18.9
	130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROTEIN [18.8
	103245 101809	X76648 M86849	Hs.28988	glutaredoxin (thioltransferase) Homo sapiens connexin 26 (GJB2) mRNA, complet	18.7 · 18.6
	105344		Hs.8645	ESTs	18.4
65	135225		Hs.9667	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
	116786		Hs.83429	tumor necrosis factor (ligand) superfamily; m	18.3
	131510		Hs.27842	ESTs; Weakly similar to similar to 1-acyl-gly ESTs	18.2 18.0
	124059 103352		Hs.99769 Hs.78853	uracil-DNA glycosylase	17.9
70	132742		Hs.55901	ESTs; Weakly similar to C43H8.1 [C.elegans]	17.9
	135242		Hs.9700	cyclin E1	17.9
	123494		Hs.112110	ESTs	17.8
	129168 128517		Hs.109052 Hs.100861	chromosome 14 open reading frame 2 ESTs; Weakly similar to p60 katanin [H.sapien	17.7 17.6
75	130160		Hs.151344	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransfe	17.6
. –	103448		Hs.204238	lipocalin 2 (oncogene 24p3)	17.5
	119708	W67810	Hs.57904	mago-nashi (Drosophila) homolog; proliferatio	17.5
	122946		Hs.105341 Hs.251871	ESTs CTP synthase	17.5 17.5
80	125819 131689		Hs.30696	CTP synthase transcription factor-like 5 (basic helix-loop	17.5
	115061		Hs.41271	ESTs	17.3
	113702	T97307	Hs.161720	ESTs; Moderately similar to !!!! ALU SUBFAMIL	17.3
	115291		Hs.122579	ESTs TRAF family member-associated NFKB activator	17.3 17.2
	102567	U59863	Hs.146847	"TONE IGHT IN THE THE PERSONNEL WE'VE BETTAGET	11.2

	400000	44044044	11- 400042	policed and state the discount of the continuous	47.0
	129229 129351	AA211941 AA167268	Hs.109643 Hs.62349	polyadenylate binding protein-interacting pro Human ras inhibitor mRNA; 3' end	17.2 17.2
	110769	N22222	NS.02343	yw34b06.s1 Morton Fetal Cochlea Homo sapiens	17.1
	113182	T55234	Hs.9676	Human DNA sequence from clone 30M3 on chromos	17.0
5	115892	AA435946	Hs.50831	ESTs	17.0
_	123114	AA486407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598803	Hs.111496	ESTs	17.0
	123339	AA504253	Hs.101515	ESTs	16.9
10	123689	AA609556	Hs.256562	ESTs	16.9
10	131941	D62657	Hs.35086	ubiquitin-specific protease 1	16.8
	120649	AA287115	Hs.99697	ESTs	16.8 16.8
	102139	U15932 AA331393	Hs.2128 Hs.47378	dual specificity phosphatase 5 ESTs	16.7
	115522 135243	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
15	131257	AA256042	Hs.24908	ESTs	16.5
10	109508	AA233892	Hs.55902	ESTs; Weakly similar to IIII ALU SUBFAMILY SX	16.3
	132701	AA279359	Hs.55220	BCL2-associated athanogene 2	16.3
	134449	L34155	Hs.83450	taminin; alpha 3 (niceln (150kD); kalinin (16	16.3
20	126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske iron	16.3
20	106124	AA423987	Hs.7567	ESTs	16.2
	115363	AA282071	Hs.152759	activator of S phase kinase	16.2 16.1
	117588 131245	N34895 AA620599	Hs.44648 Hs.24766	ESTs DKFZP564E1962 protein	16.1
	101674	M61916	Hs.82124	laminin; beta 1	16.0
25	126819	AA305536	Hs.161489	ESTs	16.0
	134039	S78569	Hs.78672	laminin; alpha 4	16.0
	130648	AA075427	Hs.17296	ESTs; Weakly similar to Iprediction	15.9
	102823	U90914	Hs.5057	carboxypeptidase D	15.8
20	128470	AA447504	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from cl	15.8
30	115844	AA430124	Hs.234607	ESTs	15.7 15.7
	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
	130155 101008	L33404 J04162	Hs.151254 Hs.763	kallikrein 7 (chymotryptic; stratum comeum) Fc fragment of IgG; low affinity Illa; recept	15.7
	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [15.6
35	116844	H64938	Hs.38331	ESTs	15.6
	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
	114768	AA149007	Hs.182339	Ets homologous factor	15.5
40	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	15.5
40	101507	M27492	Hs.82112	interleukin 1 receptor; type I	15.4 15.4
	102519 102610	U52969 U65011	Hs.80296 Hs.30743	Purkinje cell protein 4 preferentially expressed antigen in melanoma	15.4
	111244	N69556	Hs.24724	MFH-amplified sequences with leucine-rich tan	15.4
	120404	AA234921	Hs.96427	KIAA1013 protein	15.3
45	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA298786	Hs.112242	ESTs .	15.1
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
50	115967 104636	AA446887 AA004415	Hs.42911 Hs.106106	ESTs ESTs	14.9 14.9
50	134133	X93920	Hs.180383	dual specificity phosphatase 6	14.9
	134444	X04470	Hs.251754	secretory leukocyte protease inhibitor (antil	14.8
	132998	Y00062	Hs.170121	protein tyrosine phosphatase; receptor type;	14.8
	131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequence	14.6
55	134056	R27358	Hs.7886	ESTs; Weakly similar to Pelle associated prot	14.6
	101249	L33881	Hs.1904	protein kinase C; iota	14.5 14.5
	105298	AA233459	Hs.26369	ESTs	14.5
	107119 115839	AA620307 AA429038	Hs.27379 Hs.40541	ESTs ESTs	14.5
60	122802	AA460530	Hs.256579	ESTs	14.5
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosyltransf	14.3
	130269	AA284694	Hs.168352	nucleoporin-like protein 1	14.3
	134374	D62633	Hs.8236	ESTs	14.3
65	106370	AA443841	Hs.18676	sprouty (Drosophila) homolog 2	14.2
65	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antig	14.1 14.1
	132923	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
	107968 125390	AA034020 H95094	Hs.61539 Hs.75187	ESTs translocase of outer mitochondrial membrane 2	14.1
	107148	AA621131	Hs.5889	ESTs; Weakly similar to W01A11.2 gene product	14.1
70	110788	N24730	Hs.15420	ESTs	14.0
	109481	AA233342	Hs.90680	ESTs; Weakly similar to WD40 protein Ciao 1 [13.9
	105646	AA282147	Hs.5888	ESTs	13.9
	106030	AA412251	Hs.12802	development and differentiation enhancing fac	13.8
75	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
75	133230	S82240	Hs.6838	ras homolog gene family; member E	13.7 13.6
	124803	R45480 AA405747	Hs.164866 Hs.97865	cyclin K ESTs; Weakly similar to WASP-family protein [13.6
	121381 105200	AA405747 AA195399	Hs.24641	ESTs veakly similal to VVASP-tailing protein (13.5
	105200	AA281245	Hs.23317	ESTs	13.5
80	114986	AA251010	Hs.87807	ESTs	13.5
-	118036	N52844	Hs.196008	ESTs	13.5
	134672	N79749	Hs.87627	ESTs; Weakly similar to cDNA EST EMBL:T00542	13.5
	110915	N46252	Hs.29724	ESTs	13.3
	· 117984	N51919	Hs.47368	ESTs	13.3
				1.0	

	132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
	124315 102547	H94892	Hs.6906 Hs.46638	v-ral simian leukemia viral oncogene homolog	13.2 13.2
	125134	U57911 W19228	Hs.100748	chromosome 11 open reading frame 8 ESTs	13.2
5	111806	R33468	Hs.24651	ESTs	13.1
	106983	AA521195	Hs.10887	similar to lysosome-associated membrane glyco	13.0
	106498 110787	AA452141 N24716	Hs.7171 Hs.12244	ESTs ESTs; Weakly similar to C44B9.1 [C.elegans]	13.0 13.0
	122860	AA464414	Hs.112159	ESTs	13.0
10	131535	AA504642	Hs.28436	ESTs; Weakly similar to coded for by C. elega	13.0
	116188	AA464728	Hs.184598	ESTs	13.0
	107243 129300	D59489 C20976	Hs.34727 Hs.110165	ESTs ESTs; Highly similar to ribosomal protein L26	12.9 12.9
	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
15	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	12.8
	131839	H80622	Hs.33010	KIAA0633 protein	12.8
	119620 120802	W47620 AA343533	Hs.56009 Hs.128777	2'-5'digoadenylate synthetase 3 ESTs; Weakly similar to predicted using Genef	12.8 12.7
	102250	U28014	Hs.74122	caspase 4; apoptosis-related cysteine proteas	12.7
20	105539	AA258873	Hs.25242	ESTs	12.7
	114965	AA250737	Hs.72472	ESTs	12.7
	118001 100448	N52151 D87469	Hs.47447 Hs.57652	ESTs . EGF-like-domain; multiple 2	12.7 12.6
	130920	D50975	Hs.75525	calreticulin	12.6
25	131075	Y00757	Hs.2265	secretory granule; neuroendocrine protein 1 (12.6
	105496	AA256323	Hs.25264	DKFZP434N126 protein	12.5
	109235	AA193592	Hs.42300 Hs.77910	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ 3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5 12.5
	118215 134388	N62195 M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	12.5
30	106897	AA489790	Hs.167496	RAN binding protein 6	12.4
	133050	S67325	Hs.63788	propionyl Coenzyme A carboxylase; bela polype	12.4
	109683 121463	F09308 AA411745	Hs.27607 Hs.239681	ESTs ESTs; Weakly similar to KIAA0554 protein [H.s	12.3 12.3
	102876	X03663	Hs.174142	colony stimulating factor 1 receptor; formed	12.2
35	101804	M86699	Hs.169840	TTK protein kinase	12.2
	129017	H13108	Hs.107968	ESTs	12.1
•	105812 106459	AA394126 AA449741	Hs.20814 Hs.4029	ESTs; Highly similar to CGI-27 protein (H.sap glioma-amplified sequence-41	12.1 12.0
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	12.0
40	107080	AA609210	Hs.19221	ESTs	12.0
	110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0 12.0
	112253 116760	R51818 H11054	Hs.104222 Hs.155342	Homo saplens mRNA; cDNA DKFZp566L034 (from cl protein kinase C; delta	12.0
	120314	AA194166	Hs.221040	KIAA1038 protein	12.0
45	123005	AA479726	Hs.105577	ESTs	12.0
	132572	AA448297	Hs.237825 Hs.5199	signal recognition particle 72kD ESTs; Weakly similar to UBIQUITIN-CONJUGATING	12.0 12.0
	110561 101923	H59617 S75256	HS.3133	HNL=neutrophil lipocalin [human, ovarian canc	11.9
~~	134992	H05625	Hs.92414	ESTs	11.8
50	105516	AA257971	Hs.21214	ESTs	11.8
	105248	AA226968	Hs.22826 Hs.20161	ESTs ESTs; Weakly similar to IgE receptor beta sub	11.7 11.7
	109130 115955	AA172040 AA446121	Hs.44198	Homo saplens BAC clone RG054D04 from 7q31	11.7
	116135	AA460314	Hs.94179	ESTs	11.7
55	116284	AA487252	Hs.237809	ESTs; Weakly similar to hypothetical protein	11.7
	132384	AA479933	Hs.46967	Human DNA sequence from clone 167A19 on chrom	11.7 11.7
	134753 125136	Y09216 W31479	Hs.173135 Hs.129051	dual-specificity tyrosine-(Y)-phosphorylation ESTs	11.7
	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
60	117395	N26330	Hs.93701	ESTs	11.5
	127007 130567	AA299360	Le 1609	EST11857 Uterus tumor I Homo sapiens cDNA 5'	11.5 11.5
	135073	L07493 AA452000	Hs.1608 Hs.94030	replication protein A3 (14kD) Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	11.5
	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	11.4
65	115536	AA347193	Hs.62180	ESTs	11.4
	133240 106521	D31161 AA453431	Hs.68613 Hs.14732	ESTs malic enzyme 1; NADP(+)-dependent; cytosolic	11.3 11.3
	107674	AA011027	Hs.41143	KIAA0581 protein	11.3
70	114149	Z38814	Hs.27196	ESTs	11.3
70	132478	H20906	Hs.49500	KIAA0746 protein	11.2 11.2
	104252 102436	AF002246 U46499	Hs.210863 Hs.790	cell adhesion molecule with homology to L1CAM microsomal glutathione S-transferase 1	11.2
	106726	AA465339	Hs.7141	ESTs	11.2
75	100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	11.2
75	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA clo	11.2
	130417 132906	U58522 AA142857	Hs.155485 Hs.234896	huntingtin-Interacting protein 2 ESTs; Highly similar to geminin [H.sapiens]	11.2 11.2
	107853	AA142657 AA024427	Hs.59461	DKFZP434C245 protein	11.2
00	103467	Y00451	Hs.78712	aminolevulinate; delta-; synthase 1	11.1
80	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	11.1
	102654 103172	U68494 X68742	Hs.24385 Hs.116774	Human hbc647 mRNA sequence integrin; alpha 1	11.1 11.1
	106856	AA486183	Hs.15839	ESTs; Weakly similar to similar to oxysterol-	11.1
	108255	AA063157	Hs.172608	ESTs	11.1

	404200	LICOSTA	11- 007440	Name and an application of the DVF7a5C41442 (from all	44.4
	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from ci	11.1 11.1
	129057 128845	X62466 AA455658	Hs.214742 Hs.10649	CDW52 antigen (CAMPATH-1 antigen) basement membrane-induced gene	11.1
	129025	AA420992	Hs.103441	ESTs; Weakly similar to testicular tektin B1-	11.0
5	107638	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	11.0
•	134480	AA024664	Hs.83916	NADH dehydrogenæse (ubiquinone) 1 aipha subco	11.0
	115262	AA279112	Hs.88594	ESTs	11.0
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	10.9
	106614	AA458934	Hs.179912	ESTs	10.9
10	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein [H.sa	10.9
	115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hornolog	10.9
	121770	AA421714	Hs.11469	KIAA0896 protein	10.9
	132191	AA449431	Hs.158688	KIAA0741 gene product	10.9
16	133214	Y10659	Hs.250911	interleukin 13 receptor; alpha 1	10.9
15	133914	N32811	Hs.77542	ESTs	10.8
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	10.8
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8
	104147	AA451992	Hs.226799	ESTs; Highly similar to HSPC039 protein [H.sa	10.8 10.8
20	106474	AA450212	Hs.42484 Hs.184942	Homo sepiens mRNA; cDNA DKFZp564C053 (from cl	10.8
20	115881 129950	AA435577 M31516	Hs.1369	G protein-coupled receptor 64 decay accelerating factor for complement (CD5	10.8
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	10.8
	133784	AA214305	Hs.76173	ESTs	10.8
	134248	AA292677	Hs.80624	ESTs	10.8
25	105565	AA278302	Hs.18349	ESTs; Weakly similar to partial CDS [C.elegan	10.8
	127999	AA837495	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
	108040	AA041551	Hs.48644	ESTs	10.7
	130367	Z38501	Hs.8768	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	10.7
	108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.saplens]	10.7
30	111345	N89820	Hs.14559	ESTs	10.7
	115583	AA398913	Hs.45231	LDOC1 protein	10.7
	128965	T17440	Hs.107418	ESTs	10.7
	101396	M15796	Hs.78996	proliferating cell nuclear antigen	10.6
25	132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxygen	10.6
35	101275	L37936	Hs.3273	Ts translation elongation factor; milochondri	10.6 10.6
	104660	AA007160	Hs.14846 Hs.69499	Homo sapiens mRNA; cDNA DKFZp564D016 (from cl Human DNA sequence from BAC 15E1 on chromosom	10.6
	108609 112041	AA100694 R43300	Hs.22929	ESTs	10.6
	114208	Z39301	Hs.7859	ESTs	10.6
40	118537	N67974	Hs.75431	fibrinogen; gamma polypeptide	10.6
	106919	AA490885	Hs.21766	ESTs	10.6
	115984	AA447687	Hs.91109	ESTs	10.6
	105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	10.6
	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
45	116710	F10577	Hs.70312	ESTs	10.5
	119780	W72967	Hs.191381	ESTs: Weakly similar to hypothetical protein	10.5
	112996	T23539	Hs.7165	zinc finger protein 259	10.5
	103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
50	101255	L34600	Hs.149894	mitochondrial translational initiation factor	10.4
3 0	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subun	10.4 10.4
	125617	Al287461	Hs.164950 Hs.27263	ESTs ESTs	10.4
	131475 132073	Z39053 N67408	Hs.38516	ESTs	10.4
	101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene; comple	10.3
55	102437	U46569	Hs.221986	equaporin 5	10.3
	104301	D45332	Hs.6783	ESTs	10.3
	127236	AI341818	Hs.98658	budding uninhibited by benzimidazoles 1 (yeas	10.3
	101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
	113805	W42957	Hs.250617	ESTs	10.2
60	133536	Y00264	Hs.177486	amylold beta (A4) precursor protein (protease	10.2
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; complete	10.2
	113523	T90037	Hs.16686	ESTs	10.2
	116195	AA465148	Hs.72402	ESTs	10.2
65	134542	X57025	Hs.85112	insulin-like growth factor 1 (somatomedin C)	10.2
65	125298	Z39255	Hs.235350	YDD19 protein	10.2
	119367	T78324	Hs.90905	ESTs	10.2 10.2
	134470	X54942	Hs.83758	CDC28 protein kinase 2	10.1
	134288	AA430008	Hs.8117	ESTs ESTs: Weakly similar to contains similarity t	10.1
70	105127 110627	AA158132 H70485	Hs.11817 Hs.35225	ESTs; Weakly similar to MBNL protein [H.sapie	10.1
, ,	115188	AA261819	Hs.88367	ESTs	10.1
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	10.1
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	10.1
	100079	AB002365	Hs.23311	KIAA0367 protein	10.0
75	113987	W87494	Hs.9641	ESTs; Moderately similar to COMPLEMENT C1Q SU	10.0
	117280	N22107	Hs.172241	ESTs	10.0

TABLE 98: Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers 80

CAT Number 23182_1 Pkey 100661

Accession BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655

5 ABB06983 ARAZESETS WINDS IECDROSOT AASDOSB AITSTAN ASHQETZA AAJESTA ARAGESTA ARAZESTA ARAGESTA ARAZESTA ARAGESTA ARA		101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI755634 AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838
AAR9849 AW957919 AW975196 AV1975196 AV1975196 AV197519 A8003319 AL042776 AW074313 Al887722 AU32284 AA447521 A1123885 N29334 A1354911 AW090687 AL256763 AA455358 AL256910 AA074724 AA3267374 AK962007 A4457673 A127259 A18587374 AL858731 AA702453 A1858757 AA216786 A1251819 A162527 AA866022 A1092324 N71686 AA69674 AA69696 AA69674 AA728280 AA66827 AW768817 N71679 A369672 A369697 A185803919 AA686974 A1082074 A185961 A86974 A1472840 AA69686 AA834316 AW7689101 AW063376 AW2694770 A1300266 A1356094 A669874 A1688160 BEICHS915 AW466315 AA731314 AA69568 AA69468 AA834316 AW7689101 AW063376 AW26969 AA35789 A669874 A185968 AW764280 A185968 AA834316 AW3689101 AW063376 AW26969 AA30789 A1393237 A1821317 A761348 AF025841 D4368 AW9949871 A4598 AF025841 D89789 D89788 D89780 AW989822 A1871742 A1310238 AW069154 A1392237 A1821317 A761348 AF025841 D43688 AW9949871 L4598 AF025841 D89780 AW989280 A495686 AW76290 A495623 AA69567 A86952 AA66570 AA66571 A7665240 AW6780 D89780 A466570 AW76292 A466570 A466570 AA66571 A7665240 AW6780 D89780 AA66570 AW76292 A466570 AA66571 AV6780 AA66570 AA66570 AW76292 AA66570 AA66	5			AA806983 AA625673 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 A1635399 AA605313 A1624669 AW594319 A1221834 A1337434 AA307708 BE550282 A1760467 A1630636 A1221521 AW674314 AW0778889 A1933732 A1686969 A1186928 AW074595 A1127486 AL079644 A1910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW3833422 AW3833427 AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA30521 H93904 AA089612 AW391543 AW402915 AW173382 AW4027D1 AW403113 R94438 N73126 H93466 AA099928 AA095051 T29025 AW951071 L47277 L47276 A1375913 BE384156 W24652
15	10			AA583483 AW873194 AW575166 A1128799 A1803319 AL042776 AW074313 A1887722 A1032284 AA447521 A1123885 N29334 A1354911 AW090687 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93467 AA962007 A1446783 AA127259 A1613495 A1686720 A1587374 AA936731 AA702453 A1859757 AA216786 A1251819 A1469227 AA806022 A1092324 N71868 AA968782 AA236919
20	15	100824	5_36	AA668974 Al688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 Al300266 Al336094 Al560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 Al457474 AW466316 AA550969 AA630788 Al393237 Al521317 Al761348 AF025841 D48968 AW994987 L34598 AF025841 D489789 D89789 D89790 AW998932 Al971742 Al310238 X90976 AW199668 AW674280 Al365552 AA877452 AV657554 C75229 AA376077 Al798056 AW609213 W25566 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145
25 101809 32963_1	20			AW449154 AA130232 AI458720 AA962511 AI700627 R70437 AW004008 AA045229 AI671572 H99599 AA043768 AI685454 AI871685 N29937 X90977 AA524240 AI142114 AI825750 AI567805 AI631365 AI347893 AA134740 F20669 AA046707 AW793216 AW963298
25 101809 32963_1		101714	30725_1	
30	25	101809	32963_1	M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544 AW384566 AW378307 AW378323 AW839085 AA457102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114 AW264544 AU18136 AW021810 AA961504 AW076214 AW771489 AW192469 AW392488 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 AI783695 AI589498 AI917637 AW264471 AW384491 AI816732 AW368530 AW368521 AW368463
AA837575 NN_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120 AW062884 AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076148 BE182636 AA169569 AA167499 AI283967 AA167783 AA076140 A1749649 AA166792 A1708618 AA09739 AA514789 AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 AI284506 AW193324 AA148194 AW589341 AI669077 AW264913 AA074902 AI680515 AA169974 AA169614 AA079651 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 AI306666 AA074727 N79823 AA524360 AI826800 AA713827 BE140374 BE004062 AW265060 BE184103 AI199258 AA857863 AA29459 AA837890 AI626104 AA503624 BE183618 BE183717 AA573267 AI833071 AW270590 AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418 AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635 AA165649 AA165663 AW418534 AW997510 AW995640 AA504426 D79223 D79621 AI276062 AI973155 AA653470 AA337887 AI382521 AW084427 D57078 W37628 AI61567034 AA766091 H25097 H25078 AW991507 AA319736 BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 AI066624 AI478955 AI863075 AI073744 AA490170 R46651 AI075653 F02865 N22222 AW972956 AA976503 AI917802 AA952564 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA4275910 AI017004 AI241295 AA40816 AA291468	30			. AA490466 AW243772 AW316636 Al076554 AW511702 N69323 H88912 AA257017 Al952506 H88913 Al912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
40 40 40 40 40 40 40 40 40 40 40 40 40 4	25	101923	30543_1	AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120 AW062884 AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076188 BE182636 AA169569 AA167439
45 127007	35			AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 AI284506 AW193324 AA148194 AW583341 AI669077 AW264913 AA074902 AI680515 AA169874 AA169614 AA079651 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 AI306666 AA074727 N79823 AA524360 AI826800
45 127007 19921_1 AB037777 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 AI522058 BE326323 AA374890 AW418534 AW997510 AW995214 AW9595649 AA504426 D79223 D79621 AI276062 AI973155 AA653470 AA337887 AI382521 AW084427 D57078 AW991507 AA319736 BE000831 AA541787 AW175038 AA327931 AW117510 AW664665 AI066624 AI478955 AI863075 AI073744 AA490170 R46651 AI075653 F02865 N22222 AW972956 AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA475910 AI017004 AI241295 AA402816 AA291468	40			BE183717 AA573267 AIB33071 AW270590 AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418 AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635
110769 229824_1 BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 Al066624 Al478955 Al863075 Al073744 AA490170 R46651 Al075653 F02865 N22222 AW972956 120695 9683_3 AA976503 Al917802 AA953664 AA404613 AA42871 BE280542 AW194691 Al927301 Al740458 Al796100 Al935603 AW052210 AA970201 Al633384 AA4275910 Al017004 Al241295 AA402816 AA291468	45	127007	19921_1	AB037771 BE005079 AA394189 AW959650 AA299360 AA398081 W37627 AW750817 AW630138 Al522058 BE326323 AA374890 AW418534 AW997510 AW995214 AW959649 AA504426 D79223 D79621 Al276062 Al973155 AA653470 AA337887 Al382521 AW084427
120695 9683_3 AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210 AA970201 AI633384 AA425910 AI017004 AI241295 AA402816 AA291468		110769	229824_1	BE000831 AA541787 AW173038 AA327931 AW117510 AW664665 Al066624 Al478955 Al863075 Al073744 AA490170 R46651 Al075653
EU WARREN (M0000004 WARDA IN VIDE LOVE WARDE IN WARREN OF WARDE IN WARREN OF		120695	9683_3	AA976503 AI917802 AA953664 AA404613 AA428771 BE280542 AW194691 AI927301 AI740458 AI796100 AI935603 AW052210
30	50			Mai 0201 M000004 M1200 IO M011004 M241220 M1402010 M251400

Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to the about the 80th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

60 Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID

Title: UniGene title ratio: ratio tumor vs normal tissues

65 Pkey 432938 ratio T27013 X51630 56.1 33.5 Hs.3132 Hs.1145 steroidogenic acute regulatory protein Wilms tumor 1
BMPR-lb; bone morphogenetic protein receptor 418179 400292 AA250737 Hs.72472 30.0 29.5 28.1 28.1 27.4 25.2 23.7 22.7 452838 415511 422956 U65011 AI732617 BE545072 Hs.30743 Hs.182362 Hs.122579 Preferentially expressed antigen in melanoma 70 **ESTs** ESTs 410929 H47233 Hs.30643 Matrix Metalloproteinase 10 (Stromolysin 2) gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA collagen; type X; alpha 1 (Schmid metaphyseal secretory granule, neuroendocrine protein 1 X07820 Al624049 400289 Hs.2258 Hs.277523 Hs.179729 449034 427585 75 D31152 428392 H10233 Hs.2265 Hs.77496 Hs.103538 Hs.62180 21.3 21.2 AW369771 C14187 448243 **ESTs** 430591 444783 **ESTs** AK001468 20.8 **ESTs** AJ404672 AA398155 AB018305 80 407638 Hs.288693 EST Hs.97600 Hs.5378 423739 **ESTs** 19.7 spondin 1, (f-spondin) extracellular matrix p 19.0 436982 Hs.301584 451110 A1955040 ESTs 18.8 M86699 Hs.169840 . TTK protein kinase 18.7

	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
	439706		Hs.59761	ESTs	18.3
_	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
5	410247	AF181721	Hs.61345	RU2S .	17.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
10	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
10	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
	428187	A1687303	Hs.285529	ESTs	15.9
	438817	A1023799	Hs.163242	ESTs	15.9
	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	15.9
1.0	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
15	412723	AA648459	Hs.179912	ESTs	15.3
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	15.2
	443646	AI085198	Hs.298699	ESTs	15.1
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
00	428976	AL037824	Hs.194695	ras homolog gene family, member I	14.6
20	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
	427356	AW023482	Hs.97849	ESTs	13.9
0.5	418601	AA279490	Hs.86368	calmegin	13.8
25	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
	428532	AF157326	Hs.184786	TBP-interacting protein	13.6
	402408			0	13.6
	447350	Al375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
20	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
30	423575	C18863	Hs.163443	ESTs	13.2
	443211	A1128388	Hs.143655	ESTs	13.2
	437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
25	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from c	12.7
35	442655	AW027457	Hs.30323	ESTs	12.5
	452096	BE394901	Hs.226785	ESTs	12.4
	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
40	447033	AI357412	Hs.157601	EST - not in UniGene	12.3
40	433764	AW753676	Hs.39982	ESTs	12.2
	442611	BE077155	Hs.177537	ESTs	12.0
	408562	A1436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	11.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
15	421478	A1683243	Hs.97258	ESTs	11.8
45	426635	BE395109	Hs.129327	ESTs	11.8
	415989	Al267700	Hs.111128	ESTs	11.7
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.5
	452249	8E394412	Hs.61252	ESTs	11.4
50	418506	AA084248	Hs.85339	G protein-coupled receptor 39	11.3
50	442353	BE379594	Hs.49136	ESTs	11.3
	447700	Al420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	450480	X82125	Hs.25040	zinc finger protein 239	11.3
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
E E	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-relate	11.2
55	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
	445258	AI635931	Hs.147613	ESTs	11.1
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-blnd	10.9
60	404567	ALAMONEON	Un ENGOE	0 homes hav C4	10.8 10.7
UU	423811	AW299598	Hs.50895	homeo box C4	10.6
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.3
	441627	AA947552	Hs.58086	ESTs ESTs, Moderately similar to GNPI_HUMAN GLUCOS	10.3
	443555	N71710	Hs.21398	RAB6 interacting, kinesin-like (rabkinesin6)	10.3
65	412140	AA219691	Hs.73625		10.1
UJ	427469	AA403084	Hs.269347	ESTs ESTs	10.1
	415227	AW821113 AA151342	Hs.72402	CGI-147 protein	10.0
	445413		Hs.12677	peptidylglycine alpha-amidating monooxygenase	10.0
	425734	AF056209	Hs.159396	ESTs	10.0
70	421451	AA291377	Hs.50831	highly expressed in cancer, rich in leucine h	9.8
70	410044	BE566742	Hs.58169	CGI-07 protein	9.7
	427878 408460	C05766 AA054726	Hs.181022 Hs.285574	ESTs	9.7
	408460		Hs.285574 Hs.145404	ESTs	9.7
	422972 443715	N59319 Al583187		cyclin E1	9.7
75			Hs.9700	ESTs	9.6
13	440901	AA909358	Hs.128612	ESTs	9.6
	453160 415311	AI263307	Hs.146228	ESTS; Highly similar to SPERM SURFACE PROTEIN	9.5
	415211	R64730.comp		huntingtin interacting protein 2	9.5
	425282	AW163518	Hs.155485	namengan microsing protein z N	9.5
80	400250	AW162049	No SAEAD	pre-mRNA cleavage factor îm (68kD)	9.3
Ģυ	410568	AW162948	Hs.64542	ESTs	9.3
	442957 453022	A1949952 AF053306	Hs.49397	budding uninhibited by benzimidazoles 1 (yeas	9.3
	453922 434401	AP053306 AI864131	Hs.36708	Putative prostate cancer tumor suppressor	9.2
	434401 453628	AW243307	Hs.71119	ESTs	9.1
	453628	WIENOGI	Hs.170187		5.1

	452055	Al377431	U _{0.} 202772	ESTs	9.1
	424086	AJ351010	Hs.293772 Hs.102267	lysyl oxidase	9.1
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.1
_	416208	AW291168	Hs.41295	ESTs	9.0
5	407168	R45175	Hs.117183	gb:yg40f01.s1 Soares infant brain 1NIB Homo s	9.0
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	8.9
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC10	8.9
	433527	AW235613	Hs.133020	ESTs	8.9
10	409928 423020	AL137163 AA383092	Hs.57549 Hs.1608	hypothetical protein dJ47384 replication protein A3 (14kD)	8.8 8.7
10	425665	AK001050	Hs.159066	ESTs	8.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	8.6
	449433	AI672096	Hs.9012	ESTs	8.6
	453878	AW964440	Hs.19025	ESTs	8.6
15	450505	NM_004572	Hs.25051	plakophilin 2	8.6
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	8.5
	414315	Z24878	Un 450474	gb:HSB65D052 STRATAGENE Human skeletal muscle	8.5
	425492 435181	AL021918 AA669339	Hs.158174 Hs.28838	zinc finger protein 184 (Kruppel-like) KIAA1571 protein	8.5 8.5
20	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HEMBA10	8.5
	418384	AW149266	Hs.25130	ESTs	8.4
	453370	Al470523	Hs.182356	ESTs, Moderately similar to translation initi	8.4
	409041	AB033025	Hs.50081	KIAA1199 protein	8.4
25	447078	AW885727	Hs.301570	ESTs .	8.4
25	448674	W31178	Hs.154140	ESTs	8.3
	433393 433496	AF038564 AF064254	Hs.98074 Hs.49765	atrophin-1 interacting protein 4 VERY-LONG-CHAIN ACYL-COA SYNTHETASE	8.3 8.3
	433496 421155	H87879	Hs.102267	lysyl oxidase	8.2
	438394	BE379623	Hs.27693	CGI-124 protein	8.2
30	400298	AA032279	Hs.61635	STEAP1	8.1
	409092	A1735283	Hs.172608	ESTs	8.1
	440250	AA876179	Hs.134650	ESTs	8.1
	409143	AW025980	Hs.138965	ESTs	8.1
35	407771	AL138272	Hs.62713	ESIS	8.1
33	419088 431725	AI538323 X65724	Hs.77496 Hs.2839	ESTs Norrie disease (pseudoglioma)	8.1 7.9
	431750	AA514986	Hs.283705	ESTs .	7.9
	435635	AF220050	Hs.181385	uncharacterized hematopoietic stem/progenitor	7.9
	441826	AW503603	Hs.129915	phospholriesterase related	7.9
40	417728	AW138437	Hs.24790	KIAA1573 protein	7.8
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
	421039	NM_003478	Hs.101299	cullin 5	7.8
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
45	429609 415139	AF002246 AW975942	Hs.210863 Hs.48524	cell adhesion molecule with homology to L1CAM ESTs	7.8 7.7
1.5	450192	AA263143	Hs.24596	RAD51-Interacting protein	7.7
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	7.7
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	7.5
50	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA, subu	7.5
	433330	AW207084 AL359055	Hs.132816	ESTS Home seniors mPNA full longth insert aDNA do	7.5 7.5
	439759 427660	AL355055 AI741320	Hs.67709 Hs.114121	Homo sapiens mRNA full length insert cDNA clo Homo sapiens cDNA: FLJ23228 fis, clone CAE066	7.5
	422095	A!868872	Hs.288966	ceruloplasmin (ferroxidase)	7.5
55	436476	AA326108	Hs.53631	ESTs	7.5
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
60	439262	AA832333	Hs.124399	ESTs	7.4 7.3
J	435420 422892	AI928513 AA988176	Hs.59203 Hs.121553	ESTs hypothetical protein FLJ20641	7.3
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	7.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	7.2
~~	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled diva	7.2
65	418007	M13509	Hs.83169	Matrix metalloprotease 1 (Interstitial collag	7.2
	420900	AL045633	Hs.44269	ESTs	7.2
	424001	W67883 X03635	Hs.137476	KIAA1051 protein Estrogen receptor 1	7.2 7.1
	400301 400238	V02022	Hs.1657	0	7.1
70	413573	AJ733859	Hs.149089	ESTs	7.1
	428071	AF212848	Hs.182339	transcription factor ESE-3B	7.1
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	7.1
	453062	AW207538	Hs.61603	ESTs	7.1
75	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical protein	7.1
75	442500	AI819068 AI754693	Hs.209122	ESTs ESTs	7.1 7.0
	446142 417791	AV965339	Hs.145968 Hs.111471	ESTS ESTS	7.0
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	7.0
	451797	AW663858	Hs.56120	ESTs	7.0
80	452909	NM_015368	Hs.30985	pannexin 1	7.0
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	7.0
	436281	AW411194	Hs.120051	ESTs	7.0
	449897	AW819642	Hs.24135 He 150042	transmembrane protein vezatin; hypothetical p	6.9 6.9
	414142	AW368397	Hs.150042	, ESTs	0.5

	440770	25222121			
	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	6.9
	419423	D26488	Hs.90315	KIAA0007 protein	6.9
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from d	6.8
5	452971	A1873878	Hs.91789	ESTs	6.8
3	413597	AW302885	Hs.117183	ESTs	6.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.8
	437478	AL390172	Hs.118811	ESTs	6.7
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
IO	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	446608	N75217	Hs.257846	ESTs	6.6
	438167	R28363	Hs.24286	ESTs	6.6
	445459	Al478629	Hs.158465	ESTs	6.6
1.0	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	6.6
15	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	6.6
	410292	AA843087	Hs.124194	ESTs	6.5
	415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fls, clone HEMBA10	6.5
	424770	AA425562		gb:zw46e05.r1 Soares_total_fetus_Nb2HF8_9w Ho	6.5
	438122	A1620270	Hs.129837	ESTs	6.5
20	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	6.5
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molety X	6.5
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.5
	439901	N73885	Hs.124169	ESTs	6.5
25	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	6.4
	404552			0	6.4
	404599			0	6.4
	419503	AA243642	Hs.137422	ESTs	6.4
	420149	AA255920	Hs.88095	ESTs	6.4
30	440411	N30256	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	Al140683	Hs.98328	ESTs	6.4
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and metallopr	6.4
	453619	H87648	Hs.33922	H.sapiens novel gene from PAC 117P20, chromos	6.4
	410273	BE326877	Hs.281523	ESTs	6.3
35	434486	AA678816	Hs.117142	ESTs	6.3
55	454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein produ	6.3
	403381	777314130	1 15.55500	0	6.2
	421308	AA687322	Hs.192843	ESTs	6.2
	419346	AI830417	16.102040	ab;wh94d12.x1 NCL CGAP, CLL1 Homo sapiens cDNA	6.2
40	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone HEP038	6.2
40	453047	AW023798	Hs.286025	ESTs	6.2
	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic,	6.1
	410102	AW248508	Hs.279727	ESTs;	6.1
	410004	Al298027	Hs.299115	ESTs	6.1
45		A1613318	Hs.48442	ESTs .	6.1
45	413335	A1221919	Hs.173438		6.1
	424945			hypothetical protein FLJ10582	
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	6.1
	451229	AW967707	Hs.48473	ESTs	6.1
50	452641	AW952893	Hs.237825	signal recognition particle 72kD	6.1
50	433172	AB037841	Hs.102652	hypothetical protein ASH1	6.1
	425465	L18964	Hs.1904 Hs.122593	protein kinase C; iota	6.1
	437117 423440	AL049256		ESTs contactin 1	6.0
	430510	R25234 AW162916	Hs.143434 Hs.241576	hypothetical protein PRO2577	6.0 6.0
55	433252	AB040957	Hs.151343		6.0
55	434699	AA643687	Hs.149425	KIAA1524 protein Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	6.0
	436954	AA740151	Hs.130425	ESTs	5.9
	436032	AA150797	Hs.109276	latexin protein	5.9
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	5.9
60	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bindi	5.9
	418379	AA218940	Hs.137516	fidgetin-like 1	5.9
	438081	H49546	Hs.298964	ESTs	5.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	5.8
	450459	Al697193	Hs.299254	ESTs	5.8
65	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
00	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced ge	5.8
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	5.7
	429181	AW979104	Hs.294009	ESTs	5.7
	454933	BE141714	. ~	gb:QV0-HT0101-061099-032-c04 HT0101 Homo sapi	5.7
70	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated guanin	5.7
. •	430371	D87466	Hs.240112	KIAA0276 protein	5.7
	425371	D49441	Hs.155981	mesothelin	5.7
	424513	8E385864	Hs.149894	mitochondrial translational initiation factor	5.7 5.6
	432015	AL157504	Hs.159115	ESTs	5.6
75	438109	Al076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
, ,		T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	5.6
	407137		Hs.606		
	407945	X69208	Hs.44970	ATPase, Cu++ transporting, alpha polypeptide ESTs	5.6 5.6
	416565	AW000960			5.5
80	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	
O U	419752	AA249573	Hs.152618	ESTs .	5.5 5.5
	422093	AF151852	Hs.111449	CGI-94 protein fucose-1-phosphate guanylyttransferase	5.5 5.6
	424583	AF017445	Hs.150926	nuclear cap binding protein subunit 2, 20kD	5.5 5.5
	430388	AA356923	Hs.240770		5.5 5.5
	452534	AW083022	Hs.149425	. Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	5.5

	453279	AW893940	Hs.59698	ESTs	5.5
	424188	AW954552	Hs.142634	zinc finger protein	5.5
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.5
_	424641	AB001106	Hs.151413	glia maturation factor, beta	5.5
5	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
	427975	AI536065	Hs.122460	ESTs	5.5
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	5.5
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y79AA10	5.5
10	417995	AW974175	Hs.188751	ESTs	5.4
10	418946	Al798841	Hs.132103	ESTs ESTs	5.4 5.4
	419963 420362	AA743276 U79734	Hs.301052 Hs.97206		5.4
	422670	AA371612	Hs.115351	huntingtin interacting protein 1 ESTs	5.4
	432837	AA310693	Hs.279512	HSPC072 protein	5.4
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
10	458027	L49054	Hs.85195	ESTs, Highly similar to I(3;5)(q25.1;p34) fus	5.4
	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, homolo	5.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	5.4
	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.elegan	5.4
20	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMAN ALU SU	5.4
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.3
	420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein) horn	5.3
	436586	Al308862	Hs.167028	ESTs	5.3
	435793	AB037734	Hs.4993	ESTs	5.3
25	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	5.3
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.2
	453293	AA382267	Hs.10653	ESTS	5.2
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
	434891	AA814309	Hs.123583	ESTs	5.2
30	415263	AA948033	Hs.130853	ESTs	5.2
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTs	5.2
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pro	5.2
25	431548	A1834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	5.2
35	412719	AW016610	Hs.129911	ESTs	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
	424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
	433558	AA833757	Hs.201769	ESTS	5.1 5.1
40	434265	AA846811 AW503857	Hs.130554	Horno saplens cDNA: FLJ23089 fis, clone LNG070 Sarcolemmal-associated protein	5.1 5.1
70	453911 415539	AI733881	Hs.4007 Hs.72472	BMPR-lb; bone morphogenetic protein receptor	5.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	5.1
	432358	AI093491	Hs.72830	ESTs	5.0
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	5.0
45	419699	AA248998	Hs.31246	ESTs	5.0
٠,٠	420313	AB023230	Hs.96427	KIAA1013 protein	5.0
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell deat	5.0
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	5.0
	434160	BE551196	Hs.114275	ESTs	5.0
50	435094	Al560129	Hs.277523	EST	5.0
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Ho	5.0
	432415	T16971	Hs.289014	ESTs	4.9
	406117			0	4.9
55	438018	AK001160	Hs.5999	hypothetical protein FLJ 10298	4.9
55	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
	448621	Al097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g [D.melanog	4.9
	453001	AW131636	Hs.191260	ESTs	4.9
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	4.9
60	418811	AK001407 Al061288	Hs.88663 Hs.133437	hypothetical protein FLJ 10545 ESTs, Moderately similar to gonadotropin indu	4.9 4.8
00	436754 437212	AI765021	Hs.133437 Hs.210775	ESTs, Moderately Similar to gonadoiropin mou	4.8
	447312	AJ434345	Hs.36908	activating transcription factor 1	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
	434690	AI867679	Hs.148410	ESTs	4.8
65	444172	BE147740	Hs.104558	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.8
	418677	\$83308	Hs.87224	SRY (sex determining region Y)-box 5	4.8
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from cl	4.8
	420179	N74530	Hs.21168	ESTs	4.7
70	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.7
	420850	BE139590	Hs.122406	ESTs	4.7
	425420	BE536911	Hs.234545	ESTs	4.7
75	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.7
75	419131	AA406293	Hs.301622	ESTs	4.7
	422278	AF072873	Hs.114218	ESTs	4.7
	451684	AF216751	Hs.26813	CDA14	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR/MRP)	4.6
80	408425	AW058674	Hs.44787	Homo sapiens mRNA; cDNA DKFZp43400227 (from c	- 4.6
ου	417168	AL133117 AF155827	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	4.6 4.6
	429486 442917	AA314907	Hs.203963 Hs.85950	hypothetical protein FLJ10339 ESTs	4.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.6
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.6
	-02100		5010	·	

	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone COL088	4.6
	459551	Al472808		gb:ti70e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom	4.6
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.6
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	4.6
5	449722	BE280074	Hs.23960	cyclin B1	4.6
_	431689	AA305688	Hs.267695	UDP-Gal:betaGicNAc beta 1,3-galactosyltransfe	4.5
	425178	H16097	Hs.161027	ESTs	4.5
•	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
	436556	Al364997	Hs.7572	ESTs	4.5
10	400534	74004001	113.1012	0	4.5
10	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from c	4.5
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium d	4.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	4.5
15	441006	AW605267	Hs.7627	CGI-60 protein	4.5
15	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	4.5
	447924	AI817226	Hs.170337	ESTs	4.5
	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (JEM-1)	4.5
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.4
	432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.4
20	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	4.4
	414699	Al815523	Hs.76930	synuclein, alpha (non A4 component of amyloid	4.4
	412733	AA984472	Hs.74554	KIAA0080 protein	4.4
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitocho	4.4
	433377	Al752713	Hs.43845	ESTs	4.4
25	449535	W15267	Hs.23672	low density lipoprotein receptor-related prot	4.4
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.4
	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, done NT2RP40	4.4
	423025	AA831267	Hs.12244	Homo sapiens cDNA: FLJ23581 fis, clone LNG136	4.4
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	4.3
30	416241		Hs.32683		4.3
50		N52639		ESTS	
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
	435532	AW291488	Hs.117305	ESTs	4.3
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
25	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo sapi	4.3
35	418478	U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (melanom	4.3
	406069			0	4.3
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone LNG055	4.3
	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the monocl	4.3
	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	4.3
40	418693	A1750878	Hs.87409	thrombospondin 1	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.2
	409763	AL043212		gb:DKFZp434H0623_r1 434 (synonym: htes3) Homo	4.2
	455601	Al368680	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
	408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2
45	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP057	4.2
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
	425024	R39235	Hs.12407	ESTs	4.2
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
	447406		Hs.282882		4.2
50		BE618060		ESTs	4.2
J U	449347	AV649748	Hs.295901	ESTs	
	414279	AW021691	Hs.3804	DKFZP564C1940 protein	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	4.2
55	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	4.2
55	436406	AW105723	Hs.125346	ESTs	4.2
	438209	AL120659	Hs.6111	KIAA0307 gene product	4.2
	443653	AA137043	Hs.9663	programmed cell death 6-Interacting protein	4.1
	454556	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo sapi	4.1
C C	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	4.1
60	412593	Y07558	Hs.74088	early growth response 3	4.1
	416566	NM_003914	Hs.79378	cyclin A1	4.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	4.1
	428417	AK001699	Hs.184227	F-box only protein 21	4.1
	429317	AA831552	Hs.268016	solute carrier family 5 (inosito) transporter	4.1
65	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT2RM40	4.1
	422988	AW673847	Hs.97321	ESTs	4.0
	434657	AA641876	Hs.191840	ESTs	4.0
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1, 64k	4.0
•	443271	BE568568	Hs.195704	ESTs	4.0
70	421437	AW821252	Hs.104336	ESTs	4.0
	401644	F111061606	, 10. 1 54000	0	4.0
	405095			0	4.0
		D77102			4.0
	418417	R77182	Un 570#6	gb:yi65e02.r1 Soares placenta Nb2HP Homo sapi	
75	420807	AA280627	Hs.57846	ESTS EST- Madesolahi similar to endused expressio	4.0
13	429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
	457726	AI217477	Hs.194591	ESTs	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PLACE10	4.0
00	442768	AL048534	Hs.48458	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM	4.0
80	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT2RP30	4.0
	424081	NM_006413	Hs.139120	ribonudease P (30kD)	4.0
	425692	D90041	Hs.155956	NAT1; arytamine N-acetyltransferase	4.0
	407792	A1077715	Hs.39384	putative secreted tigand homologous to fix1	4.0
	408353	BE439838	Hs.44298	. hypothetical protein	4.0

	421175	Al879099	Hs.102397	GIOT-3 for gonadotropin inducible transcripti	3.9
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.9
5	400195	00212100	10.2112	0	3.9
•	401480			ŏ	3.9
	410360	AW663690	•	gb:hj21g03.x1 NCI_CGAP_Li8 Homo sapiens cDNA	3.9
	410908	AA121686	Hs.10592	ESTs	3.9
					3.9
1Λ	420159	AI572490	Hs.99785	ESTs	
10	422805	AA436989	Hs.121017	H2A histone family; member A	3.9
'	424639	AI917494	Hs.131329	ESTs	3.9
	428555	NM_002214	Hs.184908	Integrin, beta 8	3.9
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis, clone NT2RP20	3.9
1.5	· 433703	AA210863	Hs.3532	nemo-like kinase	3.9
15	437144	AL049466	Hs.7859	ESTs	3.9
	452728	AI915676	Hs.239708	ESTs	3.9
	430447	W17064	Hs.241451	SWI/SNF related, matrix associated, actin dep	3.9
	440594	AW445167	Hs.126036	ESTs	3.9
	408938	AA059013	Hs.22607	ESTs	3.9
20	427051	BE178110	Hs.173374	ESTs	3.9
	447568	AF155655	Hs.18885	CGi-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP I	3.9
	443475	AI066470	Hs.134482	ESTs	3.9
	433447	U29195	Hs.3281	neuronal pentraxin II	3.9
25	428093	AW594506	Hs.104830	ESTs -,	3.8
	437938	A1950087	110.104000	ESTs; Weakly similar to Gag-Pol polyprotein [3.8
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
		AW194364			3.8
30	441859		Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	
30	437700	AA766060	Hs.122848	ESTs	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	409564	AA045857	Hs.54943	fracture callus 1 (rai) homolog	3.8
	429474	AA453441	Hs.31511	ESTs	3.8
25	431965	BE175190		gb:QV2-HT0577-010500-165-g04 HT0577 Homo sapi	3.8
35	454018	AW016892	Hs.241652	ESTs	3.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
	439635	AA477288	Hs.94891	Homo saplens cDNA: FLJ22729 fis, clone HSI156	3.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisiae	3.8
	446402	Al681145	Hs.160724	ESTs	3.8
40	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxi	3.8
	400268			0	3.8
	418217	Al910647	Hs.13442	ESTs	3.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	3.8
45	417300	Al765227	Hs.55610	solute carrier family 30 (zlnc transporter),.	3.8
	414136	AA812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.36908	activaling transcription factor 1	3.7
	400240		110.0000	n	3.7
	407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone HS1073	3.7
50	450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
-	418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta-5-de	3.7
55	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
33	402820	DE 470004	11- 000470	0	3.7
	408090	BE173621	Hs.292478	ESTs	3.7
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor 4E	3.7
	418282	AA215535	Hs.98133	ESTs	3.7
C C	418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell line	3.7
60	418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repeal-con	3.7
	422290	AA495854	Hs.48827	hypothetical protein FLJ12085	3.7
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
	439907	AA853978	Hs.124577	ESTs	3.7
	447479	AB037834	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, parti	3.7
65	451073	A1758905	Hs.206063	ESTs	3.7
	450377	AB033091	Hs.24936	ESTs	3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
	448807	A1571940	Hs.7549	ESTs	3.7
	442821	BE391929	Hs.8752	Putative type II membrane protein	3.7
70	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	3.7
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.7
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	3.7
		AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PLACE10	3.7
75	421154 411402				. 3.7
, 5		BE297855	Hs.69855	NRAS-related gene	
	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	3.6
00	434164	AW207019	Hs.148135	ESTs	3.6
80	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kinas	3.6
	402222			· 0	.3.6
	404915			0	3.6
	404996			0	3.6
	411560	AW851186		. gb:iL3-CT0220-150200-071-H05 CT0220 Homo sapi	3.6
				170	
				172	

	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	3.6
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone CAE038	3.6
	427038	NM_014633	Hs.173288	KIAA0155 gene product	3.6
_	439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo sapi	3.6
5	458242	BE299588	Hs.28465	Homo saplens cDNA: FLJ21869 fis, clone HEP024	3.6
•	415115	AA214228	Hs.127751	hypothetical protein	3.6
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.6
	441205	AW137827	Hs.176904	ESTs	3.6
	452693	T79153	Hs.48589		3.6
10				zinc finger protein 228 .	
10	417389	BE260964	Hs.82045	Midkine (neurite growtin-promoting factor 2)	3.6
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	3.5
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
15	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from c	3.5
	400666			0	3.5
	422646	H87863	Hs.151380	ESTs	3.5
	407845	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	3.5
		AV660717	Hs.47144		3.5
20	408730	A4000111	NS.47 144	OKFZP586N0819 protein	3.5
20	401517	4141400004	11- 20000	0	
	413775	AW409934	Hs.75528	nucleolar GTPase	3.5
	417177	NM_004458	Hs.81452	falty-acid-Coenzyme A ligase, long-chain 4	3.5
	427943	AW959075		gb:EST371145 MAGE resequences, MAGE Homo sapi	3.5
0.5	439107	AL046134	Hs.27895	ESTs '	3.5
25	447268	A1370413	Hs.36563	Homo saplens cDNA: FLJ22418 fis, clone HRC085	3.5
	412604	AW978324	Hs.47144	DKFZP586N0819 protein	3.5
	427134	AA398409	Hs.173561	EST	3.5
	430273	Al311127	Hs.125522	ESTs	3.5
	436571	AW137159	Hs.146151	ESTs	3.5
30	433037	NM_014158	Hs.279938	HSPC067 protein	3.5
50	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	3.5
					3.5
	400531	AF151064	Hs.36069	hypothetical protein	
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	3.4
25	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	3.4
35	407596	R86913		gb:yq30f05.r1 Soares fetal liver spieen 1NFLS	3.4
	453779	N35187	Hs.43388	ESTs	3.4
	444858	A1199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta subcom	3.4
	424856	AA347746	Hs.9521	ESTs, Weakly similar to KIAA1015 protein [H.s	3.4
40	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
	404108			0	3.4
	403729			Ŏ	3.4
	404232			Ö	3.4
		A A 220022	Hs.133011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
45	423687	AA329633			
40	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.4
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clo	3.4
	441447	AA934077	Hs.126980	ESTs	3.4
	448358	R44433	Hs.106614	Human DNA sequence from clone RP4-534K7 on ch	3.4
c 0	450926	A1744361	Hs.205591	ESTs, Weakly similar to zinc finger protein P	3.4
50	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone HS1056	3.4
	441111	AI806867	Hs.126594	ESTs	3.4
	447519	U46258	Hs.23448	ESTs	. 3.4
55	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
	449581	Al989517	Hs.181605	ESTs	3.4
	456132	BE219771	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT2RP40	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP30	3.4
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	3.4
60	441433	AA933809	Hs.42746	ESTs	3.4
00					3.4
	417837	AL079905	Hs.1103	transforming growth factor, beta 1 NIF3 (Ngg1 interacting factor 3, S.pombe homo	3.4
	450516	AA902656	Hs.21943		
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
CE	419200	AW966405	Hs.288856	prefoldin 5	3.3
65	423161	AL049227	Hs.124776	Homo saplens mRNA; cDNA DKFZp564N1116 (from c	3.3
	445679	AI343868	Hs.58800	Homo sapiens cDNA FLJ12488 fis, clone NT2RM20	3.3
	435014	BE560898	Hs.10026 ·	ribosomal protein L17 isolog	3.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	3.3
	439170	AA332365	Hs.165539	ESTs	3.3
70	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.3
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein IH.s	3.3
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.3
	408805	H69912	Hs.48269	vaccinia related kinase 1	3.3
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	3.3
75					3.3
13	408532	Al453137	Hs.63176	ESTs	
	409517	X90780	Hs.54668	troponin 1, cardiac	3.3
	414304	AI621276	Hs.165998	DKFZP564M2423 protein	3.3
	436427	Al344378	Hs.143399	ESTs	3.3
00	436662	A1582393	Hs.126695	ESTs	3.3
80	440304	BE159984	Hs.125395	ESTs	3.3
	447385	F12863		gb:HSC3FE081 normalized infant brain cDNA Hom	3.3
	451177	Al969716	Hs.13034	ESTs	3.3
•	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.	3.3
	451743	AW074266	Hs.23071	. ESTs	3.3

	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	3.3
	446351	AW444551	Hs.258532	ESTs	· 3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
-	418216	AA662240	Hs.283099	AF15q14 protein	3.3
5	401508			0	3.3
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HSi009	3.3
	416530	U62801	Hs.79361	kallikrain 6 (neurosin, zyme)	3.3
	443171	BE281128	Hs.9030	TONDU	3.3
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.3
10	412078	X69699	Hs.73149	paired box gene 8	3.3
	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	3.3
	401197	741100201	113.41700	0	3.3
	422134	AW179019	Hs.112110	ESTs	3.3
	409044	Al129586	Hs.33033	ESTs	3.3
15					3.2
IJ	416198	H27332	Hs.99598	ESTS	3.2
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	
	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis, clone MAMMA10	3.2
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	3.2
20	428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
20	428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
	421261	AA600853	Hs.98133	ESTs	3.2
	446219	A1287344	Hs.149827	ESTs	3.2
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC086 [H	3.2
	409172	Z99399	Hs.118145	ESTs	3.2
25	419388	T67012	Hs.75323	prohibitin	3.2
	434187	AA627098	Hs.99103	ESTs, Weakly similar to I38428 T-complex prot	3.2
	445060	AAB30811	Hs.88808	ESTs	3.2
	448254	AI829900	Hs.22929	ESTs .	3.2
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.2
30	411393	AW797437	Hs.69771	B-factor, properdin	3.2
50	453775		Hs.35120		3.2
		NM_002916		replication factor C (activator 1) 4 (37kD)	3.2
	408418	AW963897	Hs.44743	KIAA1435 protein	
	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans]	3.2
25	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.2
35	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.183001	ESTs	3.2
	402829			0	3.2
	451593	AF151879	Hs.26706	CGI-121 protein	3.2
40	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.2
40	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2
	445929	AI089660	Hs.7838	makorin, ring finger protein, 1	3.2
	409365	AA702376	Hs.226440	Homo saplens clone 24881 mRNA sequence	3.2
	418836	A1655499	Hs.161712	ESTs	3.2
	441020	W79283	Hs.35962	ESTs	3.1
45	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
	410486	AW235094	Hs.193424	ESTs, Weakly similar to KIAA1064 protein [H.s	3.1
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	3.1
50	409178	BE393948	Hs.50915	kallikrein 5	3.1
-	439480	AL038511	Hs.125316	ESTs	3.1
	417848	AA206581	Hs.39457	ESTs	3.1
	446293	Al420213	Hs.149722	ESTs	3.1
		A1580492	Hs.42743	hypothetical protein	3.1
55	408108				3.1
55	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	3.1
	410519	AW612264	Hs.131705	ESTs CCI 101 amin'n	
	421987	AI133161	Hs.286131	CGI-101 protein	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
60	453931	AL121278	Hs.25144	ESTs	3.1
UU	454423	AW603985	Hs.179662	nucleosome assembly protein 1-like 1	3.1
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (from c	3.1
	418735	N48769	Hs.44609	ESTs .	3.1
	414245	BE148072	Hs.75850	WAS protein family, member 1	3.1
	410909	AW898161	Hs.53112	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.1
65	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	3.1
	409239	AA740875	Hs.44307	ESTs .	3.1
	429017	AA463605	Hs.238995	ESTs	3.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	3.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic prot	3.1
70	448133	AA723157	Hs.73769	folate receptor 1 (adult)	3.1
	418792	AB037805	Hs.88442	KIAA1384 protein	3.1
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	402077			0	3.1
	440671	AW297920	Hs.130054	ESTs	3.1
75	419890	X17360	Hs.278255	homeo box D4	3.1
, ,	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. cerevi	3.1
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B; yeast)	3.1
	443584	A1807036	Hs.101619	ESTs	3.1
80	445525	BE149866		ESTs	3.1
50			Hs.14831		3.1
	410441	BE298210	Un 440024	gb:601118016F1 NIH_MGC_17 Homo sapiens cDNA c	3.1
	422634	NM_016010	Hs.118821	CGI-62 protein	
	420022	AA256253	Hs.120817	ESTs	3.0
	453912	AL121031	Hs.32556	KIAA0379 protein	3.0

					••
	456844	Al264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	3.0
	414941	C14865	Hs.182159	ESTs	3.0
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on chrom	3.0
-	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone NT2RP30	3.0
5	444420	Al148157	Hs.146766	ESTs	3.0
	431742	NM_016652	Hs.268281	CGI-201 protein	3.0 3.0
	412519	AA196241	Hs.73980 Hs.96322	troponin T1, skeletal, slow	3.0
	418348 444261	AI537167 AA298958		Homo sapiens cDNA: FLJ23560 fis, clone LNG098 MDS023 protein	3.0
10	457465	AW301344	Hs.10724 Hs.195969	ESTs	3.0
10	443933	AV001344 AJ091631	Hs.135501	Homo sapiens two pore potassium channel KT3.3	3.0
	442150	Al368158	Hs.128864	ESTs	3.0
	414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.0
	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.0
15	437949	U78519	Hs.41654	ESTs	3.0
13	403515	070013	113.41004	0	3.0
	403864			ŏ	3.0
	407785	AW207285	Hs.98279	ESTs	3.0
	426199	AA371865	Hs.97090	ESTs	3.0
20	426324	AW291787	Hs.200933	ESTs	3.0
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweg	3.0
	427837	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)	3.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.0
~~	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicus]	3.0
25	446978	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-bindin	3.0
	452431	U88879	Hs.29499	toll-like receptor 3	3.0
	452841	T17431	Hs.65412	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	3.0
	432114	AL036021	Hs.225597	ESTs	3.0
20	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	3.0
30	442607	AA507576	Hs.288361	KIAA0741 gene product	3.0
	453920	AI133148	Hs.36602	I factor (complement)	3.0
	430000	AW205931	Hs.99598	ESTs	3.0
	429164	AI688663	Hs.116586	ESTs	3.0
35	453331	AI240665	Hs.8895	ESTs	3.0 3.0
33	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar to syn	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2 0	3.0
	401714 400903			ŏ	3.0
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
40	443761	AI525743	Hs.160603	ESTs	3.0
••	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on chrom	3.0
	442580	A1733682	Hs.130239	ESTs	3.0
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	TABLE 10	B:			
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	Accession	i: Genbank acce	assion numbers	•	
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	407596 409763	1003489_1 115392_1	R86913 AL0432	R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093	
	407596 409763 410360	1003489_1 115392_1 11972252	R86913 AL0432 AW5638	R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 590	
	407596 409763	1003489_1 115392_1	R86913 AL0432 AW5638 BE2982	R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 390 10 Al672315 AW086489 BE298417 AA455921 AA902537 BE3:	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658
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60 65 70 75	407596 409763 410360 410441 411560 414315 418417 418454 419346 424770 427943 431965 436812 437938 439255 447385 454193	1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1 175699_1 184129_1 243504_1 284802_1 33959_2 427323_1 44573_2 470321_1 719912_1 1050256_1	R86913 AL0432 AW6631 BE2982 Al88505 AW8511 Z24878 R77182 AA3153 BE1751 AW258 AI95000 AA2518 AI95000 AA2518 AY9578 AI74133 AW103 AW656 AA90877 AW103 BE1645 F12863 BE1411 AW178	R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077675 AA077655 R19502 BE545457 Al638421 R14093 390 10 Al672315 AW086489 BE298417 AA455921 AA902537 BE3: 15 Al476470 Al287650 Al885299 Al985381 AW592624 AW3401 16 AW969697 BE143456 AA494098 F13654 AA494040 AA143127 R77197 R80484 08 AA223392 BE538098 BE087173 7 AA236612 62 Al880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863 90 BE003348 067 AA731645 AA810101 AW194180 Al690673 AW978773 07 N70208 R97040 N36809 Al308119 AW967677 N35320 Al25 75 Al820501 Al820532 W87891 T85904 U71456 T82391 BE32 F13493 AA927794 Al560251 AW874068 AL134043 AW23536: 16 Al689062 AA282915 AW102898 AI872193 Al763273 AW178 13 AL539642 AA642799 AA856975 AW505512 Al961530 AW6 538 AA180009 AA337499 AW961101 AA251669 AA251874 Al8 41 AW072629 AW513996 AA293273 AA969759 N75628 N223 4566 Al373032 Al564269 F00531 H83488 W37181 W76802 R66 000 AA832198 BE164502 Al377223 T75099 83 AW178167 AW178162 AW178166 AW178172 AW845893 A 161 AW178207 AW178165 AW178166 AW178172 AW845893 A 161 AW178207 AW178162 AW178168 AW178160 AW178136 BIO AW845828 AW178165 AW178114 AW178212 BE140918 E 206 AW178203 AW178165 AW178168 AW178160 AW178136 BIO AW845828 AW178218 AW178171 AW178157 AW178156 1073 AW807055 AW807067 AW807276 AW807030 AW807363 195 AW807055 AW807067 AW807276 AW807030 AW807363	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951 51473 H59397 AW971573 R97278 W01059 AW967671 AA908598 28571 T75102 R34725 AA884922 BE328517 Al219788 AA884444 33 AA663345 AW008282 AA488964 AA283144 Al890387 Al950344 3629970 BE612881 AW276997 AW513601 AW512843 AA044209 B19225 AW205862 Al683338 Al858509 AW276905 Al633006 AA972584 888 H64729 H60052 T92487 Al022058 AA780419 AA551005 W80701 6056 Al002839 R67840 AA300207 AW959581 T63226 F04005 AW178159 AW178159 AW178222 AW178213 AW178209 AW178223 AW178220 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 BE140915 AW178221 AW178130 AW178134 AW178096 AW178156 AW178108 AW178108 BE141189 AW178170 AW845816 BE141586 AW178156 AW178159 BE141592 AW845901 BE141580 AW178155 BE141598
60 65 70 75	407596 409763 410360 410441 411560 414315 418417 418454 419346 424770 427943 431965 436812 437938 439255 447385 454193	1003489_1 115392_1 1197225_2 120358_1 1249443_1 143512_1 1750818_1 175699_1 184129_1 243504_1 284802_1 33959_2 427323_1 44573_2 470321_1 719912_1 1050256_1	R86913 AL0432 AW6631 BE2982 Al88505 AW8511 Z24878 R77182 AA3153 BE1751 AW258 AI95000 AA2518 AI95000 AA2518 AY9578 AI74133 AW103 AW656 AA90877 AW103 BE1645 F12863 BE1411 AW178	R86901 H25352 R01370 H43764 AW044451 W21298 12 AA077575 AA077655 R19502 BE545457 Al638421 R14093 390 10 Al672315 AW086489 BE298417 AA455921 AA902537 BE3: 65 Al476470 Al287650 Al885299 Al985381 AW592624 AW3401 86 AW996967 BE143456 AA494098 F13654 AA494040 AA143127 R77197 R80484 08 AA223392 BE538098 BE087173 77 AA236612 62 Al880208 AA346646 N22655 AW811775 AW811786 075 W06838 AA417863 90 BE003348 107 AA731645 AA810101 AW194180 Al690673 AW978773 17 N70208 R97040 N36809 Al308119 AW967677 N35320 Al25 75 Al820501 Al82052 W87891 T85904 U71456 T8231 BE32 F13433 AA927794 Al560251 AW874068 AL 134043 AW23536: 16 Al689062 AA282915 AW102898 Al872193 Al763273 AW173 813 Al539642 AA642789 AA856975 AW505512 Al961530 AW6 538 AA180009 AA337499 AW961101 AA251669 AA251874 Al8 41 AW072629 AW513996 AA293273 AA969759 N75628 N223 456 Al373032 Al564269 F00531 H83488 W37181 W78802 R66 000 AA832198 BE164502 Al377223 T75099 83 AW178167 AW178162 AW178168 AW178172 AW845893 A 161 AW178207 AW178210 AW178214 AW178212 BE140918 E 206 AW178203 AW178165 AW178168 AW178178 AW178184 1810 AW845828 AW178216 AW178114 AW178211 AW178224 133 AW178164 AW178218 AW178171 AW178157 AW178168 104 AW8758163 AW178218 AW178171 AW178157 AW178168 104 AW178163 AW178093 AW178171 AW178157 AW178168 1057 AW807055 AW807067 AW807276 AW807030 AW807363	27124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 136 Al266556 AA456390 Al310815 AA484951 51473 H59397 AW971573 R97278 W01059 AW967671 AA908598 28571 T75102 R34725 AA884922 BE328517 Al219788 AA884444 33 AA663345 AW008282 AA488964 AA283144 Al890387 Al950344 3629970 BE612881 AW276997 AW513601 AW512843 AA044209 B19225 AW205862 Al683338 Al858509 AW276905 Al633006 AA972584 888 H64729 H60052 T92487 Al022058 AA780419 AA551005 W80701 6056 Al002839 R67840 AA300207 AW959581 T63226 F04005 AW178159 AW178159 AW178222 AW178213 AW178209 AW178223 AW178220 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 BE140915 AW178221 AW178130 AW178134 AW178096 AW178156 AW178108 AW178108 BE141189 AW178170 AW845816 BE141586 AW178156 AW178159 BE141592 AW845901 BE141580 AW178155 BE141598

TABLE 10C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons 5

	Pkey	Ref	Strand	Nt_position
• •	400534	6981826	Minus	278637-279292
10	400666	8118496	Plus	17982-18115,20297-20456
	400903	2911732	Plus	59112-59228
	401197	9719705	Plus	176341-176452
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401508	7534110	Minus	110779-110983
15	401517	7677912	Plus	29278-29770
	401644	8576138	Pius	82655-83959
	401714	6715702	Plus	96484-96681
	402077	8117414	Plus	65014-65195
•	402222	9958106	Plus	3261-3834,3939-4269
20	402408	9796239	Minus	110326-110491
	402820	6456853	Minus	82274-82443
	402829	8918414	Plus	101532-101852,102006-102263
	403381	9438267	Minus	26009-26178
0.5	403515	7656757	Minus	173358-179553
25	403729	7543752	Minus	37662-37909.,
	403864	7709019	Minus	51753-51890,79290-79445
	404108	8247074	Minus	63603-64942
	404232	8218045	Minus	71800-71956
20	404552	7243881	Plus	19854-20010
30	404567	7249169	Minus	101320-101501
	404599	8705107	Plus	110443-110733
	404915	7341766	Minus	100915-101087
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
25	405095	8072599	Plus	138877-139066
35	406069	9117732	Plus	68880-69374
	406117	9142932	Plus	54304-54584

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted. 40

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES TABLE 11A: ABOUT 222 UP-Re
Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title

45

PFAM domains: predicted protein structural domains io: ratio tumor vs normal tissue

5 A	tauu.	Iauu	wind	49 IM
50				

20						
	Pkey	Ex. Accn	UGID	Title	PFAM domains	ratio
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	30.0
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	25.2
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1q,Collagen	22.7
55	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular m	tsp_1	19.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	17.4
	443646	AI085198	Hs.298699	ESTs	TSPN,vwc,tsp_1,EGF	15.1
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
	418601	AA279490	Hs.86368	calmegin	SS,calreticulin	13.8
60	428532	AF157326	Hs.184786	TBP-interacting protein	TM	13.6
	427344	NM 000869	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
	432677	NM 004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamin	TM,Glycos_transf_2,Ri	11.0
	404567	NM 015902	Hs.278428	progestin induced protein (DD5)	TM.HECT.2f-UBR1	10.8
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,MAM,EGF	8.9
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM,MSP_domain	8.8
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSPN,vwc,lsp_1,EGF	8.5
	453370	A1470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran,ABC_membr	8.4
	400298	AA032279	Hs.61635	STEAP1	TM	8.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_knot	7.9
70	429609	AF002246	Hs.210863	cell adhesion molecule with homolo	TM,fn3.ig	7.8
	412170	D16532	Hs.73729	very low density lipoprotein recepto	TM,ldl_recept_a,ldl_rec	7.4
	428954	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,IGFBP,Cys_knot,tsp	7.4
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS,hemopexin,Peptidas	7.2
	424001	W67883	Hs.137476	KIAA1051 protein	Pep_M12B_propep,Rep	7.2
75	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetica	TM	7.1
	446142	AI754693	Hs.145968	ESTs	Cadherin_C_term,cadhe	7.0
	415138	C18356	Hs.78045	tissue factor pathway Inhibitor 2 TFP	Kunitz_BPTI,G-gamma	6.8
	438167	R28363	Hs.24286	ESTs	7tm_1	6.6
	452097	AB002364	Hs.27916	ADAM-TS3; a disintegrin-like and	Pep_M12B_propep,Rep	6.4
80	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucose in	SS	5.8
	425371	D49441	Hs.155981	mesothelin	SS	5.7
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha p	TM,E1-E2_ATPase,Hy	5.6
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum c	SS,trypsin	5.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,I_LWEQ	5.4
				J		-

	413384	NM_000401	Un 75224	exostoses (multiple) 2	TM	5.3
	425154	NM_001851	Hs.75334 Hs.154850	collagen, type IX, alpha 1	Collagen,TSPN	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral	TGF-beta,TGFb_propep	5.1
_	415539	A1733881	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	5.1
5	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.9
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8 4.7
	450375 451684	AA009647 AF216751	Hs.8850 Hs.26813	a disintegrin and metalloproteinase d CDA14	disIntegrin,Reprolysin,P TM	4.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran,ABC_m	4.6
10	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase d	TM	4.5
	400534	AP000541		predicted exons	TM,KRAB,zf-C2H2	4.5
	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1	TM,Folate_carrier	4.5
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high aff	TM,SDF	4.4
15	449535	W15267	Hs.23672	low density lipoprotein receptor-rela	SS,ldl_recept_b,ldl_rece	4.4 4.3
13	452028 418693	AK001859 AI750878	Hs.27595 Hs.87409	hypothetical protein FLJ10997 thrombospondin 1	Zn_carbOpept,Propep_M EGF,TSPN,tsp_1,tsp_3,	4.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interfer	TM,GBP	4.2
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	Frizzled,Fz,7tm_2	4.2
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium pho	TM,Na_Pi_cotrans	4.2
20	412494	AL133900	Hs.792	ADP-ribosylation factor domain pro	arf,zf-B_box,zf-C3HC4	4.0
	405095	NM_014479	Hs.145296	disintegrin protease	Reprolysin, disintegrin	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pro	SS,wap	4.0 4.0
	407792 408829	Al077715 NM_006042	Hs.39384 Hs.48384	putative secreted ligand homologous heparan sulfate (glucosamine) 3-0-s	SS TM	3.8
25	450581	AF081513	Hs.25195	endometrial bleeding associated fact	SS,TGF-beta,TGFb_pro	3.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3,	TM,Sterol_desat	3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	TM,ANF_receptor,guan	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	TM	3.6
20	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting	TM,PTN_MK	3.6
30	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	3.5 3.4
	406400 407864	AA343629 AF069291	Hs.104570 Hs.40539	kallikrein 8 (neuropsin/ovasin) chromosome 8 open reading frame 1	SS,trypsin TM,FHA,BRCT	3.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,fn3,pkinase	3.4
	446913	AA430650	Hs.16529	transmembrane 4 superfamily memb	TM,transmembrane4	3.4
35	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fuc	SS	3.4
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZ	cadherin_Cadherin_C_te	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	TM,Sec7	3.3 · 3.3
	416530 401197	U62801	Hs.79361	kallikrein 6 (neurosin, zyme) predicted exons	SS,TM,trypsin arf,Ets	3.3
40	436525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fis,	TM	3.2
. •	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	3.2
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fib	3.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-s	SS	3.2
45	418836	A1655499	Hs.161712	ESTs	pkinase,Activin_recp	3.2
43	409178 421987	BE393948	Hs.50915 Hs.286131	kallikrein 5 CG1-101 protein	SS,trypsin TM	3.1 3.1
	447072	A(133161 D61594	Hs.17279	tyrosylprotein sulfotransferase 1	SS	3.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteo	SS,TGFb_propeptide,T	3.1
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	3.1
50	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,hem	3.1
	456844	Al264155	Hs.152981	CDP-diacylglycerol synthase (phosp	TM, Cytidylyltrans	3.0 3.0
	414725 407785	AA769791 AW207285	Hs.120355 Hs.98279	Homo saplens cDNA FLJ13148 fis, ESTs	SPRY,7tm_1 Sema,ig	3.0
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35	TM,zf-C3HC4	3.0
55	452431	U88879	Hs.29499	toll-like receptor 3	TM,TIR,LRRCT	3.0
	453920	AI133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRC	3.0
	453331	AI240665	Hs.8895	ESTs	disintegrin,Reprofysin,P	3.0
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	3.0 3.0
60	428428 407910	AL037544 AA650274	Hs.184298 Hs.41296	cyclin-dependent kinase 7 (homolog fibronectin teucine rich transmernbra	TM,pkinase TM,LRRCT,LRRNT,LR	2.9
-	408380	AF123050	Hs.44532	diubiquitin	TM,ubiquitin,7tm_3,AN	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase d	disintegrin,Reprolysin	2.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestostero	TM,Androgen_recep,ho	2.9
65	424406	D54120	Hs.146409	wingless-type MMTV integration sit	cadherin,Cadherin_C_te	2.9
65	428549	AA430064 U33635	Hs.220929 Hs.90572	ESTs, Moderately similar to ARF-fa PTK7 protein tyrosine kinase 7	arf TM,pkinase,ig	2.9 2.9
	419452 452281	T93500	Hs.28792	ESTs	TGFb_propeptide,TGF-	2.9
	420440	NM_002407	Hs.97644	mammaglobin 2	SS, Uteroglobin	2.9
	418848	AI820961	Hs.193465	ESTs	pkinase,Activin_recp	2.9
70	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	2.9
	433190	M26901	Hs.3210	renin	SS,asp	2.9
	424538	NM_005095	Hs.150390	zinc finger protein 262	TM SS	2.8 2.8
	433002 444342	AF048730 NM_014398	Hs.279906 Hs.10887	cyclin T1 similar to lysosome-associated mem	TM,Lamp	2.8
75	430598	AK001764	Hs.247112	hypothetical protein FLJ 10902	TM	2.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,pkinase,KA1	2.8
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C03	TM	2.8
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate tran	TM,GATase_2,SIS	2.8
QΛ	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus	TM Callagos COLELTSEN	2.8 2.8
80	417866 424894	AW067903 H83520	Hs.82772 Hs.153678	collagen, type XI, alpha 1 reproduction 8	Collagen, COLFI, TSPN SS, UBX	2.8 2.8
	424894 430651	AA961694	Hs.105187	kinesin protein 9 gene	SS	27
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-	TM	2.7
	448595	AB014544	Hs.21572	. KIAA0644 gene product	TM,LRRCT,LRR	2.7
					100	

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	452835	AK001269	Hs.30738	ESTs	TM	2.7
	403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	SS,Anti_proliferat	2.7
	420281	AI623693	Hs.191533	ESTs	Cation_efflux	2.7
5	434815 432201	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalact	SS tenfoil transin	2.6 2.6
,	430450	AI538613 R23553	Hs.135657 Hs.241489	TMPRSS3a mRNA for serine protea hypothetical protein	trefoil,trypsin SS	2.6 2.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras,arf	2.6
	421802	BE261458	Hs.108408	CGI-78 protein	TM	2.6
10	452355	N54926	Hs.29202	G protein-coupled receptor 34	TM,7tm_1	2.6
10	417742	R64719	Un acata	gb:EST22d11 WATM1 Homo saple	ank,death,RHD,TIG	2.6 2.6
	451346 433147	NM_006338 AF091434	Hs.26312 Hs.43080	glioma amplified on chromosome 1 platelet derived growth factor C	TM,Ig,LRR,LRRNT,LR TM,PDGF,CUB	2.6 2.6
	420079	NM_014051	Hs.94896	PTD011 protein	SS,TM,	2.6
1.0	419918	X80700	Hs.93728	pre-B-cell leukemia transcription fac	homeobox,ig,Acyitransf	2.5
15	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS shipped Same Diagin so	2.5
	406671 417412	AA129547 X16896	Hs.285754 Hs.82112	met proto-oncogene (hepatocyte gro interleukin 1 receptor, type I	pkinase,Sema,Plexin_re SS,T(R,ig	2.5 2.5
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	2.5
00	433929	Al375499	Hs.27379	ESTs	EGF,ldi_recept_a,ldl_re	2.5
20	443562	AF118838	Hs.9599	solute carrier family 25, member 13	TM,mito_can	2.5
	414386 417576	X00442 AA339449	Hs.75990 Hs.82285	haptoglobin phosphoribosylglycinamide formyltr	sushi,trypsin AlRS,formyl_transf,GA	2.5 2.5
	449207	AL044222	Hs.23255	nucleoporin 155kD	TM	2.5 2.5
	416107	AA173846	Hs.79015	antigen Identified by monoclonal ant	TM,ig	2.4
25	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	TM,PH	2.4
	414812	X72755	Hs.77367	monokine induced by gamma interfe	SS,IL8 TM,MulS_C,MulS_N,P	2.4 2.4
	406137 450710	R42764 AW953381	Hs.3248 Hs.18627	mutS (E. coli) homolog 6 ESTs, Weakly similar to G01447 GP	TM	24
	430291	AV660345	Hs.238126	CGI-49 protein	TM	2.4
30	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b a	ig	2.4
	451418	BE387790	Hs.26369	ESTs	TM C alaba	2.4
	412277 413719	BE277592 BE439580	Hs.73799 Hs.75498	guanine nucleotide binding protein (small inducible cytokine subfamily A	TM,G-alpha SS,IL8	2.4 2.4
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TMRCT	2.3
35	416224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bi	SS,efhand	2.3
	452268	NM_003512	Hs.28777	H2A histone family, member L	histone, Calc_CGRP_IA4	2.3
	451668 400880	Z43948 M84349	Hs.26789 Hs.119663	ASPIC (acidic secreted protein in ca CD59 antigen	SS,TM, SS,UPAR_LY6	2.3 2.3
	421340	F07783	Hs.1369	decay accelerating factor for comple	ideua, 22	2.3
40	443986	AI381750	Hs.283437	HTGN29 protein	TM	2.3
	443037	AW500305	Hs.8906	syntaxin 7	TM,Syntaxin	2.3
	440516 404877	S42303 A1394145	Hs.161 Hs.18048	cadherin 2, type 1, N-cadherin (neur melanoma antigen MAGE-10	HNH,cadherin,Cadherin TM,MAGE	2.3 2.3
	440704	M69241	Hs.162	insulin-like growth factor binding pr	SS,thyroglobulin_1,1GF	2.3
45	437952	D63209	Hs.5944	solute carrier family 11 (proton-coup	TM	2.3
	418624	A1734080	Hs.104211	ESTs	Sema,ig	2.2
	410434 424687	AF051152 J05070	Hs.63668 Hs.151738	toll-like receptor 2 matrix metalloproteinase 9 (gelatina	SS,TIR,LRRCT,LRR SS,fn2,hemopexin,Pepti	2.2 2.2
	431457	NM_012211	Hs.256297	integrin, alpha 11	TM,FG-GAP,vwa	2.2
50	407907	A1752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5	SS,Lysyl_hydro	2,2
	400898	AF220030	Hs.125300	Homo sapiens tripartite motif protein	SPRY,7tm_1	2.2
	400303 411789	AA242758 AF245505	Hs.79136 Hs.72157	Human breast cancer, estrogen regul Homo sapiens mRNA; cDNA DKFZ	SS,TM, ig,LRRCT	2.2 2.2
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	TM,PA,Ribosomal_S2	2.2
55	401131	NM_001651	Hs.298023	Homo sapiens aquaporin 5 (AQP5),	TM,MIP	2.2
	400277	Y00281	Hs.2280	Human mRNA for ribophorin I	TM	2.1
	409317 409956	U20165 AW103364	Hs.53250 Hs.727	bone morphogenetic protein recepto H.saplens activin bela-A subunit (ex	TM,pkinase TGF-beta,TGFb_propep	2.1 2.1
	451253	H48299	Hs.26126	claudin 10	TM,PMP22_Claudin	2.1
60	429638	AI916662	Hs.211577	Kinectin 1 (kinesin receptor)	TM .	. 21
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	TMWD40	2.1
	418414 449057	J04977 AB037784	Hs.84981 Hs.22941	X-ray repair complementing defectiv ESTs	SS TM	2.1 2.1
	417666	Al345001	Hs.82380	menage a trois 1 (CAK assembly fac	zf-C3HC4	2.1
65	428485	NM_002950	Hs.2280	ribophorin I	TM	2.1
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1 2.1
	430057 425189	AW450303 H16622	Hs.2534	bone morphogenetic protein recepto gb:ym26c07.r1 Soares infant brain 1	TM,Activin_recp,pkina RasGEF,PH,fibrinogen_	2.1 2.1
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
70	421343	BE246444	Hs.283685	hypothetical protein FLJ20396	. TM	2.1
	425627 426261	AF019612	Hs.297007 Hs.168670	ESTs peroxisomal famesylated protein	TM,Peptidase_M50 E1-E2_ATPase,Cation_	2.1 2.1
	431638	AW242243 NM_000916	Hs.2820	oxytocin receptor	TM,7tm_1	2.1
	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-rela	TM	2.1
75	421685	AF189723	Hs.106778	calcium transport ATPase ATP2C1	TM,E1-E2_ATPase,Hy	2.1
	424099	AF071202	Hs.139336 Hs.153203	ATP-blnding cassette; sub-family C MyoD family inhibitor	TM,ABC_tran,ABC_m TM	2.1 2.1
	424800 410007	AL035588 AW950887	Hs.153203 Hs.57813	zinc ribbon domain containing, 1	TFIIS	21
00	436135	D85390	Hs.5057	carboxypeptidase D	SS,Zn_carbOpept	2.1
80	420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM lipocalin	2.1
	420162 426156	BE378432	Hs.95577 Hs.167382	cyclin-dependent kinase 4 natriuretic peptide receptor A/guany	pkinase,ank,ArfGap,PH TM,ANF_receptor,guan	2.1 2.0
	442711	BE244537 AF151073	Hs.8645	hypothetical protein	TM	2.0
	411872	AW327356	Hs.90918	. chromosome 11 open reading frame	TM	2.0
					179	

5	427801 430268 431183 431846 404210 435640 447906 412666	AW979155 AK000737 NM_006855 BE019924 U02478 AF220053 AL050062 AL080116	Hs.234433 Hs.237480 Hs.250696 Hs.271580 Hs.100469 Hs.54960 Hs.19999 Hs.74420	hypothetical protein PRO1068 hypothetical protein FLJ20730 KDEL (Lys-Asp-Glu-Leu) endoplas Uroplakin 1B Human AF-6 mRNA uncharacterized hematopoletic stem/ DKFZP566K023 protein ortgin recognition complex, subunit	TM,Aa_trans TM TM,ER_Jumen_recept,I TM,Ernanmembrane4 TM,RA,DIL,PDZ,FHA TM,SET,zf-CXXC,PHD SS TM	20 20 20 20 20 20 20 20 20		
10	417181 423945 411773 448350 401093	L10123 AA410943 NM_006799 L14561 AI955244	Hs.1071 Hs.72472 Hs.72026 Hs.78546 Hs.121520	surfactant protein A binding protein BMPR-lb; bone morphogenetic pro protease, serine, 21 (testisin) Homo sapiens clone 24411 mRNA s HYPOTHETICAL 16.4 kDa PROTE	TM TM.pkinase,Activin_rec SS,typsin TM,E1-E2_ATPase,Hy TM,LRRCT	20 20 20 20 20 20		
15	415664 448165 416391 422926 446849	NM_004939 NM_005591 AI878927 NM_016102 AU076617	Hs.78580 Hs.202379 Hs.79284 Hs.121748 Hs.16251	DEAD/H (Asp-Glu-Ala-Asp/His) bo metotic recombination (S. cerevisiae mesoderm specific transcript (mouse ring finger protein 16 cleavage and polyadenylation specif	DEAD,helicase_C,SPRY DNA_repair,Glyco_tran TM,abhydrolase SPRY,zf-C3HC4,zf-B_ TM	2.0 2.0 2.0 2.0 2.0		
20	427617 411678 432554	D42063 Al907114 Al479813	Hs.179825 Hs.71465 Hs.278411	RAN binding protein 2-like 1 squalene epoxidase NCK-associated protein 1	TM,Ran_BP1,zf-RanBP TM,Monooxygenase TM	2.0 2.0 2.0		
25	Pkey: Un CAT num	TABLE 11B: Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers						
30	Pkey 417742 425189	CAT Number 1696282_1 247825_1	R64719 Z4	4680 R12451 17322 AA351959				
35	TABLE 11C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495 Strand: Indicates DNA strand from which exons were predicted Nt_position: Indicates nucleotide positions of predicted exons							
40	Pkey 400534 401197	Ref 6981826 9719705	Strand Minus Plus	Nt_position 278637-279292 176341-176452				
45	small mol	ecules. These w	vere selected as	s for Table 10A, except that the ratio was g	reater than or equal to 2.0, and th	ode either enzymes or proteins amenable to modulation to ne predicted protein contained a structural domain that is porters). Predicted protein domains are noted.		
	TABLE 12	A: ABOUT 57 U	IP-REGULATEI	O GENES ENCODING EXTRACELLULAR	CELL SURFACE PROTEINS, O	VARIAN CANCER VERSUS NORMAL ADULT TISSUES		

SUES TABLE 12A: ABOUT 57 UP-REGULATED GEI Pkey: Primekey Ex. Accr.: Exemplar Accession UG ID: UniGene ID Tilde: UniGene II Tilde: UniGene II Tilde: UniGene II Tilde: Traditional Institution II Tradition II Tra

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55	ratio: rat	ratio; ratio tumor vs. normal							
	Pkev	Ex. Accn	UGID	Title	PFAM domains	ratio			
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase, Activin_recp	30.0			
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, Peptidase_M10	25.2			
	426427	M86699	Hs.169840	TTK protein kinase	pkinase	18.7			
60	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-rela	nkinase	16.2			
	433159	AB035898	Hs.150587	kinesin-like protein 2	kinesin	11.5			
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran	8.4			
	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitia	SS, Peptidase_M10	7.2			
	425465	L18964	Hs.1904	protein kinase C, iota	Ski_Sno,pkinase_C	6.1			
65	409506	NM_006153	Hs.54589	NCK adaptor protein 1	SH2,SH3	5.2			
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic pro	pkinase,Activin_recp	5.1			
	424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8			
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	4.6			
	431699	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 fis,	RhoGAP,FF,ras	3.9			
70	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	C2,PI-PLC-Y,PI-PLC-X	3.8			
	450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor ,pkinase	3.6			
	400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS, Peptidase_M10	3.5			
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis,	EGF,fn3,pkinase	3.4			
75	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SS,TM,trypsin	3.3			
	411393	AW797437	Hs.69771	B-factor, properdin	SS,sushi,trypsin,vwa,fn3,	3.2			
	444755	AA431791	Hs.183001	ESTs	AAA	3.2			
	418836	AI655499	Hs.161712	ESTs	pkinase,Activin_recp	3.2			
	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	3.1			
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10, ,ig	3.1			
80	453920	AI133148	Hs.36602	I factor (complement)	ldl_recept_a,trypsin,SRCR	3.0			
	404653	AA923729	Hs.26322	0 `	pkinase	2.9			
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkinase,ig	2.9			
	418848	A1820961	Hs.193465	ESTs	pkinase Activin_recp	2.9			
	428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,pkinase,KA1	2.8			
	179								
					•				

	401323	AL158037		predicted exon	lactamase_B	2.7
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3,pkinase ,ABC_tran	2.7
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protea	trefoil,trypsin	2.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene fam	ras.arf	2.6
5	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte gro	pkinase,Sema	2.5
_	453448	AL036710	Hs.209527	ESTs	CNH,pkinase	2.5
	414386	X00442	Hs.75990	haptoglobin	sushi trypsin	2.5
	421270	H56037 -	Hs.108146	ESTs	RhoGAP	2.4
	414695	BE439915	Hs.76913	proteasome (prosome, macropain) su	proteasome	2.4
10	431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA,Viral_helicase1	2.2
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatina	SS,fn2, ,Peptidase_M10	2.2
	416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26	AAA	2.2
	417601	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
15	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
	430057	AW450303	Hs.2534	bone morphogenetic protein recepto	Activin_recp.pkinase	2,1
	421841	AA908197	Hs.108850	KIAA0936 protein	TPR.pkinase	2.1
	453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	2.1
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM,ABC_tran	2.1
20	411190	AA306342	Hs.69171	protein kinase C-like 2	pkinase,pkinase_C,HR1	2.1
	407740	AA295547	Hs.62666	ESTs	p450	2.1
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	pkinase,ank,ArfGap ,ras	2.1
	420490	H69894	Hs.193041	ESTs	Pl3Ka,Pl3_Pl4_kinase	2.1
	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guany	TM,ANF_receptor ,pkinase	2.0
25	423945	AA410943	Hs.72472	BMPR-lb; bone morphogenetic pro	TM,pkinase,Activin_recp	2.0
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS,trypsin	2.0
	447298	BE617527	Hs.180450	ribosomal protein S24	PI3Ka, PI4_kinase	2.0
	427617	D42063	Hs.179825	RAN binding protein 2-like 1	TPR,pro_isomerase	2.0
	453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_isomerase,rm	. 2.0
30						

TABLE 12C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleofide positions of predicted exons

35

Pkey 401323 Strand Nt_position 9212516 .Plus 213509-214450 40

Table 13A lists about 1086 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

45 TABLE 13A: About 1086 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Pkey: Primekey
Ex. Accn: Exemplay Accession
UG ID: UniGene ID

Title: UniGene title

50 ratio: ration tumor vs. normal ovary

	Pkey	Ex. Accn	UG ID	Title	ratio
	439706	AW872527	Hs.59761	ESTs	109.2
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
55	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	104.4
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (Intestinal)	88.3
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	82.8
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (antil	81.9
	413859	AW992356	Hs.8364	ESTs	73.9
60	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	72.7
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcription f	68.1
	411469	T09997	Hs.70327	cysteine-rich protein 2	66.6
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	65.7
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, proton c	64.9
65	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	62.5
	446441	AK001782	Hs.15093	hypothetical protein	60.7
	428758	AA433988	Hs.98502	Homo saplens cDNA FLJ14303 fis, clone PLACE20	59.7
	441406	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fis, clone NT2RP10	57.8
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	56.7
70	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076	55.7
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264	55.2
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxylase	54.B
	428330	L22524	Hs.2256	matrix metalloprotelnase 7 (matrilysin, uteri	53.4
	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	51.4
75	430634	AI860651	Hs.26685	ESTs	50.7
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	50.7
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.6
	407786	AA687538	Hs.38972	tetraspan 1	50.4
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (endobr	49.7
80	417308	H60720	Hs.81892	KIAA0101 gene product	48.9
	436876	Al124756	Hs.5337	Isocitrate dehydrogenase 2 (NADP+), mitochond	48.4
	439180	Al393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	47.1
	428289	M26301	Hs.2253	complement component 2	46.3
	405484			. 0	46.1

	405074	D40444	11- 455004		45.7
	425371 403912	D49441	Hs.155981	mesothelin 0	45.7 45.0
	443021	AA368546	Hs.8904	lg superfamily protein	44.6
5	427697	T18997	Hs.180372	BCL2-like 1	44.3
5	428227 404678	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN 0	44.0 43.9
	404078	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	43.8
	451035	AU076785	Hs.430	plastin 1 (I isoform)	43.8
10	440848	BE314650	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar	42.8
10	436278 413936	BE396290 AF113676	Hs.5097 Hs.75621	synaptogyrin 2 serine (or cysteine) proteinase inhibitor, cl	42.4 42.1
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	42.1
	428411	AW291464	Hs.10338	ESTs	41.8
16	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
15	412477	AA150864 AW276858	Hs.790 Hs.81256	microsomal glutathione S-transferase 1 S100 calcium-binding protein A4 (calcium prot	40.7 40.1
	417130 424673	AA345051	Hs.294092	ESTs	39.8
	416530	U62801	Hs.79361	kaliikrein 6 (neurosin, zyme)	39.7
20	443162	T49951	Hs.9029	ESTs; Highly similar to KERATIN; TYPE I CYTO	39.5
20	413719	BE439580 J05070	Hs.75498 Hs.151738	small Inducible cytokine subfamily A (Cys-Cys matrix metalloproteinase 9 (gelatinase B, 92k	39.3 38.9
	424687 413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein-39	38.5
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	38.1
25	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid	37.9
25	415511	AI732617 AI885516	Hs.182362 Hs.95612	ESTs ·	37.7 37.7
	409453 445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	37.3
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone HSI116	37.3
20	408243	Y00787	Hs.624	interleukin 8	37.3
30	419092	J05581	Hs.89603	mucin 1, transmembrane ESTs	36.7 36.0
	444172 412115	BE147740 AK001763	Hs.104558 Hs.73239	hypothetical protein FLJ10901	. 35.8
	420440	NM_002407	Hs.97644	mammaglobin 2	35.7
25	414386	X00442	Hs.75990	haptoglobin	35.3
35	423225	AA852604 H13032	Hs.125359 Hs.103378	Thy-1 cell surface antigen ESTs, Weakly similar to DRR1 [H.saplens]	35.1 35.0
	440596 413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	34.9
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	34.8
40	445919	T53519	Hs.290357	ESTs	34.7
40	416854	H40164 U33446	Hs.80296 Hs.75799	Purkinje cell protein 4 protease, serine, 8 (prostasin)	34.4 34.2
	414186 434371	AA631362	ns.13133	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	33.9
	421937	AI878857	Hs.109706	HN1 protein	33.9
15	449722	BE280074	Hs.23960	cyclin B1	33.8
45	400965	VETETO	Hs.158164	0 ATP-binding cassette, sub-family B (MDR/TAP),	33.7 33.5
	452203 411945	X57522 AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	33.5
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
50	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	33.3
50	438461 422963	AW075485 M79141	Hs.286049 Hs.13234	phosphoserine aminotransferase ESTs	33.3 33.3
	422503	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	33.2
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	32.8
55	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
55	431211 436552	M86849 NM_014038	Hs.5566 Hs.5216	Homo sapiens connexin 26 (GJB2) mRNA, complet HSPC028 protein	32.5 32.5
	442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subu	32.5
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	32.4
60	450353	A1244661	Hs.103296	ESTs	32.4
60	422158 433412	L10343 AV653729	Hs.112341 Hs.8185	protease inhibitor 3, skin-derived (SKALP) CGI-44 protein; sulfide dehydrogenase like (y	32.4 32.3
	441020	W79283	Hs.35962	ESTs	32.2
	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine protease (ECHOS1) (T	32.0
65	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	31.9
65	453309 408380	Al791809 AF123050	Hs.32949 Hs.44532	defensin, beta 1 diubiquitin	31.8 31.7
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	31.6
	409231	AA446644	Hs.692	GA733-2; epithelial glycoprotein (EGP) (KSA)	31.6
70	423961	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specific fac	31.2 30.8
70	413840 440943	Al301558 AW082298	Hs.290801 Hs.146161	ESTs ESTs. Weakly similar to KIAA0859 protein [H.s	30.8
•	419239	AA468183	Hs.184598	Homo saplens cDNA: FLJ23241 fis, clone COL013	30.4
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	30.2
75	418203	X54942	Hs.83758	CDC28 protein kinase 2	30.1
75	412719	AW016610	Hs.129911 Hs.50724	ESTs Homo sapiens cDNA FLJ10934 fis, clone OVARC10	30.0 30.0
	407862 431563	BE548267 AI027643	Hs.50724 Hs.120912	ESTs	29.9
	431743	AW972642	Hs.293055	ESTs	29.8
οΛ	443295	AI049783	Hs.241284	ESTs	29.7
80	413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7 29.6
	441028 442315	AI333660 AA173992	Hs.17558 Hs.7956	ESTs ESTs	29.6
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5

	100000				
	432280	BE440142	Hs.2943	signal recognition particle 19kD	29.4
	420158	A1791905	Hs.95549	hypothetical protein	29.3
	445033	AV652402	Hs.155145	ESTs	29.2
_	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	29.1
5	432706	NM_013230	Hs.286124	CD24	29.0
	422163	AF027208	Hs.297332	prominin (mouse)-like 1	28.7
	447035	NM_004753	Hs.17144	short-chain dehydrogenase/reductase 1	28.6
	443958	BE241880	Hs.10029	cathepsin C	28.2
10	422956	BE545072	Hs.122579	ESTs	28.1
10	450377	AB033091	Hs.24936	ESTs	28.0
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	28.0
	444725	AW952022	Hs.234174	Homo sapiens cDNA FLJ13819 fis, clone THYRO10	27.8
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	27.7
1.5	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	27.6
15	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	27.5
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cys-X-C	27.4
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
00	442993	BE018682	Hs.44343	ESTs	27.2
20	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	27.0
•	419356	A1656166	Hs.7331	ESTs	27.0
	433662	W07162	Hs.150826	CATX-8 protein	26.7
	422576	BE548555	Hs.118554	CGI-83 protein	26.4
~ =	423271	W47225	Hs.126256	Interleukin 1, beta	26.3
25	443715	Al583187	Hs.9700	cyclin E1	26.1
	420186	NM_015925	Hs.95697	liver-specific bHLH-Zip transcription factor	26.0
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) homolog	25.9
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate dioxyge	25.8
20	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	25.3
30	408474	AA188823	Hs.83196	Homo sapiens cDNA: FLJ23597 fis, clone LNG152	25.3
	411825	AK000334	Hs.72289	hypothetical protein FLJ20327	25.3
	400881			0	25.2
	440594	AW445167	Hs.126036	ESTs	25.1
0.5	414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1
35	411925	AW014588	Hs.72925	chromosome 11 open reading frame 13	25.1
	417869	BE076254	Hs.82793	proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Hs.3281	neuronal pentraxin II	25.0
	450858	C18458	Hs.25597	elongation of very long chain fatty acids (FE	24.8
40	410619	BE512730	Hs.65114	keratin 18	24.8
40	434094	AA305599	Hs.238205	hypothetical protein PRO2013	24.6
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	24.6
	446859	A1494299	Hs.16297	COX17 (yeast) homolog, cytochrome c oxidase a	24.5
	421451	AA291377	Hs.50831	ESTs	24.3
4.5	433929	Al375499	Hs.27379	ESTs	24.3
45	438930	AW843633	Hs.81256	S100 calcium-binding protein A4 (calcium prot	24.2
	444212	AW503976	Hs.10649	basement membrane-induced gene	24.2
	441633	AW958544	Hs.112242	ESTs	24.2
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	24.2
50	417715	AW969587	Hs.86366	ESTs	24.1
50	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	24.1
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reduc	24.1
	430125	U46418	Hs.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW880709	Hs.283683 ~	EST	23.8
	408669	Al493591	Hs.78146	platelet/endothetial cell adhesion molecule (23.8
55	439413	Al598252	Hs.37810	ESTs	23.7
	449034	AI624049	Hs.277523	gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	23.7
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
~	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated prot	23.5
60	451267	A1033894	Hs.117865	solute carrier family 17 (anlon/sugar transpo	23.4
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	23.4
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport regulato	23.4
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth factor 8	23.4
15	451110	A1955040	Hs.301584	ESTs	23.3
65	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	23.2
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to sign	23.1
	424670	W61215	Hs.116651	epithelial V-like antigen 1	23.1
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 ffs, clone HRC052	23.1
70	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	23.1
70	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiquitous)	23.1
	433159	AB035898	Hs.150587	kinesin-like protein 2	23.0
	411393	AW797437	Hs.69771	B-factor, properdin	23.0
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamine-alp	22.8
75	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal	22.7
75	445721	H92136	Hs.13144	HSPC160 protein	22.6
	448258	BE386983	Hs.85015	ESTs, Weakly similar to A4P_HUMAN INTESTINAL	22.6
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidate cy	22.6
	452698	NM_001295	Hs.301921	ESTs	22.5
90	418693	A1750878	Hs.87409	thrombospondin 1	22.4
80	414880	AW247305	Hs.119140	eukaryotic translation initiation factor 5A	22.4
	401519			0	22.3
	402496	45400174	U= 00744	0	22.3
	420324	AF163474	Hs.96744	DKFZP586D0823 protein, Prostate androgen-regu	22.3 22.2
	403022			. 0	22.2

	434042	Al589941	Hs.8254	hypothetical protein PRO0899	22.1
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	22.1
	406545	AB018249	Hs.10458	small inducible cytokine subfamily A (Cys-Cys	22.1
_	447362	AW176120	Hs.9061	ESTs	22.0
5	429547	AW009166	Hs.99376	ESTs	22.0
	427954	J03060	Hs.247551	metaxin 1	22.0
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	22.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (21.9
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polypeptide	21.7
10	414421-	Al521130	Hs.55567	ESTs, Weakly similar to LAK-4p [H.sapiens]	21.5
~ ~	412589	R28660	Hs.24305	ESTs	21.5
	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone HEP162	21.5
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like docking	21.5
	436972	AA284679	Hs.25640	claudin 3	21.5
15					21.5
13	428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.sapiens]	21.4
	421340	F07783	Hs.1369	decay accelerating factor for complement (CD5	
	413966	AA133935	Hs.173704	ESTs	21.4 21.3
	448243	AW369771	Hs.77496	ESTs	
20	421928	AF013758	Hs.109643	polyadenylate binding protein-interacting pro	21.3
20	403399			<u>.</u> .	21.3
	435793	AB037734	Hs.4993	ESTs	21.3
	432629	AW860548	Hs.280658	ESTs	21.2
	449057	AB037784	Hs.22941	ESTs	21.2
~ ~	437575	AW954355	Hs.36529	ESTs ·	21.2
25	401131			0	21.0
	407207	T03651	Hs.179661	tubulin, beta polypeptide	20.8
	444783	AK001468	Hs.62180	ESTs	20.8
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	20.8
••	447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
30	409041	AB033025	Hs.50081	KIAA1199 protein	20.6
	421305	BE397354	Hs.289721	diptheria toxin resistance protein required f	20.6
	411704	Al499220	Hs.71573	hypothetical protein FLJ10074	20.5
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncog	20.5
	432827	Z68128	Hs.3109	Rho GTPase activating protein 4	20.4
35	410174	AA306007	Hs.59461	DKFZP434C245 protein	20.4
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen incl	20.4
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	20.3
	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte chemota	20.2
	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
40	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	20.1
40	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activating e	20.1
	429083	Y09397	Hs.227817	BCL2-related protein A1	20.0
	410173	AA706017	Hs.119944	ESTs	19.8
	433047	M86135	Hs.279946	methionine-tRNA synthetase	19.8
45					19.7
72	419088	Al538323	Hs.77496	ESTs 0	19.6
	403381	UNEESO.	Un EOOCO		19.5
	409162	H25530	Hs.50868	solute carrier family 22 (organic cation tran	
	426150	NM_003658	Hs.167218	BarH-like homeobox 2	19.4
50	449292	AI990292	Hs.225457	ESTs	19.4
30	425207	AB014551	Hs.155120	rho/rac guanine nucleotide exchange factor (G	19.4
	419950	AK001645	Hs.93871	hypothetical protein FLJ10783	19.3
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	19.3
	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2
55	446608	N75217	Hs.257846	ESTs	19.1
55	425222	M85430	Hs.155191	villin 2 (ezrin)	19.1
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	19.1
	420005	AW271106	Hs.133294	ESTs	19.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	19.0
60	407142	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2, neutral me	19.0
60	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood Leuke	18.9
	446293	Al420213	Hs.149722	ESTs	18.9
	444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
	407634	AW016569	Hs.301280	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosami	18.9
CF	445200	AA084460	Hs.12409	somatostatin	18.9
65	418917	X02994	Hs.1217	adenosine dearninase	18.8
	435777	AW419202	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene	18.7
	426427	M86699	Hs.169840	TTK protein kinase	18.7
70	436281	AW411194	Hs.120051	ESTs	18.6
70	425907	AA365752	Hs.155965	ESTs	18.6
	459720			ESTs	18.6
	421242	AW161386	Hs.13561	ESTs, Weakly similar to dJ37E16.5 [H.sapiens]	18.5
	457715	AA642402	Hs.59142	ESTs	18.5
	451668	Z43948	Hs.26789	ASPIC (acidic secreted protein in cartilage)A	18.4
75	437142	Al791617	Hs.145068	ESTs	18.4
	418588	BE387040	Hs.182476	ESTs, Weakly similar to similar to alpha/beta	18.3
	433068	NM_006456	Hs.288215	sialyltransferase	18.3
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RP5-1087M19 from 7q11.	18.3
	444726	NM_006147	Hs.11801	interferon regulatory factor 6	18.3
80	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA-2C-2	18.2
	451428	AW083384	Hs.11067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	18.2
	418742	AW451197	Hs.113418	ESTs	18.1
	446627	Al973016	Hs.15725	ESTs; hypothetical protein SBBI48	18.1
	770027	74373010		in bonnesse bearing and in	

	424885	Al333771	Hs.82204	ESTs	18.1
	402926			0	18.0
	405452			0	18.0
	428641	AA431367	Hs.234546	GMPR2 for guanosine monophosphate reductase i	18.0
5	454390	AB020713	Hs.56966	KIAA0906 protein	18.0
	441784	Al522132	Hs.28700	ESTs	18.0
	418758	AW959311	Hs.87019	ESTs	17.9
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8; fetal br	17.9
	426201	AW182614	Hs.128499	ESTs	17.8
10	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
10	456423	AW748920	115.03700	gb:CM2-BT0306-171199-034-g02 BT0306 Homo sapi	17.8
	422867	L32137	De 4504		17.8
	448110	AA626937	Hs.1584	cartilage oligomeric matrix protein	17.7
			Hs.181551	ESTs	
15	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
13	405224	41000440		0	17.7
	447630	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	17.7
	407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	17.7
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	17.6
00	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
20	427691	AW194426	Hs.20726	ESTs	17.6
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	17.5
	439841	AF038961	Hs.6710	mannose-P-dolichol utilization defect 1	17.5
	425810	AI923627	Hs.31903	ESTs	17.5
~ ~	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	17.5
25	456098	AW747800	Hs.55016	hypothetical protein FLJ21935	17.4
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	17.4
	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cosmid F	17.3
30	405295			0	17.3
	408340	AB037762	Hs.44268	myelin gene expression factor 2	17.3
	456068	AI677897	Hs.76640	RGC32 protein	17.3
	448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [H.sap	17.2
	441829	AL117482	Hs.7978	DKFZP434C131 protein	17.2
35	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
75	412078	X69699	Hs.73149	paired box gene 8	17.2
					17.1
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	17.0
40	426805	AB032945	Hs.172506	myosin VB	
40	410247	AF181721	Hs.61345	RU2S	17.0
	434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apopto	16.9
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-	16.9
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
45	454163	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo sapi	16.9
43	415402	AA164687	Hs.297889	ESTs	16.9
	420309	AW043637	Hs.21766	ESTs	16.9
	419201	M22324	Hs.1239	alanyl (membrane) aminopeptidase (aminopeptid	16.9
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	16.9
50	457705	AW974668		gb:EST386757 MAGE resequences, MAGM Homo sapl	16.8
50	412723	AA648459	Hs.179912	ESTs	16.8
	435774	R88066	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
	408753	AJ337192	Hs.47438	SH3 domain binding glutamic acid-rich protein	16.8
	447783	AF054178	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
	418085	R40328	Hs.258822	ESTs	16.7
55	452472	AW957300	Hs.294142	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	16.7
	409112	BE243971	Hs.50649	quinone oxidoreductase homolog	16.7
	410250	A1082777	Hs.61384	KIAA1445 protein	16.7
	446219	Al287344	Hs.149827	ESTs	16.6
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithelial)	16.6
60	425812	AA364128	Hs.245633	ESTs*	16.6
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
•	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	16.6
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	16.6
65	430375	AW371048	Hs.93758	H4 histone family, member H	16.6
	419607	R52557	Hs.91579	Homo sapiens clone 23783 mRNA sequence	16.6
	410328	BE080190	Hs.62275	CGI-141 protein	16.5
	405426	22000.00		0	16.5
	432636	AA340864	Hs.278562	claudin 7	16.5
70	434725	AK000796	Hs.4104	hypothetical protein	16.5
, 0	414683	S78296	Hs.76888	internexin neuronal intermediate filament pro	16.5
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	16.5
	449944	AF290512	Hs.58215	Homo sapiens rhotekin mRNA, partial cds	16.4
	400666	M-200012	113.30213	0	16.4
75		DESENSON	Hs.105509	CTL2 gene	16.4
, 5	421536	BE250690			16.4
	436032	AA150797	Hs.109276	latexin protein	
	418196	AI745649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p	16.4
	452323	W44356	Hs.292812	ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4
90	407699	AA825974	Hs.32646	Homo saplens cDNA: FLJ21901 fis, clone HEP034	16.4
80	414617	AI339520	Hs.20524	ESTs, Moderately similar to hexokinase I [H.s	16.3
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, member	16.3
	452650	AW270150	Hs.254516	ESTs	16.3
	432906	BE265489	Hs.3123	tethal giant larvae (Drosophila) homolog 2	16.3
	402408			. 0	16.3
				4	

	408805	H69912	Hs.48269	vaccinia related kinase 1	16.3
	447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041 1 SGC32445 p	16.3
	405699		110.12.100.	0	16.2
		M22406			16.2
5	406893			gb:Human intestinal mucin mRNA, partial cds,	
3	418629	BE247550	Hs.86859	growth factor receptor-bound protein 7 (GRB7)	16.2
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
	424243	Al949359	Hs.301837	ESTs, Highly similar to cls Golgi-localized c	16.2
	418462	BE001596	Hs.85266	integrin, beta 4	16.1
	457205	Al905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
10	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epidermal t	16.1
10					
	449845	AW971183	Hs.60054	ESTs	16.1
	406429			0	16.1
	407375	AA091354		gb:li0815.seq.F Human fetal heart, Lambda ZAP	16.1
	448377	Al494514	Hs.171380	ESTs	16.1
15	431156	NM_002220	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	16.0
13					
	450043	AA885699	Hs.24332	CGI-26 protein	16.0
	403121			0	16.0
	40021 <i>4</i>			0	. 15.9
	453252	R02436	Hs.215725	ESTs	15.9
20	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate, RC3)	15.9
	416855	AA188763	Hs.36793	Homo sapiens cDNA: FLJ23188 fis, clone LNG120	15.9
					15.9
	424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interacting pro	
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, parti	15.9
	428187	AJ687303	Hs.285529	ESTs '	15.9
25	438817	Al023799	Hs.163242	ESTs	15.9
	425692	D90041	Hs.155956	NAT1; arylamine N-acetyltransferase	15.9
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	15.9
	439999	AA115811	Hs.6838	ras homolog gene family, member E	15.9
	411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase	15.9
30	413027	NM_002885	Hs.75151	RAP1, GTPase activating protein 1	15.9
	453884	AA355925	Hs.36232	KIAA0186 gene product	15.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-bet	15.8
			Hs.129349		15.8
	422748	AA316266		ESTs	
25	414591	Al888490	Hs.55902	ESTs	15.8
35	421877	AW250380	Hs.109059	mitochondrial ribosomal protein L12	15.8
	404780			0	15.8
	401192			0	15.8
	447519	U46258	Hs.23448	ESTs .	15.8
	434262	AF121858	Hs.12169	sorting nextn 8	15.7
40					15.7
40	451253	H48299	Hs.26126	claudin 10	
	435499	R89344	Hs.14148	ESTs	15.7
	422424	AI186431	Hs.116577 ·	prostate differentiation factor; placental bo	15.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	15.7
	424562	Al420859	Hs.150557	basic transcription element binding protein 1	15.7
45	443247	BE614387	Hs.47378	ESTs	15.7
73					
	430696	AA531276	Hs.59509	ESTs	15.6
	437044	AL035864	Hs.69517	ESTs, highly similar to differentially expres	15.6
	428237	AF175206	Hs.183125	killer cell lectin-like receptor F1	15.6
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	· 15.6
50	414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethy	15.6
-	422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
	408716	AI567839	Hs.151714	ESTs	15.5
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	15.5
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
55	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	15.5
	409015	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5
	447549	AI871120 ·		ESTs	15.5
			Hs.23900		15.4
	449704	AK000733		GTPase activating protein	15.4
60	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity Ilib, recept	
60	421630	NM_001956	Hs.1407	endothelin 2	15.4
	433018	AI669760	Hs.188881	ESTs	15.4
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	15.3
	407014	U38268		gb:Human cytochrome b pseudogene, partial cds	15.2
		AF080157	Hs.198998	conserved helix-loop-helix ubiquitous kinase	15.2
65	429311			epithelial protein up-regulated in carcinoma,	15.2
05	431842	NM_005764	Hs.271473		
	406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	15.2
	458495	A1202029	Hs.148593	ESTs	15.2
	420551	AL137692	Hs.98790	Homo sapiens mRNA; cDNA DKFZp434P182 (from cl	15.1
	448443	AW167128	Hs.231934	ESTs	15.1
70	443646	A1085198	Hs.298699	ESTs	15.1
, 0			Hs.259619	Homo sapiens mRNA; cDNA DKFZp434B1120 (from c	15.1
	431538	AL137547			
	436687	AA868643	Hs.120461	ESTs	15.1
	420917	AW135716	Hs.117330	ESTs	15.0
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibitor, cl	15.0
75	403482			0	15.0
. •	421499	AI271438	Hs.105022	Homo sapiens PAC clone RP4-701016 from 7q33-q	15.0
		MIZ! 1400	113.103022		
	401047			0	14.9
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	14.9
	416693	Al373204	Hs.79531	Homo sapiens TTF-I Interacting peptide 20 mRN	14.9
80	428474	AB023182	Hs.184523	KIAA0965 protein	14.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
				heat shock cognate 40	14.9
	430271	T06199	Hs.237506		
	414328	Z21666	Hs.75900	aconitase 2, mitochondrial	14.9
	415314	N88802	Hs.5422	glycoprotein M6B	14.8

	453735	A1066629	Hs.125073	ESTs	14.8
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	14.8
	423575	C18863	Hs.163443	ESTs	14.8
	438081	H49546	Hs.298964	ESTs	14.8
5	403485			0	14.8
_	452114	N22687	Hs.8236	ESTs	14.8
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412869	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
	452101	T60298	1.0.02.00	gb:yb87f12.r1 Stratagene liver (937224) Homo	14.7
10	420505	AW967984	Hs.291612	ESTs	14.7
10	426125	X87241	Hs.166994	FAT turnor suppressor (Drosophila) homolog	14.7
	433336	AF017986	Hs.31386	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
	428977	AK001404	Hs.194698	cyclin B2	14.7
	420371	H82114	Hs.301769	ESTs	14.7
15	402424	1102114	113.501705	0	14.7
IJ		AA479005	Hs.154036	tumor suppressing subtransferable candidate 3	14.7
	424971		Hs.279938		14.6
	433037	NM_014158		HSPC067 protein	14.6
	421670	BE207318	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
20	438598	AI805943	Hs.5723	Homo saplens cDNA: FLJ23439 fis, clone HSI001	14.6
20	453370	Al470523	Hs.182356	ESTs, Moderately similar to translation initi	
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	14.6
	402287			0	14.6
	419741	NM_007019	Hs.93002	ublquitin carrier protein E2-C	14.6
25	442047	AA974598	Hs.150324	ESTs .	14.5
25	428582	BE336699	Hs.185055	BENE protein	14.5
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
	406851	AA609784	Hs.180255	major histocompatibility complex, class II, D	14.5
	457316	Al123657	Hs.127264	ESTs	14.5
20	420453	AL157500	Hs.97840	Homo sapiens mRNA; cDNA DKFZp434G015 (from cl	14.5
30	436406	AW105723	Hs.125346	ESTs	14.5
	420736	AI263022	Hs.82204	ESTs	14.5
	419743	AW408762	Hs.127478	ESTs	14.5
	429113	D28235	Hs.196384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-rich tan	14.5
35	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untr	14.5
	. 427414	F11750	Hs.6647	Homo saplens cDNA FLJ13088 fis, clone NT2RP30	14.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activat	14.4
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	14.3
	429414	A1783656	Hs.202095	empty spiracles (Drosophila) homolog 2	14.3
40	424669	AA417181	Hs.120858	Homo saplens cDNA FLJ13945 fis, clone Y79AA10	14.3
	408989	AW361666	Hs.49500	KIAA0746 protein	14.3
	406788	Al911841	Hs.5184	TH1 drosophila homolog	14.3
	417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
	402104			0	14.3
45	416368	R88849		gb:ym96a06.r1 Soares adult brain N2b4HB55Y Ho	14.2
	405802		•	Ŏ	14.2
	448357	N20169	Hs.108923	ESTs	14.2
	444261	AA298958	Hs.10724	MDS023 protein	14.2
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	14.2
50	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	14.1
	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
55	427036	AA397625	Hs.163913	ESTs	14.1
	444381	BE387335	Hs.283713	ESTs	14.1
	432090	AW972855	Hs.292853	ESTs	14.0
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (from cl	14.0
	404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (afla	14.0
60	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	14.0
	429942	Al338993	Hs.134535	ESTs	14.0
	403165			0	13.9
	442150	Al368158	Hs.128864	ESTs	13.9
65 ·	439709	AW401433	Hs.6649	hypothetical protein FLJ20128	13.9
	456799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
	427356	AW023482	Hs.97849	ESTs	13.9
	448982	A1638164	Hs.225520	ESTs	13.9
	432025	BE407132	Hs.111286	hypothetical protein FLJ22512	13.8
70	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	13.8
	402965			0	13.8
	418601	AA279490	Hs.86368	calmegin	13.8
	436954	AA740151	Hs.130425	ESTs	13.8
	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	N46466	Hs.58879	ESTs	13.8
	401735	11-10-100	,	0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
	425007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
80	409463	AI458165	Hs.17296	ESTs	13.7
-	430193	AI826653	Hs.102928	Homo sapiens cDNA FLJ13479 fis, clone PLACE10	13.7
	458869	Al637934	Hs.224978	ESTs	13.7
	426769	AA075596	Hs.172153	glutathione peroxidase 3 (plasma)	13.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7
	710001	14/00/1010		· · · · · · · · · · · · · · · · · · ·	

	420004	MAJOUE	11- 404400	FCT-	127
	439901 431374	N73885	Hs.124169	ESTs	13.7 13.7
		BE258532	Hs.251871	CTP synthase	
	432861	- AA339526	Hs.279593	HSPC171 protein	13.7
5	441172	A1279652	Hs.132879	ESTs	13.7 13.7
,	410001	AB041036	Hs.57771	kallikrein 11; serine protease (TLSP)	13.6
		NM_004293	Hs.239147	guanine deaminase	13.6
	422769	AA938905	Hs.289112	CGI-43 protein	
	402389	V04000	11- 00000	•	13.6
10	448977	X91809	Hs.22698	regulator of G-protein signalling 19	13.6
10	459648	4404200	11-04040	gb:lL3-CT0220-150200-070-B02 CT0220 Homo sapi	13.6
	452972	M31732	Hs.31210	B-cell CLL/lymphoma 3	13.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6
	448585	AB020676	Hs.21543	KIAA0869 protein	13.6
	428385	AF112213	Hs.184062	putative Rab5-Interacting protein	13.6
15	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEM8810	13.6
	447238	AW451676	Hs.158564	ESTs	13.6
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fis, clone HS1009	13.6
	425749	AW328587	Hs.159448	surfelt 2	13.5
00	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
20	413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin (140	13.5
	419034	NM_002110	Hs.89555	hemopoletic cell kinase	13.5
	448361	H82028	Hs.238707	Homo sapiens cDNA: FLJ22457 fis, clone HRC099	13.5
	412754	AW160375	Hs.74565	amylold beta (A4) precursor-like protein 1	13.5
~ -	419081	AI798863	Hs.87191	ESTs	13.5
25	407732	AW138839	Hs.24210	ESTs	13.5
	423329	AF054910	Hs.127111	tektin 2 (testicular)	13.5
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439636	AF086467		gb:Homo sapiens full length Insert cDNA clone	13.4
••	417605	AF006609	Hs.82294	regulator of G-protein signalling 3	13.4
30	445861	BE293423	Hs.11809	single Ig IL-1R-related molecule	13.4
	447350	AI375572	Hs.172634	ESTs; HER4 (c-erb-84)	13.4
	451807	W52854	Hs.27099	DKFZP564J0863 protein	13.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long f	13.4
	422443	NM_014707	Hs.116753	histone deacetylase 7B	13.4
35	412504	Z44496	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10	13.4
	453344	BE349075	Hs.44571	ESTs	13.4
	402885			0	13.4
	438712	AW978161	Hs.169877	ESTs	13.4
	421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
40	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	401897			0	13.3
	425601	AW629485	Hs.293352	ESTs	13.3
	450779	AW204145	Hs.156044	ESTs	13.3
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
45	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 protein x	13.3
	434263	N34895	Hs.44648	ESTs	13.3
	426059	BE292842	Hs.166120	interferon regulatory factor 7	13.3
	407467	D55638		gb:Human B-cell PABL (pseudoautosomal boundar	13.3
	412560	R24601	Hs.108300	CCR4-NOT transcription complex, subunit 3	13.2
50	442986	Al025990	Hs.285520	ESTs	13.2
	420317	AB006628	Hs.96485	KIAA0290 protein	13.2
	443211	AI128388	Hs.143655	ESTs	13.2
	434361	AF129755	Hs.117772	ESTs	13.2
	423493	Al815965	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologou	13.2
55	414183	AW957446	Hs.301711	ESTs	13.2
	447778	BE620592	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box prot	13.1
	439490	AW249197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	13.1
<i>~</i>	409606	AW444594	Hs.2387	transglutaminase 4 (prostate)	13.1
60	421308	AA687322	Hs.192843	ESTs	13.1
	414950	C15407		gb:C15407 Clontech human aorta polyA+ mRNA (6	13.1
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-associ	13.1
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
~ ~	422605	H16646	Hs.118666	Human clone 23759 mRNA, partial cds	13.0
65	430427	AA296701	Hs.241413	opticin	13.0
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	13.0
	421693	X71490	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP564M082 protein	13.0
70	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
70	406709	Al355761	Hs.242463	keratin 8	13.0
	405353			0	13.0
	453060	AW294092	Hs.21594	ESTs	13.0
	459299	BE094291	Hs.155651	hepalocyte nuclear factor 3, beta	13.0
~~	447843	AW337186	Hs.224891	ESTs	13.0
75	446576	AI659477	Hs.51820	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
	449700	L02867	Hs.78358	ESTs	13.0
	436476	AA326108	Hs.53631	ESTs	13.0
	432532	AW058459	Hs.162246	ESTs	13.0
0.0	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
80	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40 co-ch	12.9
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitoc	12.9
	447210	AF035269	Hs.17752	phosphalidylserine-specific phospholipase A1a	12.9
	427923	AW274357	Hs.268384	Fzr1 protein	12.9
	437395	AL365408	Hs.10632	hypothetical protein DKFZp762M136	12.9
				·	

	444007	A A D 47552	He FOOD	FOT-	42.0
	441627	AA947552 AA496539	Hs.58086	ESTs	12.9 12.9
	419084	AA321355	Hs.179902	transporter-like protein	12.9
	423067		Hs.285401	ESTS	12.8
5	423070 441344	R55677 BE250144	Hs.155569	ESTs ESTs	12.8
5	423527	Al206965	Hs.41514	Homo sapiens cDNA FLJ13824 fis, clone THYRO10	12.8
	417006	AW673606	Hs.105861 Hs.80758	aspartyHRNA synthetase	12.8
	453552	AL041941	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.8
	453657	W23237	Hs.296162	ESTs	12.8
1.0	434414	A1798376	113.200102	gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA	12.7
1,0	456051	T85626	Hs.76239	hypothetical protein FLJ20608	12.7
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
	418216	AA662240	Hs.283099	AF15q14 protein	12.7
	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
15	424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
	440062	Al350518	Hs.129692	ESTs	12.7
	444371	BE540274	Hs.239	Forkhead box M1	12.7
	412520	AA442324	Hs.795	H2A histone family, member O	12.7
	413349	BE086692		gb:QV1-BT0678-130400-156-g07 BT0678 Homo sapi	12.7
20	414500	W24087	Hs.76285	DKFZP564B167 protein	12.6
	429261	AW176254	Hs.143475	ESTs	12.6
	402238			0	12.6
	400280			0	12.6
	421246	AW582962	Hs.300961	ESTs, Highty similar to AF151805 1 CGt-47 pro	12.6
25	442029	AW956698	Hs.14456	neural precursor cell expressed, developmenta	12.6
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl O-as	12.6
	409964	AW368226	Hs.67928	ESTs	12.6
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
20	452117	AJ421760	Hs.77870	Homo sapiens cDNA FLJ12750 fis, clone NT2RP20	12.5
30	448074	BE621355	Hs.27160	ESTs	12.5
	442655	AW027457	Hs.30323	ESTs	12.5
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	12.5
	400240			0	12.5
25	413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
35	426215	AW963419	Hs.155223	ESTs	12.5
	430024	AI808780	Hs.227730	integrin, alpha 6	12.5
	445655	AA873830	Hs.167746	B cell linker protein	12.5 12.5
	419941	X98654	Hs.93837	phosphatidylinositol transfer protein, membra	12.5
40	425280	U31519 Al879283	Hs.1872 Hs.180714	phosphoenolpyruvate carboxykinase 1 (soluble) cytochrome c oxidase subunit VIa polypeptide	12.4
40	427767 450243	AW119084	Hs.201037	ESTs	12.4
	408930	AA146721	Hs.49005	hypothetical protein	12.4
	418783	T41368	115.45550	gb:ph1d1_19/1TV Outward Alu-primed hncDNA lib	12.4
	452096	BE394901	Hs.226785	ESTs	12.4
45	424513	BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
	422306	BE044325	Hs.227280	Homo sapiens mRNA for Lsm5 protein	12.4
	409031	AA376836	Hs.76728	ESTs	12.4
	435515	N40080	Hs.6879	DC13 protein	12.4
	429583	NM_006412	Hs.209119	1-acylglycerol-3-phosphate O-acyltransferase	12.3
50	449643	R05989	Hs.19603	ESTs	12.3
	440313	AL050060	Hs.7158	DKFZP566H073 protein	12.3
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	12.3
	447357	Al375922	Hs.159367	ESTs	12.3
	405089			0	12.3
55	414972	BE263782	Hs.77695	KIAA0008 gene product	12.3
	435039	AW043921	Hs.130526	ESTs	12.3
	447033	Al357412	Hs.157601	EST - not in UniGene	12.3
	427521	AW973352	Hs.299056	ESTs	12.3
60	409377	AA300274	Hs.115659	Homo sapiens cDNA: FLJ23461 fis, clone HSI077	12.3 12.3
00	400116	41 127510	No 42222	hypothetical protein FLJ22059	12.2
	445806	AL137516	Hs.13323		12.2
	457817	AA247751 AW996503	Hs.79572 Hs.197680	cathepsin D (lysosomal aspartyl protease) ESTs	12.2
	442410 445404	Al261687	Hs.145541	ESTs, Weakly similar to JC4974 sodium todide	12.2
65	403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
UJ	427082	AB037858	Hs.173484	hypothelical protein FLJ10337	12.2
	433764	AW753676	Hs.39982	ESTs	12.2
	400268	711100010	110.00002	0	12.2
	433190	M26901	Hs.3210	renin	12.2
70	444863	AW384082	Hs.301323	ESTs	12.2
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
	451346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein (leu	12.2
	430262	AA218780	Hs.237323	N-acetylglucosamine-phosphate mutase	12.2
76	421071	Al311238	Hs.104476	ESTs	12.2
75	426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
	409178	BE393948	Hs.50915	kallikrein 5	12.1
	400250			0	12.1
	428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1
0Λ	414531	T69387	Hs.76364	allograft inflammatory factor 1	12.1
80	448210	AW247775	Hs.7393	hypothetical protein from EUROIMAGE 1987170	- 12.1 12.1
	440081	AA863389	Hs.135643	ESTs NADU debudoscensce (ubiquinone) 1 alcha subco	12.1
	413179	N99692	Hs.75227 Hs.929	NADH dehydrogenase (ubiquinone) 1 alpha subco myosin, heavy polypeptide 7, cardiac muscle,	12.1
	447551	BE066634 AF242388	Hs.149585	lengsin	12.1
	400517	CA 545900	110.143303	, icilifant	14.1

	401610			0	12.0
	454381	A103E003	Un 102429	ESTs	12.0
		A1935093	Hs.193428	ESTs	12.0
	443997 402944	AW081465	Hs.299644	0	12.0
5	430637	DE160001	Ha assagn	<u> </u>	12.0
	415099	BE160081	Hs.256290 Hs.77917	S100 calcium-binding protein A11 (calgizzarin	12.0
	445422	Al492170 AV653731	Hs.282829	ubiquitin carboxyl-terminal esterase L3 (ubiq ESTs	12.0
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	12.0
	442611	BE077155	Hs.177537	ESTs	12.0
10	443271	BE568568	Hs.195704	ESTs	12.0
10	415120	N64464	Hs.34950	ESTs	12.0
	439574	A1469788	Hs.165190	ESTs	12.0
	405804	M403100	115.105150	0	12.0
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow .	12.0
15	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	12.0
15	447075	AV662037	Hs.124740	ESTs	12.0
	416841	N33878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	12.0
	402943	1400010	110.240400	0	11.9
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypeptide A	11.9
20	439744	AL389994	Hs.301272	ESTs, Weakly similar to homologue of Drosphil	11.9
20	405762	VEDODO	10.001212	n	11.9
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg	11.9
	455102	BE005496	113.000	gb:CM1-BN0117-110400-183-b09 BN0117 Horno sapl	11.9
	402840	02000430		80.0001-010-11-110-00-100-000-0110-111-110-000-00b	11.9
25	449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone CAS072	11.9
23	439273	AW139099	Hs.269701	ESTs	11.9
	450484	BE220675	113.203701	gb:ht98f11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	11.9
	445431	AF137386	Hs.12701	plasmolipin	11.9
	401888	AI-137300	113.12701	n .	11.9
30	426037	AW160780	Hs.166071	cyclin-dependent kinase 5	11.9
50	416742	R38644	Hs.248420	ESTs	11.9
	418324	AW246273	Hs.84131	threonyl-tRNA synthetase	11.8
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	11.8
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	11.8
35	421478	AI683243	Hs.97258	ESTs	11.8
55	426635	BE395109	Hs.129327	ESTs	11.8
	420523	AA262999	Hs.42788	ESTs	11.8
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mRNA; 3	11.8
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	11.8
40	441816	AI401807	Hs.149997	ESTs	11.8
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
	400640	ADOLOGO	110.101011	0	11.8
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	11.8
	401532		(1.0.701.00	0	11.8
45	400161			Ö	11.8
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c	11.7
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	11.7
	401879			0	11.7
	415989	Al267700	Hs.111128	ESTs	11.7
50	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	11.7
-	410616	AW873401	Hs.273599	ESTs	11.7
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	11.7
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (from cl	11.7
	436877	AA931484	Hs.121255	ESTs, Weakly similar to cDNA EST EMBL:067419	11.7
55	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	11.7
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	11.7
	400279			0	11.6
	440497	AA887266	Hs.144979	ESTs	11.6
	451260	AW750773		gb:CM0-CN0044-260100-164-h03 CN0044 Homo sapi	11.6
60	429175	AI953040	Hs.127714	ESTs, Moderately similar to SOX30 protein [H.	11.6
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule)	11.6
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP066	11.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	11.6
	428760	Al351459	Hs.192398	ESTs	11.6
65	421401	AW410478	Hs.104019	transforming, addic coiled-coil containing p	11.6
	404502			0	11.6
	430423	Al190548	Hs.143479	ESTs, Weakly similar to hypothetical protein	11.6
	405192			0	11.6
7 0	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	11.6
70	401714			0	11.5
	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen alpha	11.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (Isoform	11.5
	401010			0	11.5
75	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	11.5
75	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester	11.5
	459684			gb:ao86a08.x1 Schiller meningioma Homo sapien	11.5
	451051	BE254309	Hs.125262	DKFZP586G1624 protein	11.5
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chronic	11.5
00	412153	R87934		gb:yo47b10.r1 Soares adult brain N2b4HB55Y Ho	11.5
80	427256	AL042436	Hs.97723	ESTs	11.5
	406708	Al282759	Hs.242463	keratin 8	11.4
	457644	AA770080	Hs.144962	ESTs, Moderalely similar to 159365 ubiquitin	11.4
	422848	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Thomsen	11.4
	424134	AF070637	Hs.140950	hypothetical protein	11.4

	451931	AK000208	Un 27267	Homo sapiens cDNA FLJ20201 fis, clone COLF121	11.4
	400438	AF185611	Hs.27267 Hs.115352	growth hormone 1	11.4
	412994	D32257	Hs.75113	general transcription factor IIIA	11.4
_	408124	U89337	Hs.42853	cAMP responsive element binding protein-like	11.4
5	452249	BE394412	Hs.61252	ESTs	11.4
	424627	AA344555		gb:EST50715 Gall bladder I Homo sapiens cDNA	11.4
	405626			0	11.4
	436690	AA373970	Hs.183096	ESTs.	11.4 11.4
10	415862	R51034 N80129	Hs.144513 Hs.94360	ESTs metallothionein 1L	11.4
10	406755 433657	AI244368	Hs.8124	PH domain containing protein in retina 1	11.4
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	11.4
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	11.4
	433053	BE301909	Hs.279952	glutathione S-transferase subunit 13 homolog	11.4
15	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exch	11.3
	442353	BE379594	Hs.49136	ESTs	11.3
	447700	AJ420183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3 11.3
	402077 409203	A A 700 472	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
20	405203	AA780473	H3.001	O	11.3
20	428248	Al126772	Hs.40479	ESTs	11.3
	425508	AA991551	Hs.97013	EST8	11.3
	428340	AF261088	Hs.154721	aconitase 1, soluble	11.3
0.5	431452	Al073641	Hs.152372	ESTs	11.3
25	446651	AA393907	Hs.97179	ESTs	11.3
	443755	C18397	Hs.9730	tachykinin 3 (neuromedin K, neurokinin beta)	11.3 11.3
	436209 401020	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p 0	11.3
	456724	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	11.2
30	407227	H94949	Hs.171955	trophinin associated protein (tastin)	11.2
-	402066		*.•	0	11.2
	442721	AI015892	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from cl	11.2
	401025			0	11.2
25	452423	AA991724	Hs.180535	Homo sapiens cDNA: FLJ22711 fis, clone HSI133	11.2
35	431685	AW296135	Hs.267659	vav 3 oncogene	11.2 11.2
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC ESTs, Weakly similar to transformation-relate	11.2
	435496 409079	AW840171 W87707	Hs.265398 Hs.82065	interleukin 6 signal transducer (gp130; oncos	11.2
	456995	T89832	Hs.170278	ESTs	11.2
40	419223	X60111	Hs.1244	CD9 antigen (p24)	11.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	11.2
	407604	AW191962	Hs.288061	actin, beta	11.2
	437929	T09353	Hs.106642	ESTs, Weakly similar to hypothetical protein	11.1
45	415789	H01581	11- 447200	gb:yj33f08.r1 Soares placenta Nb2HP Homo sapi	11.1 11.1
43	424447	AL137376 AF282693	Hs.147368 Hs.150185	Homo sapiens mRNA; cDNA DKFZp434J0226 (from c inflammation-related G protein-coupled recept	11.1
	436034 404931	AF202053	[13.130103	0	11.1
	445979	AI695047	Hs.202395	ESTs	11.1
	446733	AA863360	Hs.26040	ESTs; Highly similar to CYTOCHROME P45 IVA2	11.1
50	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
	445258	AI635931	Hs.147613	ESTs	11.1
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YKR074w [S.cerevi	11.1 11.1
	421041	N36914 AB007913	Hs.14691 Hs.158291	ESTs KIAA0444 protein	11.1
55	425537 435763	Al243929	Hs.190419	ESTs	11.1
55	444790		Hs.11955	B9 protein	11.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.1
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11.1
~ 0	405358			0	11.1
60	435814	AW615179	Hs.152870	ESTs	11.0 11.0
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549 Homo sapiens cDNA FLJ11672 fis, clone HEMBA10	11.0
	446772 456694	AW294404 AW016382	Hs.144515 Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone HEP001	11.0
	441128	AA570256	Hs.54628	ESTs	11.0
65	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
	412576	AA447718	Hs.107057	ESTs	11.0
	411122	F00809	Hs.143696	coactivator-associated arginine methyltransfe	11.0
	427225	AA432391	Hs.258903	Homo sapiens mRNA for KIAA1640 protein, parti	11.0
70	426260	NM_002541	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	11.0 11.0
70	444652 431947	BE513613 AL359613	Hs.11538 Hs.49933	actin related protein 2/3 complex, subunit 1A hypothetical protein DKFZp762D1011	11.0
	414432	BE378174	Hs.26506	Homo sapiens clone CDABP0005 mRNA sequence	11.0
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [10.9
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
75	447627	AF090922	Hs.285902	CGI-113 protein	10.9
	447656	NM_003726		src kinase-associated phosphoprotein of 55 kD	10.9 10.9
	454227	AW963897	Hs.44743	KIAA1435 protein 0	10.9
	402927 422380	AA309881	Hs.136246	ESTs	10.9
80	455986	BE177736		gb:RC1-HT0598-140300-021-g06 HT0598 Homo sapi	10.9
	410962	BE273749	Hs.752	FK506-binding protein 1A (12kD)	10.9
	450361	BE327108	Hs.202512	ESTs (Additional ANTI S	10.9
	457484	H57645	11- 4-1-5-	gb:yr21e01.r1 Soares fetal liver spleen 1NFLS	10.9
	407903	Al287341	Hs.154029	. bHLH factor Hes4	10.9

	403398 401405			0	10.9
	405570			0	10.9 10.9
	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOGLYCA	10.9
5	403649			0	10.9
	447824	BE620800	/ 6.	gb:601483379T1 NIH_MGC_69 Homo sapiens cDNA c	10.9
	450935	BE514743	Hs.25664	tumor suppressor deleted in oral cancer-relat	10.9
	439853 451852	AL119566 R51928	Hs.6721	lysophospholipase-like gb:yj71c05.r1 Soares breast 2NbHBst Homo sapi	10.9 10.9
10	431218	NM_002145	Hs.2733	homeo box B2	10.9
	457794	AA689292	Hs.246850	ESTs .	10.9
	444374	AA009841	Hs.11039	Homo sapiens cDNA FLJ12798 fis, clone NT2RP20	10.9
	456566	AW235317	Hs.259214	ESTs	10.8
15	405552 439436	BE140845	Hs.57868	0 ESTs	10.8 10.8
13	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprotein	10.8
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	10.8
	415807	H03139	Hs.24683	ESTs	10.8
20	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	10.8
20	417033 418464	H83784 R87580	Hs.40532	ESTs, Weakly similar to PEBP MOUSE PHOSPHATID gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	10.8 10.8
	404567	101300		0	10.8
	418384	AW149266	Hs.25130	ESTs	10.8
0.5	421971	U63127	Hs.110121	SEC7 homolog	10.8
25	428769	AW207175	Hs.106771	ESTs .,	10.8
	459104 410896	R19238 AW809637	Hs.282057	ESTs qb:MR4-ST0124-261099-015-b07 ST0124 Homo sapi	10.8 10.8
	416969	Al815443	Hs.283404	organic cation transporter	10.8
	408796	AA688292	Hs.118553	ESTs	10.8
30	426298	AW965058	Hs.111583	ESTs	10.8
	421595	AB014520	Hs.105958	Homo sapiens cDNA: FLJ22735 fis, clone HUV001	10.8
	408007 400167	AW135965	Hs.246783	ESTs 0	10.8 10.7
	445243	AI217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	10.7
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	10.7
	412241	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	10.7
	425827 420255	W28316 NM_007289	Hs.1298	gb:45b6 Human retina cDNA randomly primed sub membrane metallo-endopeptidase (neutral endop	10.7 10.7
	430891	U22492	Hs.248118	G protein-coupled receptor 8	10.7
40	402883	OLL 10L	1.0.2.01.0	0	10.7
	423811	AW299598	Hs.50895	homeo box C4	10.7
	447078	AW885727	Hs.301570	ESTs	10.7
	414343 446913	AL036166 AA430650	Hs.75914 Hs.16529	coated vesicle membrane protein transmembrane 4 superfamily member (tetraspan	10.7 10.7
45	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	10.7
	401220		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	0	10.7
	459259	AJ003294		gb:AJ003294 Selected chromosome 21 cDNA libra	10.7
	414171	AA360328 BE314567	Hs.865 Hs.211440	RAP1A, member of RAS oncogene family ESTs	10.7 10.7
50	448449 429670	L01087	Hs.211593	protein kinase C, theta	10.7
-	446759	R61463	Hs.16165	expressed in activated T/LAK lymphocytes	10.7
	400776			0	10.7
	428093	AW594506	Hs.104830	ESTs	10.7
55	412801 440545	AA121055 AW183201	Hs.190559	gb:zm22b01.rl Stratagene pancreas (937208) Ho ESTs	10.6 10.6
55	434540	NM_016045	Hs.5184	TH1 drosophila homolog	10.6
•	414273	BE269057		gb:601184231F1 NIH_MGC_8 Homo sapiens cDNA cl	10.6
	401817			0	10.6
60	410423	AW402432	Hs.63489 Hs.246381	protein tyrosine phosphalase, non-receptor ty CD68 antigen	10.6 10.6
O,O	430590 426680	AW383947 AA320160	Hs.171811	adenylate kinase 2	10.6
	445413	AA151342	Hs.12677	CGI-147 protein	10.6
	402947			0	10.6
65	457426	AW971119		gb:EST383206 MAGE resequences, MAGL Homo sapi	10.6
UJ	424148 404944	BE242274 *	Hs.1741	integrin, beta 7 O	10.6 10.6
	405421			Ŏ	10.6
	416772	Al733872	Hs.79769	protocadherin 1 (cadherin-like 1)	10.6
70	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.6
70	457588 406038	Al571225 Y14443	Hs.284171 Hs.88219	KIAA1535 protein zinc finger protein 200	10.6 10.6
	404790	1 17770	115.00215	0	10.6
	418922	AW956580	Hs.42699	Thrombospondin-1 (Hs.87409)	10.6
75	425940	AB023184	Hs.163990	KIAA0967 protein	10.6
75	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	10.6
	418870 417933	AF147204 X02308	Hs.89414 Hs.82962	CXCR4; chemokine CXC receptor 4 (fusin) thymidylate synthetase	10.5 10.5
	450538	AW297396	Hs.227052	ESTs	10.5
~~	427928	AA417662	Hs.119217	ESTs	10.5
80	432721	AL121478	Hs.3132	steroidogenic acute regulatory protein	10.5
	429267	AA299290	Hs.246857	ESTs, Highly similar to S71100 protein kinase	10.5 10.5
	439190 408975	AW978693 AW958693	Hs.293811 Hs.49391	ESTs hypothetical protein LOC54149	10.5
	415130	W85893	Hs.249867	. ESTs	10.5

	425738	H29630	Hs.159408	Homo saplens clone 24420 mRNA sequence	10.5
	440232	Al766925	Hs.112554	ESTs	10.5
	425065	AA371906	Hs.294151	ESTs, Moderately similar to KIAA0544 protein	10.5
5	420829	AW665612	Hs.221969	ESTs	. 10.5 10.5
,	430466 407771	AF052573 AL138272	Hs.241517 Hs.62713	polymerase (DNA directed), theta ESTs	10.5
	444611	AK002180	Hs.11449	DKFZP564O123 protein	10.5
	444665	BE613126	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
	448030	N30714	Hs.20161	HDCME31P protein	10.5
10	438982	AW979101	Hs.291980	ESTs	10.5
	446224	AW450551	Hs.13308	ESTs	10.5
	405108			0	10.5
	438233	W52448	Hs.56147	ESTs	10.5
1.5	401799			0	10.5
15	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
	414222	AL135173	Hs.878	sorbitol dehydrogenase	10.5
	421828	AW891965	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422626	AA344932	Hs.118786	metallothionein 2A	10.5
20	449261	AI637592	Hs.224958	ESTs	10.4 10.4
20	416218	R21499	Hs.23213	ESTs	10.4
	457848	W26524	Hs.125682	ESTs; Wealdy similar to D2092.2 [C.elegans] ESTs	10.4
	442577 406505	AA292998	Hs.163900 Hs.115418	cadherin 16, KSP-cadherin	10.4
	412258	AF016272 AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fis, clone HSI056	10.4
25	429224	Al905780	Hs.198272	NADH dehygrogenase (ubiquinone) 1 beta subcom	10.4
	447774	BE018118	Hs.19554	chromosome 1 open reading frame 2	10.4
	403914	02010110		0	10.4
	406329			Ö	10.4
	402423			Ō	10.4
30	431986	AA536130	Hs.149018	ESTs	10.4
	423145	BE264548	Hs.222190	ESTs, Weakly similar to secretory carrier mem	10.4
	414402	BE294186		gb:601172959F1 NIH_MGC_17 Homo sapiens cDNA c	10.4
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	10.4
2.5	426095	Al278023	Hs.89986	ESTs	10.4
35	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone HRC109	10.4
	442415	A1005101	Hs.129550	ESTs	10.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	10.3
	435084	D17516	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3 10.3
40	431724 456798	AA514535 AJ006422	Hs.283704 Hs.135183	ESTs centaurin-alpha	10.3
-10	417370	T28651	Hs.82030	tryptophanyi-tRNA synthetase	10.3
	422596	AF063611	Hs.118633	2'-5'oligoadenylate synthetase-like	10.3
	435226	AI248938	Hs.270106	ESTs	10.3
	433192	AB040880	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
45	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	10.3
	416228	AW505190	Hs.79089	sema domain, immunoglobulin domain (lg), tran	10.3
	453403	BE466639	Hs.61779	Homo saplens cDNA FLJ13591 fis, clone PLACE10	10.3
	447906	AL050062	Hs.19999	DKFZP566K023 protein	10.3
50	401782	NM_012434	Hs.117865	solute carrier family 17 (anion/sugar transpo	10.3 10.3
50	453927 450737	AA082465 AW007152	Hs.301751 Hs.203330	ESTs, Weakly similar to Iprediction ESTs	10.3
	421633	AF121860	Hs.106260	sorting nexin 10	10.3
	409881	AF139799	Hs.202830	ESTs	10.3
	432883	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
55	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.3
	419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl polype	10.3
	401835			0	10.3
	408896	AI610447	Hs.48778	niban protein	10.3
60	443120	AW402677	Hs.290801	ESTs	10.3
60	400208	4.4.000000	11-00404	0	10.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
	400166	14/25720	Hs.135287	0 ESTs	10.2 10.2
	434642 424837	W25739 BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
65	435075	R51094	Hs.12400	ESTs	10.2
05	425912	AL137629	Hs.162189	serine/threonine kinase with Obl- and pleckst	10.2
	435080	A1831760	Hs.155111	ESTs	10.2
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin-like	10.2
	410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver, eosin	10.2
70	411410	R20693	Hs.69954	laminin, gamma 3	10.2
	450294	H42587	Hs.238730	ESTs	10.2
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, done PLACE10	10.2
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
75	400812	DE244000	11- 450000	D	10.2
75	425843	BE313280	Hs.159627	death associated protein 3	10.2
	449392	Z41698	Hs.26039	Homo sapiens cDNA FLJ13937 fis, clone Y79AA10 KIAA0203 gene product	10.2 10.2
	409089 401383	NM_014781	Hs.50421	0	10.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosoph	10.2
80	442912	A1088060	Hs.131450	ESTs	10.2
	400954	D25969	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone LNG082	10.2
	401029	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related on	10.2
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	10.2
	421905	AI660247	Hs.32699	. ESTs, Weakly similar to LIV-1 protein [H.sapi	10.2

	405094			0	10.2
	450832 440076	AW970602 R32052	Hs.105421	ESTs Markly similar to AE1E1940 1 CC1 93 pm	10.2 10.2
	447563	BE536115	Hs.178617 Hs.160983	ESTs, Weakly similar to AF151840 1 CGI-82 pro ESTs	10.2
5	421238	AB033101	Hs.102796	KIAA1275 protein	10.2
	400882			0	10.2
	415738 445464	BE539367 AW172389	Hs.295953 Hs.249999	ESTs, Weakly similar to AF220049 1 uncharacte ESTs	10.1 10.1
	459042	AW272058	Hs.210338	ESTs	10.1
10	414469	R51952	Hs.32587	steriod receptor RNA activator 1 (complexes w	10.1
	434732	AI078443	11- 47/404	gb:oz05g05.x1 Soares_fetal_liver_spleen_1NFLS	10.1
	441030 446855	AW204139 BE616767	Hs.174424 Hs.16269	ESTs, Weakly similar to p140mDia [M.musculus] B-cell CLL/lymphoma 7B	10.1 10.1
	456785	AF151074	Hs.132744	hypothetical protein	10.1
15	404182			0	10.1
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
	430355 442152	NM_006219 R39246	Hs.239818 Hs.239666	phosphoinositide-3-kinase, catalytic, beta po Homo saplens cDNA FLJ13495 fls, clone PLACE10	10.1 10.1
	436354	AI879252	Hs.5151	Homo sapiens mRNA; cDNA DKFZp564C2163 (from c	10.1
20	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	10.1
	450599	AA460865	Hs.48516	ESTS	10.1
	454393 403383	BE153288		gb:PM0-HT0335-180400-008-c08 HT0335 Homo sapi n	10.1 10.1
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	10.1
25	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.1
	412116	AW402166 J00287	Hs.784	Epstein-Barr virus induced gene 2 (lymphocyte	10.1 10.0
	413808 458572	Al223423	Hs.182183 Hs.292794	caldesmon 1 ESTs	10.0
	403295		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	0	10.0
30	403910			0	10.0
	453400	A1991901	Hs.82590	ESTs, Moderately similar to ALU7_HUMAN ALU SU	10.0 10.0
	406502 404743			0	10.0
2.5	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cDNA cl	10.0
35	402679	DE440000		0	10.0
	455864 425734	BE148970 AF056209	Hs.159396	gb:CM0-HT0245-031199-085-h05 HT0245 Homo sapi peptidylglycine alpha-amidating monooxygenase	10.0 10.0
	419280	W07506	Hs.283725	Homo saplens cDNA FLJ12627 fls, clone NT2RM40	10.0
40	443503	AV645438	Hs.282927	ESTs	10.0
40	423165	AI937547	Hs.124915	Human DNA sequence from clone 380A1 on chromo	10.0
	450206 459052	Al796450 AA298812	Hs.201600 Hs.98539	ESTs ESTs	10.0 10.0
	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5	10.0
	428438	NM_001955	Hs.2271	Endothelin 1	10.0
45	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
	426127	L36983	Hs.167013	dynamin 2	10.0
	TABLE 13				
50			et identifier num	ber	
50		per: Gene cluste : Genbank acce			
	7000001011	. Consum soci	233101111111111111111111111111111111111		•
	Pkey	CAT Number	Accession		
55	410896	1226053_1		7 AW809697 AW810554 AW809707 AW809885 AW810000 A 6 AW809774 AW810023 AW810013 AW809813 AW809660 A	W810088 AW809742 AW809816 AW809749 AW809639 AW809722
55	412153	1279701_1		6 AVV809774 AVV810023 AVV810013 AVV809813 AVV809880 A W898205 AW896020 AW896035	ALCEGODANA 1 CGEROANA 90 SANON 90 1 CARONANA 1 CGEROANA 90 1 CARONANA 90 1 C
	412241	1284681_1		3 AW948341 AW902855 AW984737	
	412517	130281_1		AA112511	
60	412801 413349	132825_1 1363558_1		; AA330917 ? BE087077 BE087072	•
O	414273	1431911_1		BE513434 BE396654	
	414402	1443240_1	BE294186	BE298975	
	414950	1509777_1		81769 D61133 12850 R65905 H13053	
65	415789 416368	1555357_1 1591066_1		12650 R65505 H15053 84573 H50890	
••	418464	17590382	R87580		
	418783	1789791_1		41369 T41294	
	424627 425827	241724_1 256834_1		5 AA344312 AW963070 V26507 AA364334	
70	434371	384839_1	AA631362	2 AA631438	
	434414	38585_1	AI798376	S46400 AW811617 AW811616 W00557 BE142245 AW85823	32 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
					3345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 7168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
					188 AX 1977 18 AX 1977 19 AX 10047 2 AX 100774 AX 150756 AX 157705 12836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
75			Al829309	AW991957 N66951 AA527374 H66215 AA045564 A1694265	H60808 AA149726 AW195620 BE081333 BE073424 AW817662
				5 AW817703 AW817659 BE081531 H59570	
			A1079443	AA648102 Al765577 AW974381	
	434732	392447_1			
	439092	468554_1	AA830149	AW978407 M85983 AW503637	
80			AA830149	3 AW978407 M85983 AW503637 7 W81444 W81445	
80	439092 439636 447824 450484	468554_1 47467_1 738611 83645_1	AAB30149 AF086467 BE620800 BE220679	0 AW978407 M85983 AW503637 7 W81444 W81445 05 AA345621 AA009992	
80	439092 439636 447824 450484 451260	468554_1 47467_1 738611 83645_1 863912_1	AA830149 AF086467 BE620800 BE220679 AW75077	0 AW978407 M85983 AW503637 7 W81444 W81445 05 AA345621 AA009992 3 A1768154	
80	439092 439636 447824 450484	468554_1 47467_1 738611 83645_1	AAB30149 AF086467 BE620800 BE220679 AW75077 R51928 A	0 AW978407 M85983 AW503637 7 W81444 W81445 05 AA345621 AA009992	

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AW175997 AW176000 AW175999 AW175994 AW176004 AW175989 BE153288 BE153151 BE152925 AA078302
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1253524_1
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                                             BE148970 BE148975 BE148937
BE177736 BE177735 BE177734
AW748920 AA487506 AA248914 AA780494
AW971119 AA574265 AA513268
            455864
                         1377038_1
  5
            455986
                         1397521_1
            456423
                         187241_1
                         336189_1
            457426
                                             H57645 T19302 AA527038 Z24851 H93171
AW974668 AA661959 AA649572 AA640401 AA640402
AJ003294 AJ003315 AJ003293
            457484
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                        389383_1
            457705
10
                        966269 1
            459259
            TABLE 13C:
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
15
            Strand: Indicates DNA strand from which exons were predicted
            Nt_position: Indicates nucleotide positions of predicted exons
                                                         Nt position
                                          Strand
           Pkey
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                           8118496
                                          Plus
           400776
400812
                          8131651
                                          Plus
                           8568711
                                          Plus
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            400881
                           2842777
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            403022
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                                          Plus
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                                                          101320-101501
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	404678	9797204	Plus	115196-115448
	404743	8894169	Minus	120556-120999
	404780	9887810	Minus	175708-175871
_	404790	7230958	Plus	38611-38761
5	404931	7342203	Plus	44226-44382
	404944	6899705	Plus	4256-4581
	405024	7107727	Plus	88500-88697
	405089	8072523	Plus	103182-103973
	405094	8072579	Plus	135587-135758
10	405108	7107890	Minus	135020-135472
	405145	9438278	Plus	37883-38052,38138-38332
	405192	7230070	Plus	115629-116071
	405224	6731245	Minus	14413-15979
	405295	3818412	Plus	56933-57099
15	405353	2811095	Plus	118525-118892
	405358	2341017	Minus	18016-18315
	405421	7243869	Minus	97411-97687
	405426	7243900	Minus	37640-37817
	405452	7656638	Minus	93876-94275
20	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405552	1552506	Plus	45199-45647
	405570	2808656	Plus	98208-98331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
0.5	405699	4165331	Plus	100727-100859
25	405762	5931935	Plus	160502-161110
	405802	5924004	Minus	27743-28264
	405804	7274891	Minus	122557-123551
	406329	6982072	Minus	-607903-608271
20	406429	9256476	Minus	83206-83365,94051-94193
30	406502	7711350	Minus	63430-63602

Table 14A lists about 695 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. 35

TABLE 14A: ABOUT 695 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

40 Pkey: Primekey Ex. Accn: Exemplar Accession UG ID: UniGene ID

Title: UniGene title

ratio: ratio of tumor vs. normal tissues 45

43		•			
	Pkey	Ex. Accn	UGID	Title	ratio
•	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	70.4
	438817	Al023799	Hs.163242	ESTs	62.8
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	57.8
50	421478	A1683243	Hs.97258	ESTs	45.7
	415989	A1267700	Hs.111128	ESTs .	42.7
	418179	X51630	Hs.1145	Wilms tumor 1	36.0
	449034	A1624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo saplens cDNA clone	34.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
55	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix protei	29.4
	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid metaphyseal chon	27.0
	435094	Al560129	Hs.277523	EST	26.2
	430691	C14187	Hs.103538	ESTs	26.2
60	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clone EU	26.1
	415511	A1732617	Hs.182362	ESTs	24.8
	448243	AW369771	Hs.77496	ESTs	24.7
	428187	AI687303	Hs.285529	ESTs	23.9
	408081	AW451597	Hs.167409	ESTs	21.9
65	418007	M13509	Hs.83169	Matrix metalloprotease 1 (interstitial collagenase	20.6
	400292	AA250737	Hs.72472	BMPR-lb; bone morphogenetic protein receptor, typ	20.6
	422956	BE545072	Hs.122579	ESTs	20.0
	413335	Al613318	Hs.48442	ESTs	19.9
	423739	AA398155	Hs.97600	ESTs	18.9
70	410929	H47233	Hs.30643	ESTs	18.5
	424086	Al351010	Hs.102267	lysyl oxidase	17.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
	427356	AW023482	Hs.97849	ESTs `	17.4
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB Homo sapien	17.1
75	407638	AJ404672	Hs.288693	EST	17.1
	427469	AA403084	Hs.269347	ESTs	17.0
	438993	AA828995		integrin; beta 8	16.7
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.5
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	16.5
80	421155	H87879	Hs.102267	lysyl oxidase	16.1
	426635	BE395109	Hs.129327	ÉSTs	15.9
	431989	AW972870	Hs.291069	ESTs	15.9
	422805	AA436989	Hs.121017	H2A histone family; member A	15.9
	444783	AK001468	Hs.62180	ESTs	15.8
			-		

	424581	M62062	Un 150017	extensis (and basis associated amounts) sinks 2	45.7
	453197	Al916269	Hs.150917 Hs.109057	catenin (cadherin-associated protein), alpha 2 ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMIL	15.7 15.7
	459325	AW088369	Hs.282184	ESTs	15.6
_	428976	AL037824	Hs.194695	ras homolog gene family, member I	15.1
5	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-li	15.0
	408660	AA525775	Hs.292523	ESTs	15.0
	410247	AF181721	Hs.61345	RU2S	15.0
	418738	AW388633	Hs.6682	solute carrier family 7, member 11	15.0
10	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDNA, mR	14.8
10	413623	AA825721	Hs.246973	ESTs	14.8
	439706	AW872527	Hs.59761	ESTs	14.7 14.6
	409041 451110	AB033025 AI955040	Hs.50081 Hs.301584	KIAA1199 protein ESTs	14.5
	436775	AA731111	Hs.291891	ESTs	14.3
15	443211	AI128388	Hs.143655	ESTs	14.3
	445258	AI635931	Hs.147613	ESTs	14.2
	447350	Al375572	Hs.172634	ESTs; HER4 (c-erb-B4)	14.2
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
00	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.9
20	447033	Al357412	Hs.157601	EST - not in UniGene	13.7
	423811	AW299598	Hs.50895	homeo box C4	13.7
	452461	N78223	Hs.108106	transcription factor	13.7
	451106	BE382701	Hs.25960	N-myc	13.6
25	416208	AW291168	Hs.41295	ESTs .	13.5 13.4
23	452249 452055	BE394412 Al377431	Hs.61252 Hs.293772	ESTs	13.2
	439243	AA593254	Hs.191349	ESTs	13.1
	420149	AA255920	Hs.88095	ESTs	12.9
	429125	AA446854	Hs.271004	ESTs	12.9
30	413597	AW302885	Hs.117183	ESTs	12.8
	416566	NM_003914	Hs.79378	cyclin A1	12.8
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo saplens cDNA clon	12.7
	407710	AW022727	Hs.23616	ESTs	12.6
25	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
35	428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (7B2 p	12.4
	431725	X65724 .	Hs.2839	Norrie disease (pseudoglioma)	12.3
	447700	A1420183	Hs.171077	ESTs, Weakly similar to similar to serine/threonin ESTs, Highly similar to t(3;5)(q25.1;p34) fusion g	12.2 12.2
	458027 408460	L49054 AA054726	Hs.85195 Hs.285574	ESTs	12.2
40	424735	U31875	Hs.152677	short-chain alcohol dehydrogenase family member	12.0
	415263	AA948033	Hs.130853	ESTs	11.9
	400298	AA032279	Hs.61635	STEAP1	11.8
	452096	BE394901	Hs.226785	ESTs	11.7
	421451	AA291377	Hs.50831	ESTs	11.6
45	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-related pro	11.6
	443715	Al583187	Hs.9700	cyclin E1	11.5
	402606	#(NOCAT)			11.5
	436954	AA740151	Hs.130425	ESTs	11.5
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity gluta	11.5
50	410102	AW248508	Hs.279727 Hs.31141	ESTs;	11.4 11.4
	408562 452030	A1436323 Al.137578	Hs.27607	Homo sapiens mRNA for KIAA1568 protein, partial cd Homo sapiens mRNA; cDNA DKFZp564N2464 (from clon	11.4
	442353	BE379594	Hs.49136	ESTs	11.3
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
55	453160	AI263307	Hs.146228	ESTs	11.2
	426427	M86699	Hs.169840	TTK protein kinase	11.1
	449433	A1672096	Hs.9012	ESTS	11.1
	412723	AA648459	Hs.179912	ESTs	11.1
60	400250			0	11.1
60	419752	AA249573	Hs.152618	ESTs	11.1
	438167	R28363	Hs.24286	ESTs	11.1
	434539 429918	AW748078 AW873986	Hs.214410 Hs.119383	ESTs ESTs	10.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (me)	10.8
65	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	10.8
•••	420900	AL045633 .	Hs.44269	ESTs	10.8
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE2000132	10.8
	446142	Al754693	Hs.145968	ESTs	10.7
70	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
70	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	10.5
	433447	U29195	Hs.3281	neuronal pentraxin II	10.4
	424188	AW954552	Hs.142634	zinc finger protein	10.4
75	414245	BE148072	Hs.75850	WAS protein family, member 1	10.3 10.3
13	426462 418601	U59111 AA279490	Hs.169993 Hs.86368	dermatan sulphate proteoglycan 3 calmegin	10.3
	444170	AW613879	Hs.102408	ESTs	10.3
	453618	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypeptide	10.3
	407378	AA299264		gb:EST11752 Uterus Homo sapiens cDNA 5' end simila	10.2
80	440901	AA909358	Hs.128612	ESTs	10.2
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	10.2
	415227	AW821113	Hs.72402	ESTs	10.2
	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis, clone OVARC1002165	10.1
	450480	X82125	Hs.25040	. zinc finger protein 239	10.1

	419088	A1538323	Hs.77496	ESTs	10.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast hom	9.9
	428253	AL133640 M22440	Hs.183357	Homo sapiens mRNA; cDNA DKFZp586C1021 (from clone	9.8 9.8
. 5	426471 407881	AW072003	Hs.170009 Hs.40968	transforming growth factor, alpha heparan sulfate (glucosamine) 3-0-sulfotransferase	9.7
. 5	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolo	9.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H1663 (from clon	9.6
10	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkinesin6)	9.6
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphorylation regu	9.6
	438209	AL120659	Hs.6111	KIAA0307 gene product	9.5
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
15	424945	Al221919	Hs.173438	hypothetical protein FLJ10582	9.5 9.4
13	414972	BE263782	Hs.77695	KIAA0008 gene product	9.4 9.4
	439262 403381	AA832333 #(NOCAT)	Hs.124399	ESTs 0	9.3
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.3
	435509	AI458679	Hs.181915	ESTs	9.3
20	445413	AA151342	Hs.12677	CGI-147 protein	9.2
	414083	AL121282	Hs.257786	ESTs	9.2
	421373	AA808229	Hs.167771	ESTs	9.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	9.1
25	446999	AA151520	Hs.279525	hypothetical protein PRO2605	9.1
25	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Homo sa	9.1
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	9.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprolein 9 cell division cycle 2. G1 to S and G2 to M	9.0 9.0
	428479 408908	Y00272 BE296227	Hs.184572 Hs.48915	serine/threonine kinase 15	9.0
30	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP3000685	9.0
50	433764	AW753676	Hs.39982	ESTs	9.0
	434636	AA083764	Hs.241334	ESTs	8.9
	451807	W52854	Hs.27099	DKFZP564J0863 protein	8.8
	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.8
35	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	8.8
	420092	AA814043	Hs.88045	ESTs	8.8
	420159	AI572490	Hs.99785	ESTs	8.8
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.8
40	451254	AI571016	Hs.172967	ESTs	8.8 8.7
40	432677 450434	NM_004482 AA166950	Hs.278611 Hs.18645	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a ESTs, Weakly similar to partial CDS [C.elegans]	8.7
	400301	X03635	Hs.1657	Estrogen receptor 1	8.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-0-sulfotransferase	8.7
	434891	AA814309	Hs.123583	ESTs	8.7
45	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Sub6 Homo s	8.7
	438885	AI886558	Hs.184987	ESTs	8.7
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUBFAM	8.7
	447342	Al199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNI	8.6
50 \	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone LNG05548	8.6 8.6
50	438078 437212	AI016377 AI765021	Hs.131693 Hs.210775	ESTs ESTs	8.5
	417728	AW138437	Hs.24790	KIAA1573 protein	8.5
	438081	H49546	Hs.298964	ESTs	8.5
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
55	435663	AI023707	Hs.134273	ESTs	8.4
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, member	8.4
	425734	AF056209	Hs.159396	peplidylglycine alpha-amidating monooxygenase COOH	8.4
	450505	NM_004572	Hs.25051	plakophilin 2	8.4
60	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	8.3
UU	436396	AI683487	Hs.299112 Hs.159238	Homo sapiens cDNA FLJ11441 fis, clone HEMBA1001323	8.3 8.3
	425695	NM_005401 AA808189	Hs.159238 Hs.272151	protein tyrosine phosphatase, non-receptor type 14 ESTs	8.2
	438180 447268	A1370413	Hs.36563	Homo sapiens cDNA: FLJ22418 fis, clone HRC08590	8.2
	433159	AB035898	Hs.150587	kinesin-like protein 2	8.1
65	400195	7.000000	1.0.100001	0	8.1
	424906	Al566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3' untransla	8.1
	438202	AW169287	Hs.22588	ESTs	8.1
	438915	AA280174	Hs.23282	ESTs	8.1
~^	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
70	453884	AA355925	Hs.36232	KIAA0186 gene product	8.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone receptor; t	8.0
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clone EU	8.0 8.0
	453102 424001	NM_007197 W67883	Hs.31664 Hs.137476	frizzied (Drosophila) homolog 10 KIAA1051 protein	8.0
75	434415	BE177494	(13.13/4/0	gb;RC6-HT0596-270300-011-C05 HT0596 Homo sapiens c	8.0
. 5	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase, phosp	7.9
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapiens c	7.9
	415245	N59650	Hs.27252	ESTs	7.9
	422352		Hs.99200	ESTs	7.9
80	425492		Hs.158174	zinc finger protein 184 (Kruppel-like)	7.8
	442655	AW027457	Hs.30323	ESTs	7.8
	445657	AW612141	Hs.279575	ESTs	7.8
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	7.8
				107	

	414142	AW368397	Hs.150042	ESTs	7.7
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	7.6
_	436476	AA326108	Hs.53631	ESTs	7.6
5	414132	A1801235	Hs.48480	ESTs	7.6
	437789	AI581344	Hs.127812	ESTs, Wealdy similar to AF141326 1 RNA helicase HD	7.6
	450192	AA263143	Hs.24596	RADS1-interacting protein	7.6
	449328	AI962493	Hs.197647	ESTs	7.5
10	440238	AW451970	Hs.155644	paired box gene 2	7.5
10	403657	#(NOCAT)		0	7.5
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
	418735	N48769	Hs.44609	ESTs .	7.5
	413627	BE182082	Hs.246973	ESTs	7.4
1.5	446293	AJ420213	Hs.149722	ESTs	7.4
15	441627	AA947552	Hs.58086	ESTs	7.4
	425465	L18964	Hs.1904	protein kinase C; lota	7.3
	409242	AL080170	Hs.51692	DKFZP434C091 protein	7.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
20	440250	AA876179	Hs.134650	ESTs	7.3
20	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
	458861	A1630223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB:a	7.3
•	436032	AA150797	Hs.109276	tatexin protein	7.2
	407771	AL138272	Hs.62713	ESTs	7.2
25	435039	AW043921	Hs.130526	ESTs	7.2
25	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glycoprote	7.2
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone NT2RP3004451	7.2
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma cells	7.2
	404253	#(NOCAT)		0	7.1
20	424120	T80579	Hs.290270	ESTs	7.1
30	429126	AW172356	Hs.99083	ESTs	7.1
	413573	A1733859	Hs.149089	ESTs	7.1
	421464	AA291553	Hs.190086	ESTs	7.0
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	7.0
25	437938	A1950087		ESTs; Weakly similar to Gag-Pol polyprotein [M.mus	7.0
35	420362	U79734	Hs.97206	huntingtin interacting protein 1	7.0
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-typ	7.0
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	6.9
	410568	AW162948	Hs.64542	pre-mRNA cleavage factor Im (68kD)	6.9
40	429418	Al381028	Hs.99283	ESTs	6.9
40	409178	BE393948	Hs.50915	kallikrein 5	6.9
	446608	N75217	Hs.257846	ESTs	6.9
	425905	AB032959	Hs.161700	KIAA1133 protein	6.9
	428532	AF157326	Hs.184786	TBP-Interacting protein	6.9
15	433426	H69125	Hs.133525	ESTs	6.9
45	431322	AW970622	11. 000404	gb:EST382704 MAGE resequences, MAGK Homo sapiens	6.8
	437960	Al669586	Hs.222194	ESTS	6.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ublquitous TPR motif, Y is	6.8
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	6.8
50	448674	W31178	Hs.154140	ESTs	6.8
30	438122	A1620270	Hs.129837	ESTs	6.8
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.sapien	6.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
	407162	N63855	Hs.142634	zinc finger protein	6.7
55	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3,	6.7
55	424639	AI917494	Hs.131329	ESTS	6.7
	432415	T16971	Hs.289014	ESTs	6.7
	421470	R27496	Hs.1378	annexin A3	6.7
	445459	A1478629	Hs.158465	ESTs	6.7
60	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.6 6.6
00	432809	AA565509	Hs.131703	ESTS	
	409234	AI879419	Hs.27206	ESTs CGI-124 protein	6.6 6.6
	438394	BE379623	Hs.27693		
	452097 453745	AB002364	Hs.27916 Hs.63908	ADAM-TS3; a disintegrin-like and metalloproteas Homo sapiens HSPC316 mRNA, partial cds	6.6 6.6
65		AA952989		ESTs	6.6
UJ	414136	AA812434 AA380177	Hs.178227 Hs.125845	ribulose-5-phosphate-3-epimerase	6.6
	423248 454018	AW016892	Hs.241652	ESTs	6.6
	452281	T93500	Hs.28792	ESTs	6.5
	424620	AA101043	Hs.151254	kaliikrein 7 (chymotryptic; stratum comeum)	6.5
70	452594	AU076405	Hs.29981	solute camer family 26 (sulfate transporter), me	6.5
, 0	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit [H.sap	6.5
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	6.4
	418677	583308	Hs.87224	SRY (sex determining region Y)-box 5	6.4
	409517	X90780	Hs.54668	troponin I, cardiac	6.4
75	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein product [H	6.4
, 5	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	429163	AA884766	110121014	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone HEP05790	6.4
	419917	AA320068	Hs.93701	Homo saplens mRNA; cDNA DKFZp434E232 (from clone	6.4
80	424153	AA451737	Hs.141496	MAGE-like 2	6.4
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone LNG07061	6.4
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLI13803 fis, clone THYRO1000187	6.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H.sapi	6.4
	443539	AI076182	Hs.134074	ESTs	6.4
				100	

	443830	Al142095	Hs.143273	ESTs	6.4
	452606 418384	N45202 AW149266	Hs.90012	Homo saplens cDNA: FLJ23441 fis, clone HSI00612 ESTs	6.4 6.3
	425371	D49441	Hs.25130 Hs.155981	mesothelin	6.3
5	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), prostate	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced gene	6.3
	437117	AL049256	Hs.122593	ESTs	6.3
	449579 453370	AW207260 AI470523	Hs.134014	prostate cancer associated protein 6 ESTs, Moderately similar to translation initiation	6.3 6.3
10	426514	BE616633	Hs.182356 Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
10	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.3
	408155	AB014528	Hs.43133	KIAA0628 gene product	6.2
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone	6.2
1.5	439138	Al742605	Hs.193696	ESTs	6.2
15	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2 6.1
	436281 407385	AW411194 AA610150	Hs.120051 Hs.272072	ESTs ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	tRNA isopentenyipyrophosphate transferase	6.1
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PLACE1008369	6.1
20	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (from clone	6.1
	415139	AW975942	Hs.48524	ESTs	6.1
	417404	NM_007350	Hs.82101 Hs.133020	_pleckstrin homology-like domain, family A, member ESTs	6.1 6.1
	433527 449448	AW235613 D60730	Hs.57471	ESTs ·	6.1
25	457733	AW974812	Hs.291971	ESTs	6.1
	457979	AA776655	Hs.270942	ESTs	6.1
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1 solute carrier family 34 (sodium phosphate), membe	6.0 6.0
30	421502 412733	AF111856 AA984472	Hs.105039 Hs.74554	KIAA0080 protein	6.0
50	422095	Al868872	Hs.288966	ceruloplasmin (ferroxidase)	6.0
	449347	AV649748	Hs.295901	ESTs	6.0
	440870	Al687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO1000085	6.0
25	437478	AL390172	Hs.118811	ESTs	6.0
35	411598	BE336654	Hs.70937	H3 histone family, member K ESTs	6.0 6.0
	418134 418845	AA397769 AA852985	Hs.86617 Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
	452039	A1922988	Hs.172510	ESTs	6.0
4.0	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tum	5.9
40	412719	AW016610	Hs.129911	ESTs	5.9
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PLACE1009150	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9 5.9
	453431 408920	AF094754 AL120071	Hs.32973 Hs.48998	glycine receptor, bela fibronectin leucine rich transmembrane protein 2	5.9
45	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	5.9
	420440	NM_002407	Hs.97644	mammaglobin 2	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	5.9
	405547	#(NOCAT)	(1- 470740	O	5.9
50	427510 435793	Z47542 AB037734	Hs.179312 Hs.4993	small nuclear RNA activating complex, polypeptide ESTs	5.9 5.8
50	427975	AI536065	Hs.122460	ESTs	5.8
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.saple	5.8
	452693	T79153	Hs.48589	zinc finger protein 228	5.8
55	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
55	421246 445424	AW582962 AB028945	Hs.300961 Hs.12696	ESTs, Highly similar to AF151805 1 CGI-47 protein cortactin SH3 domain-binding protein	5.8 5.8
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, done NT2RP3003264	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha I	5.7
CO	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP2004081	5.7
60	420637	AW976153	070000	gb:EST388262 MAGE resequences, MAGN Homo sapiens	5.7
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone ADKA01954	5.7 5.7
	446868 452971	AV660737 A1873878	Hs.135100 Hs.91789	ESTs ESTs	5.7
	428927	AA441837	Hs.90250	ESTs	5.7
65	425282	AW163518	Hs.155485	huntingtin interacting protein 2	5.7
	419247	S65791	Hs.89764	fragile X mental relardation 1	5.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
	422938	NM_001809	Hs.1594	centromere protein A (17kD) ESTs	5.6 5.6
70	447078 421247	AW885727 BE391727	Hs.301570 Hs.102910	general transcription factor IIH, polypeptide 4 (5	5.6
, 0	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
	436556	Al364997	Hs.7572	ESTs	5.6
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
75	429826	N93266	Hs.40747	ESTs	5.6 5.6
75	432030	Al908400 NM_004272	Hs.143789 Hs.9192	ESTs Homer, neuronal immediate early gene, 1B	5.6 5.5
	443270 453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUB_HUMAN ALU SUBFAMIL	5.5
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.5
	419558	AW953679	Hs.278394	ESTs	5.5
80	427386	AW836261	Hs.177486	amyloid beta (A4) precursor protein (protease nexi	5.5
	427961	AW293165	Hs.143134	ESTs	5.5
	404561 429682	#(NOCAT) NM_006306	Hs.211602	0 SMC1 (structural maintenance of chromosomes 1, yea	5.5 5.5
	407216	N91773	Hs.102267	lysyl oxidase	5.5
				• • • •	

	410658	AW105231	Hs.192035	ESTs	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.5
	414315	Z24878		gb:HSB65D052 STRATAGENE Human skeletal muscle cD	5.5
5	427878	C05766	Hs.181022	CGI-07 protein	5.5
3	431041	AA490967	Hs.105276	ESTs	5.5
	441645	Al222279	Hs.201555	ESTs	5.5
	428071	AF212848	Hs.182339	transcription factor ESE-38	5.4
	436406	AW105723	Hs.125346	ESTs	5.4
10	429181	AW979104	Hs.294009	ESTS	5.4
10	410909	AW898161	Hs.53112	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAMIL	5.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP2000814	5.4 5.4
	451996	AW514021	Hs.245510	ESTs	5.4 5.4
	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanogaster] ESTs	5.4
15	441433	AA933809	Hs.42746	ESTs	5.4
13	445495	BE622641	Hs.38489 Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM4002571	5.4
	410153	BE311926 BE077155	Hs.177537	ESTs	5.4
	442611 452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4
	453161	AA628608	Hs.61656	ESTs	5.4
20	419948	AB041035	Hs.93847	NADPH oxidase 4	5.3
20	427718	AI798680	Hs.25933	ESTs	5.3
	453867	AI929383	Hs.108196	HSPC037 protein	5.3
	422634	NM_016010	Hs.118821	CGI-62 protein	5.3
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3
25 ·	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapiens cDNA c	5.3
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.3
	451177	AI969716	Hs.13034	ESTs	5.3
	408298	Al745325	Hs.271923	ESTs; Moderately similar to IIII ALU SUBFAMILY SB2	5.3
	435867	AA954229	Hs.114052	ESTs	5.3
30	423698	AA329796	Hs.1098	DKFZp434J1813 protein	5.3
_	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone	5.3
	427660	Al741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE06654	5.3
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
35	449532	W74653	Hs.271593	ESTs	5.3
	452822	X85689	Hs.288617	Homo saplens cDNA: FLJ22621 fis, clone HSI05658	5.3
	437641	AA811452	Hs.291911	ESTs	5.2
	418379	AA218940	Hs.137516	fidgetin-like 1	5.2
40	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.2
40	433589	AA886530	Hs.188912	ESTs	5.2
	409143	AW025980	Hs.138965	ESTs .	5.2
	410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 ffs, clone NT2RP2004321	5.2
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	5.2 5.2
45	424698	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
43	431229	AA496479	Hs.43845	gb:zv37h05.r1 Soares ovary tumor NbHOT Homo saplen	5.2
	433377 445236	Al752713 AK001676	Hs.12457	ESTs hypothetical protein FLJ10814	5.2
	406367	#(NOCAT)	110.12407	0	5.2
	442500	AI819068	Hs.209122	ESTs	5.2
50	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	5.2
-	419140	Al982647	Hs.215725	ESTs	5.2
	411078	Al222020	Hs.182364	ESTs, Weakly similar to 25 kDa trypsin inhibitor [5.2
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	427061	AB032971	Hs.173392	KIAA1145 protein	5.2
55	439042	AW979172		gb:EST391282 MAGE resequences, MAGP Homo saplens c	5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	417791	AW965339	Hs.111471	ESTs	5.1
	433277	W27266	Hs.151010	ESTs	5.1
	447835	AW591623	Hs.164129	ESTs	5.1
60	434401	A1864131	Hs.71119	Putative prostate cancer turnor suppressor	5.1
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone D	5.1
	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [Celegans]	5.1
	428093	AW594506	Hs.104830	ESTs	5.1
65	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8; fetal brain (5.1
65	453096	AW294631	Hs.11325	ESTs	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.1 5.1
	436787	AA908554	Hs.192756	ESTS	5.1
	446577	AB040933 AW511443	Hs.15420	KIAA1500 protein ESTs	5.0
70	437267 419423	D26488	Hs.258110 Hs.90315	KIAA0007 protein	5.0
70	404939	020400	115.50515	0	5.0
	439052	AF085917	Hs.37921	ESTs	5.0
	447020	T27308	Hs.16986	hypothelical protein FLJ11046	5.0
•	453878	AW964440	Hs.19025	ESTs	5.0
75	410824	AW994813	Hs.33264	ESTS	5.0
	427701	AA411101	Hs.221750	ESTs	5.0
	424602	AK002055	Hs.301129	Homo sapiens clone 23859 mRNA sequence	5.0
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
	417423	AA197341	Hs.111164	ESTs	5.0
80	421477	A1904743	Hs.104650	hypothetical protein FLJ10292	5.0
	433384		Hs.124244	ESTs	5.0
	434160	BE551196	Hs.114275	ESTs	5.0
	443555		Hs.21398	ESTs, Moderately similar to GNPI_HUMAN GLUCOSAM	5.0
	416198		Hs.99598	ESTs	4.9

	424539	L02911	Hs.150402	activin A receptor, type I	4.9
	436645	AW023424	Hs.156520	ESTs	4.9 4.9
	417251 447207	AW015242 AA442233	Hs.99488 Hs.17731	ESTs; Weakly similar to ORF YKR074w [S.cerevisiae] hypothetical protein FLJ12892	4.9
5	416565	AW000960	Hs.44970	ESTs	4.9
•	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
	435420	AI928513	Hs.59203	ESTs	4.9
	435532	AW291488	Hs.117305	ESTs	4.9
• •	443268	A1800271	Hs.129445	hypothetical protein FLJ12496	4.9
10	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 ffs, clone HEP03830	4.9
	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; fou	4.9 4.9
	408938	AA059013	Hs.22607	ESTs	4.9 4.9
15	432842 436754	AW674093 Al061288	Hs.279525 Hs.133437	hypothetical protein PRO2605 ESTs, Moderately similar to gonadotropin inducible	4.9
13	442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic, U215	4.9
	409049	Al423132	Hs.146343	ESTs	4.9
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	4.9
	447112	H17800	Hs.7154	ESTs	4.9
20	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [H.sap	4.8
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase,	4.8
	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR AT	4.8
	429414	AJ783656	Hs.202095	empty spiracles (Drosophila) homolog 2	4.8 4.8
25	418882 422505	NM_004996 AL120862	Hs.89433 Hs.124165	ATP-binding cassette, sub-family C (CFTR/MRP), mem ESTs; (HSA)PAP protein (programmed cell death 9;	4.8
23	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.8
	428555	NM_002214	Hs.184908	Integrin, beta 8	4.8
	452909	NM_015368	Hs.30985	pannexin 1	4.8
	449535	W15267	Hs.23672	low density lipoprotein receptor-related protein 6	4.8
30	452232	AW020603	Hs.271698	ESTs	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
	415115	AA214228	Hs.127751	hypothetical protein	4.7
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from clon	4.7
35	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200	4.7
33	423575 415211	C18863 R64730.comp	Hs.163443 Hs.155986	ESTs ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7 4.7
	418804	AA809632	115. [33300	gb:nz17h04.s1 NCI_CGAP_GCB1 Homo saplens cDNA clo	4.7
	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha polypeptide	4.7
	432865	Al753709	Hs.152484	ESTs	4.7
40	433330	AW207084	Hs.132816	ESTs	4.7
	453047	AW023798	Hs.286025	ESTs	4.7
	421308	AA687322	Hs.192843	ESTs	4.7
	456273	AF154846	Hs.1148	zinc finger protein	4.7
45	443933	Al091631	Hs.135501	Homo sapiens two pore polassium channel KT3.3	4.7
43	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
	440351 426300	AF030933	Hs.7179 Hs.169228	RAD1 (S. pombe) homolog delta-like homolog (Drosophila)	4.7 4.7
	453775	U15979 NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	4.7
	446102	AW168067	Hs.252956	ESTs	4.7
50	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA helicase	4.7
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	4.7
	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.7
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HEMBA1004610	4.7
55	434988	AI418055	Hs.161160	ESTs	4.6
22	452571	W31518	Hs,34665	ESTs	4.6 4.6
	434361	AF129755	Hs.117772	ESTs 0	4.6
	406400 410227	#(NOCAT) AB009284	Hs.61152	exostoses (multiple)-like 2	4.6
	419945	AW290975	Hs.118923	ESTs	4.6
60	428301	AW628666	Hs.98440	ESTs	4.6
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
	431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFA	4.6
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT2RP2003137	4.6
CF	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
65	448027	AI458437	Hs.177224	ESTS	4.6
	449611	AI970394	Hs.197075	ESTS	4.6
	459574 409928	Al741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT2RP4000035 hypothetical protein dJ473B4	4.6 4.6
	409387	AL137163 AW384900	Hs.57549 Hs.123526	ESTs .	4.6
70	424078	AB006625	Hs.139033	paternally expressed gene 3	4.6
. •	435244	N77221	Hs.187824	ESTs	4.6
	404996	#(NOCAT)		0	4.6
	407905	AW103655	Hs.252905	ESTs	4.6
75	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo sapiens c	4.6
75	424341	AA385074		gb:EST98673 Thyroid Homo sapiens cDNA 5' end simil	4.6
	441675	Al914329	Hs.5461	ESTs	4.6
	452172	H00797	Hs.133207	Homo sapiens mRNA for KIAA1230 protein, partial cd	4.6 4.5
	420276 402820	AA290938 #(NOCAT)	Hs.190561	ESTs, Highly similar to mosaic protein LR11 [H.sap 0	4.5 4.5
80	402820	#(NOCA1) AA248998	Hs.31246	ESTs	4.5
	422529	AW015128	Hs.256703	ESTs	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.5
	441826	AW503603	Hs.129915	phosphotriesterase related	4.5
	453931	AL121278	Hs.25144	ESTs	4.5
				001	

	435538	AB011540	Hs.4930	low density lipoprolein receptor-related protein 4	4.5
	457465	AW301344	Hs.195969	ESTs	4.5
	418848	A1820961	Hs.193465	ESTs	4.5
_	408321	AW405882	Hs.44205	cortistatin	4.5
5	447499	AW262580	Hs.147674	KIAA1621 protein	4.5
	424513	BE385864	Hs.149894	mitochondrial translational initiation factor 2	4.5 4.5
	432731 448275	R31178 BE514434	Hs.287820 Hs.20830	fibronectin 1 synaptic Ras GTPase activating protein 1 (homolog	4.5
	430371	D87466	Hs.240112	KIAA0276 protein	4.5
10	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG07690	4.5
	407289	AA135159	Hs.203349	Homo saplens cDNA FLJ12149 fis, clone MAMMA100042	4.4
	448141	Al471598	Hs.197531	ESTs	4.4
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304	4.4 4.4
15	417718 436464	T86540 Al016176	Hs.193981 Hs.269783	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.4
13	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. cerevisia	4.4
	409092	AI735283	Hs.172608	ESTs	4.4
	416241	N52639	Hs.32683	ESTs	4.4
20	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYMER	4.4
20	440234	AW117264	Hs.126252	ESTs	4.4
	448743 451389	AB032962 N73222	Hs.21896 Hs.21738	KIAA1136 protein KIAA1008 protein	4.4 4.4
	453331	AI240665	Hs.8895	ESTs	4.4
	454036	AA374756	Hs.93560	ESTs, Weakly similar to unnamed protein product [H	4.4
25	448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (met	4.4
	453279	AW893940	Hs.59698	ESTs	4.4
	409459	D86407	Hs.54481 Hs.108873	low density (ipoprotein receptor-related protein 8 ESTs	4.4 4.4
30	431708 433906	A1698136 Al167816	Hs.43355	ESTs	4.4
-	437958	BE139550	Hs.121668	ESTs	4.4
	441423	AI793299	Hs.126877	ESTs	4.4
	429876	AB028977	Hs.225974	KIAA1054 protein	4.3
25	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasmolipin [H.	4.3
35	412078	X69699	Hs.73149 Hs.111449	paired box gene 8	4.3 4.3
	422093 423123	AF151852 NM_012247	Hs.124027	CGI-94 protein SELENOPHOSPHATE SYNTHETASE; Human selenium	4.3
	448390	AL035414	Hs.21068	hypothetical protein	4.3
40	453628	AW243307	Hs.170187	ESTs	4.3
40	449722	BE280074	Hs.23960	cyclin B1	4.3
	436679	Al127483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3 4.3
	431592 432383	R69016 AK000144	Hs.293871 Hs.274449	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL Homo sapiens cDNA FLJ20137 fis, clone COL07137	4.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.3
45	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644	#(NOCAT)		0	4.3
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine heptad	4.3
	413775	AW409934	Hs.75528	nucleolar GTPase	4.3 4.3
50	424296 431118	AI631874 BE264901	Hs.169391 Hs.250502	ESTs carbonic anhydrase VIII	4.3
50	432201	AI538613	Hs.135657	TMPRSS3a mRNA for serine prolease (ECHOS1) (TADG-1	4.3
	451073	Al758905	Hs.206063	ESTs	4.3
	451592	AI805416	Hs.213897	ESTs	4.3
55	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo saplens cDNA, m	4.3
55	441020	W79283 R96696	Hs.35962	ESTs	4.2 4.2
	439024 453619	H87648	Hs.35598 Hs.33922	ESTs H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
	453459	BE047032	Hs.257789	ESTs	4.2
	408427	AW194270	Hs.177236	ESTs	4.2
60	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clo	4.2
	426460	D79721	Hs.183702	Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582	4.2
	444540	AI693927	Hs.265165	ESTS	4.2 4.2
	452943 453913	BE247449 AW004683	Hs.31082 Hs.233502	hypothetical protein FLJ10525 ESTs	4.2
65	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC05262	4.2
	428856	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fis, clone HEP06638	4.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sapiens cDNA	4.2
	441006	AW605267	Hs.7627	CGI-60 protein	4.2
70	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein produc ESTs	4.2 4.2
70	446936 406076	H10207 AL390179	Hs.47314 Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	4.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor recep	4.2
75	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	4.2
75	417048	A1088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.2
	431750	AA514986	Hs.283705	ESTs ESTe	4.2 4.2
	439314 448582	AA382413 AI538880	Hs.178144 Hs.94812	ESTs ESTs	4.2
	449554	AA682382	Hs.59982	ESTs	4.2
80	455700	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo sapiens c	4.2
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
	433929	Al375499	Hs.27379	ESTS	4.1
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1 4.1
	444381	BE387335	Hs.283713	. ESTs	4.1

	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_9w Homo sa	4.1
	415539	AI733881	Hs.72472	BMPR-lb; bane morphogenetic protein receptor; typ	4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long form	4.1
_	420736	Al263022	Hs.82204	ESTs	4.1
5	453293	AA382267	Hs.10653	ESTs	4.1
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	4.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo saplens	4.1
	429628	H09604	Hs.13268	ESTS	4.1
10	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone HSI15685	4.1
10	440452	Al925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCYPHOSIN	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal short-c	4.1
	448816	AB033052	Hs.22151	KIAA1226 protein	4.1
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.1
	443171	BE281128	Hs.9030	TONDU	4.1
15	425322	U63630	Hs.155637	protein kinase; DNA-activated; catalytic polypepti	4.1
	442717	R88362	Hs.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	4.1
	417300	Al765227	Hs.55610	solute carrier family 30 (zinc transporter), membe	4.1
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2)	4.1
20	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
	419131	AA406293	Hs.301622	ESTs	4.1
	406348	#(NOCAT)		0	4.1
	419750	AL079741	Hs.183114	Homo saplens cONA FLJ14236 fis, clone NT2RP4000515	4.1
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondria	4.1
25	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone	4.1
23	421039	NM_003478	Hs.101299	cullin 5	4.1
	426890	AA393167	Hs.41294	ESTs	4.1
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease, autosomal	4.1
	452834	A1638627	Hs.105685	ESTs	4.1
30	428771	AB028992	Hs.193143	KIAA1069 protein	4.0
50				ESTs	4:0
	437949 450568	U78519 AL050078	Hs.41654 Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448	4.0
		NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
	424081		Hs.84389	synaptosomal-associated protein, 25kD	4.0
35	418375	NM_003081		ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CL	4.0
55	447204	Al356881	Hs.157897	fibronectin leucine rich transmembrane protein 3	4.0
	407910	. AA650274	Hs.41296	heat shock factor binding protein 1	4.0
	412314	AA825247	Hs.250899	ESTs; Highly similar to protein regulating cytokin	4.0
	436291	8E568452	Hs.5101		4.0
40	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.0
40	426991	AK001536	Hs.285803	Homo saplens cDNA FLJ12852 fis, clone NT2RP2003445	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	
	410784	AW803201	11 70040	gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapiens c	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
15	413425	F20956	11 44044	gb:HSPD05390 HM3 Homo sapiens cDNA clone 032-X4-1	4.0
45	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein [H.sapien	4.0
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor,	4.0
	425024	R39235	Hs.12407	ESTs	4.0
	445941	A1267371	Hs.172636	ESTs	4.0
50	448595	AB014544	Hs.21572	KIAA0644 gene product	4.0
50	453448	AL036710	Hs.209527	ESTs	4.0
	458944	N93227	Hs.98403	ESTs	4.0
	400284		11 7070	Estrogen receptor 1	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	4.0
E E	408796	AA688292	Hs.118553	ESTs	4.0
55	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
	438913	Al380429	Hs.172445	ESTs	4.0
	402408			O D d-livetale seems burner support	4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.0
60	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MAMMA100174	4.0
60	439780	AL109688		gb:Homo sapiens mRNA full length insert cDNA clone	4.0
	418301	AW976201	Hs.187618	ESTs	4.0
	420077	AW512260	Hs.87767	ESTs	4.0
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	4.0
C E	403721		11-00/07	0	4.0
65	411945		Hs.92137	v-myc avian myelocytomatosis viral oncogene homolo	4.0
	408684		Hs.12727	hypothetical protein FLJ21610	4.0
	414869	AA157291	Hs.72163	ESTs	4.0
	·437980	R50393	Hs.278436	KIAA1474 protein	4.0
70	451050	AW937420	Hs.69662	ESTs	4.0
70					
	TABLE 1				
		inique Eos probes		ber	
		nber: Gene cluste			
7.	Accessio	on: Genbank acce	ession numbers	,	
75					
	Pkey	CAT Number	Accession		
	409073	109851_1		3 AA063018 AI444822	
	410784	1221005_1		1 BE079700 BE062940	
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	414315	143512_1		A494098 F13654 AA494040 AA143127	
	418378	174656_1	AW96208	1 AA218925 AA354237	•
	418804	179138_1		2 AI917245 AI701732 AA228406	
	419311	183793_1	AA689591	AW974261 AA236240 AI077451 AA631399 AW974262	
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195241_1
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AA385074 AA339054 AA339115 AW956359
AA418703 AA418711 BE071915 BE071920 BE071912
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AW968128 AA468102 AA468165
AA496479 T89859 AW020056 AW135251 AI221100 AA628705 AI263148 T79074
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                          313709 1
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                          330060_1
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Al950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 Al251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
AA251875 Al820501 Al820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 Al219788 AA884444 N92578
F13493 AA927794 Al560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488984 AA283144 Al890387 Al950344 AI741346
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AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456
AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
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20
             438993
                           467651_1
                                                AA828995 AA834879 AI926361
             439042
                           468079_1
                                                AW979172 AA829595 R96050
                                                AL109688 R23665 R26578
AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
             439780
                          47673_1
                          542469 1
            442438
                                                Al624049 AW117770 Al858360
             449034
                          794817_1
25
             451024
                          85565_1
                                                AA442176 AA259181
                                                Al902519 Al902518 Al902516
             452453
                          918300_1
                                                BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
                          1351264_1
             455700
                          798085_1
             458861
30
            TABLE 14C:
            Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
                     human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
            Strand: Indicates DNA strand from which exons were predicted
35
             Nt position: Indicates nucleotide positions of predicted exons
                                                            Nt_position
             401644
                            8576138
                                            Plus
                                                            82655-83959
110326-110491
             402408
                            9796239
                                            Minus
40
                                            Minus
             402606
                            9909429
                                                            81747-82094
             402820
403381
                            6456853
9438267
                                                            82274-82443
26009-26178
                                            Minus
                                            Minus
                            8843996
                                                            156223-156370
             403657
                                             Minus
             403721
                            7528046
                                             Minus
                                                            156647-157366
45
                            9367202
             404253
                                            Minus
                                                            55675-56055
                                                            69039-70100
             404561
                            9795980
                                            Minus
             404939
                            6862697
                                                            175318-175476
                                             Plus
             404996
                            6007890
                                            Plus
                                                            37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
                            1054740
9255985
                                                            124361-124520,124914-125050
71754-71944
             405547
                                            Plus
50
             406348
                                            Minus
             406367
                            9256126
                                            Minus
                                                            58313-58489
             406400
                            9256298
                                                            1553-1712,1878-2140,4252-4385,5922-6077
55
            Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected
             as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g.,
            ig, fn3, egf, 7tm domains). Predicted protein domains are noted.
             TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
60
             Pkey: Primekey
UG ID: UniGene ID
             Title: UniGene title
             Prot. Dom.: Predicted protein structural domains
             ratio: ration tumor vs normal tissues
65
             Pkey
                           Ex. Acon
                                                                                                                           Prot. Dom.
                                               Hs.111128
             415989
                           A1267700
                                                                                                                           TM
                                                                                                                                                               42.7
                           NM_005756
AW513143
                                               Hs.184942
Hs.98367
                                                                G protein-coupled receptor 64 similar to SRY-box containing gene 17
                                                                                                                                                              30.5
30.1
             428579
                                                                                                                           TM
             428153
                                                                                                                           TM
70
             436982
                           AB018305
                                               Hs.5378
                                                                spondin 1, (f-spondin) extracellular matrix
                                                                                                                           SS
                                                                                                                                                               29.4
                                                                collagen; type X; alpha 1 (Schmid metaphy
                           D31152
                                                                                                                            C1q,Collagen
                                                                                                                                                               27.0
             427585
                                               Hs.179729
                           C14187
M13509
                                               Hs.103538
Hs.83169
                                                                                                                                                               26.2
20.6
             430691
                                                                ESTs
                                                                                                                           TM
             418007
                                                                 Matrix metalloprotease 1 (interstitial collag
                                                                                                                            SS.,Peptidase_M10
                           AA250737
                                               Hs.72472
                                                                 BMPR-Ib; bone morphogenetic protein rec
                                                                                                                                                               20.6
             400292
                                                                                                                            TM
75
              424086
                           Al351010
                                                Hs.102267
                                                                 lysyl oxidase
                                                                                                                            Lysyl_oxidase
                                                                                                                                                               17.7
                           NM_002497
AW023482
                                                                 NIMA (never in mitosis gene a)-related kin
             424905
                                               Hs.153704
                                                                                                                            pkise pkinase
                                                                                                                                                               17.4
                                               Hs.97849
                                                                 ESTs
                                                                                                                            TM
                                                                                                                                                               17.4
             427356
             407638
                           AJ404672
                                               Hs.288693
              427469
                           AA403084
                                               Hs.269347
                                                                 ESTs
                                                                                                                           TM
                                                                                                                                                               17.0
80
             438993
                           AA828995
                                                                 integrin; beta 8
                                                                                                                           SS,integrin_B
                                                                                                                                                               16.7
                                                                                                                                                               16.1
                           H87879
                                               Hs.102267
                                                                 lysyl oxidase
             421155
                                                                                                                           SS
                                               Hs.291069
             431989
                           AW972870
                                                                                                                           SS
                                                Hs.194695
                                                                 ras homolog gene family, member I
                                                                                                                           ras
TM
                                                                                                                                                               15.1
              428976
                           AL037824
             416209
                           AA236776
                                               Hs.79078
                                                                 MAD2 (mitotic arrest deficient, yeast, hom
                                                                                                                                                               15.0
```

413623 AA825721 Hs.246973 ESTs 447350 AI375572 Hs.172634 ESTs; HER4 (c-erb-B4) 428227 AA321649 Hs.2248 INTERFERON-GAMMA INDUCED PRO 452461 N78223 Hs.108106 transcription factor 416208 AW291168 Hs.41295 ESTs 416208 AW291168 Hs.61252 ESTs 416566 NM_003914 Hs.61252 ESTs 416566 NM_003914 Hs.79378 cyclin A1 416661 AA634543 Hs.79440 IGF-II mRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.28557 ESTs 400298 AA032279 Hs.61635 STEAP1 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1 413472 BE242870 Hs.75379 solute carrier family 1 (gital high affinity git	TM SS,TM,Furin-like,pkinase ILB G9a,PHD Myc_N_term TM homeobox cyclin TM SS,Cys_knot TM TM histone TM	14.8 14.1 13.7 13.5 13.4 12.6 12.3 12.2 11.9 11.8 11.5 11.4 11.3 11.2 11.1
428227 AA321649 Hs.2248 INTERFERON-GAMMA INDUCED PRO 452461 N78223 Hs.108106 transcription factor 451106 BE382701 Hs.25960 N-myc 416208 AW291168 Hs.41295 ESTs 452249 BE394412 Hs.61252 ESTs 416566 NM_003914 Hs.79378 cyclin A1 416661 AA634543 Hs.79440 IGF-II mRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 458027 A94803 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 421451 AA291377 Hs.50831 ESTs 433715 A1583187 Hs.9700 cyclin E1	ILB G9a,PHD Myc_N_term TM homeobox cyclin TM SS,Cys_knot TM TM histone TM TM TM Cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	14.1 13.7 13.6 13.5 12.6 12.3 12.2 12.9 11.8 11.6 11.5 11.4 11.4 11.3 11.2 11.1
5 452461 N78223 Hs.108106 transcription factor 416208 AW291168 Hs.41295 ESTs 452249 BE394412 Hs.61252 ESTs 416566 NM_003914 Hs.79378 cyclin A1 416661 AA634543 Hs.79440 IGF-II mrRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 421451 AA291377 Hs.50831 ESTs 443715 A1583187 Hs.9700 cyclin E1	G9a,PHD Myc_N_term TM homeobox cyclin TM SS,Cys_knot TM TM histone TM TM cyclin TM,SDF SS TM	13.6 13.5 12.8 12.6 12.3 12.2 11.9 11.8 11.5 11.5 11.4 11.3 11.2 11.1
5 451106 BE382701 Hs.25960 N-myc 416208 AW291168 Hs.41295 ESTs 452249 BE394412 Hs.61252 ESTs 416566 NM_003914 Hs.79378 cyclin A1 416661 AA634543 Hs.79440 IGF-II mRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	Myc_N_term TM homeobox cyclin TM SS,Cys_knot TM TM histone TM TM cyclin TM,SDF SS TM	13.5 13.4 12.6 12.3 12.2 11.9 11.8 11.5 11.5 11.4 11.3 11.2 11.1
416208 AW291168 Hs.41295 ESTs 452249 BE394412 Hs.61252 ESTs 416566 NM_003914 Hs.79378 cyclin A1 416661 AA634543 Hs.79440 IGF-II mRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3;5)(q25.1;p34) f 48400 AA054726 Hs.285574 ESTs 408460 AA048033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	homeobox cyclin TM SS,Cys_knot TM TM histone TM TM Cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tn_1 TM	13.4 12.6 12.3 12.2 12.2 11.9 11.8 11.6 11.5 11.4 11.4 11.3 11.2 11.1
10 416566 NM_003914 Hs.79378 cyclin A1 416566 AA634543 Hs.79378 Hs.29440 IGF-II mrRNA-binding protein 3 A31725 X65724 Hs.2839 Norrie disease (pseudoglioma) ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 A1583187 Hs.9700 cyclin E1	cyclin TM SS,Cys_knot TM TM TM histone TM TM cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	128 126 123 122 11.9 11.6 11.5 11.4 11.3 11.2 11.1
10 416661 AAG34543 Hs.79440 IĞF-li mRNA-binding protein 3 431725 X65724 Hs.2839 Norrie disease (pseudoglioma) 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	TM SS,Cys_knot TM TM histone TM TM cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	12.6 12.3 12.2 11.9 11.8 11.5 11.5 11.4 11.3 11.2 11.2
10 431725 X65724 Hs.2839 Norrie disease (pseudogiloma) . 458027 L49054 Hs.85195 ESTs, Highly similar to 1(3:5)(q25.1:p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	SS,Cys_knot TM TM histone TM TM Cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	12.3 12.2 12.2 11.9 11.8 11.6 11.5 11.4 11.4 11.3 11.2 11.2
458027 L49054 Hs.85195 ESTs, Highly similar to t(3;5)(q25.1;p34) f 408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	TM TM histone TM TM Cyclin TM,SDF SS TM TM TM TM TM TM TM TM,1000 TM,1000 TM	12.2 12.2 11.9 11.8 11.5 11.5 11.4 11.4 11.3 11.2 11.1
408460 AA054726 Hs.285574 ESTs 415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 A1583187 Hs.9700 cyclin E1	TM histone TM TM cyclin TM,SDF SS TM TM TM TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	12.2 11.9 11.8 11.5 11.5 11.4 11.4 11.3 11.2 11.2
415263 AA948033 Hs.130853 ESTs 400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	histone TM TM cyclin TM,SDF SS TM TM TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.9 11.8 11.6 11.5 11.5 11.4 11.3 11.2 11.2 11.1
400298 AA032279 Hs.61635 STEAP1 15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	TM TM TM cyclin TM,SDF SS TM TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.8 11.6 11.5 11.5 11.4 11.3 11.2 11.2 11.1
15 421451 AA291377 Hs.50831 ESTs 443715 AI583187 Hs.9700 cyclin E1	TM cyclin TM,SDF SS TM TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.6 11.5 11.5 11.4 11.4 11.3 11.2 11.2 11.1
443715 AI583187 Hs.9700 cyclin E1	cyclin TM,SDF SS TM TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.5 11.5 11.4 11.4 11.3 11.2 11.2 11.1
	TM,SDF SS TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.5 11.4 11.4 11.3 11.2 11.2 11.1
413472 BE242870 Hs.75379 solute carrier family 1 (gilal high affinity gi	SS TM TM TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.4 11.3 11.2 11.2 11.1 11.1
410102 AW248508 Hs.279727 ESTs;	TM TM, TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.3 11.2 11.2 11.1 11.1
408562 Al436323 Hs.31141 Homo saplens mRNA for KIAA1568 prote	TM,neur_chan histone TM Hist_deacetyl+F105 7tm_1 TM	11.2 11.2 11.1 11.1
20 442353 BE379594 Hs.49136 ESTs	histone TM Hist_deacetyl+F105 7tm_1 TM	11.2 11.1 11.1
427344 NM_000869 Hs.2142 5-hydroxytryptamine (serotonin) receptor 3	TM Hist_deacetyl+F105 7tm_1 TM	11.1 11.1
453160 AI263307 Hs.146228 ESTs	Hist_deacetyl+F105 7tm_1 TM	11.1
412723 AA648459 Hs.179912 ESTs	7tm_1 TM	
3.5 400250 0	TM T	
25 438167 R28363 Hs.24286 ESTs		11.1 10.9
434539 AW748078 Hs.214410 ESTs		10.9
450375 AA009647 Hs.8850 a disintegrin and metalloproteinase domain 400289 X07820 Hs.2258 Matrix Metalloproteinase 10 (Stromolysin 2	SS,hemopexin	10.8
	Cadherin_C_term	10.7
446142 Al754693 Hs.145968 ESTs 30 421285 NM_000102 Hs.1363 cytochrome P450, subfamily XVII (steroid	TM,p450	10.6
433496 AF064254 Hs.49765 VERY-LONG-CHAIN ACYL-COA SYNT	SS,TM	10.6
418506 AA084248 Hs.85339 G protein-coupled receptor 39	TM	10.5
433447 U29195 Hs.3281 neuronal pentraxin II	SS	10.4
414245 RE148072 Hs.75850 WAS protein family, member 1	TM	10.3
35 426462 U59111 Hs.169993 dermalan sulphate proteoglycan 3	SS,LRRNT	10.3
418601 AA279490 Hs.86368 calmegin	SS	10.3
415227 AW821113 Hs.72402 ESTs	TM	10.2
409269 AA576953 Hs.22972 Homo sapiens cDNA FLJ13352 fis, clone O	TM	10.1
426471 M22440 Hs.170009 transforming growth factor, aipha 40 407881 AW072003 Hs.40968 heparan sulfate (glucosamine) 3-0-sulfotran	SS,EGF SS	9.8 9.7
	SS,EGF	9.7
. 445537 AJ245671 Hs.12844 EGF-like-domain; multiple 6 414972 BE263782 Hs.77695 KJAA0008 gene product	TM	9.4
435509 Al458679 Hs.181915 ESTs	TM	9.3
445413 AA151342 Hs.12677 CGI-147 protein	UPF0099	9.2
45 446999 AA151520 Hs.279525 hypothetical protein PRO2605	TM	9.1
414569 AF109298 Hs.118258 Prostate cancer associated protein 1	TM	9.1
406687 M31126 Hs.272620 pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
408908 BE296227 Hs.48915 serine/threonine kinese 15	pkise,TM	9.0
451807 W52854 Hs.27099 DKFZP564J0863 protein	TM	8.8
50 420159 AI572490 Hs.99785 ESTs	TM Sieis B Iselia	8.8 8.7
432677 NM_004482 Hs.278611 UDP-N-acetyl-alpha-D-galactosamine:poly	TM,Ricin_B_lectin TM	8.7
408829 NM_006042 Hs.48384 heparan sulfate (glucosamine) 3-O-sulfotrar 43885 Al886558 Hs.184987 ESTs	TM	8.7
430805 A000050 Hs.19322 ESTs; Weakly similar to IIII ALU SUBFAM	TM	8.6
55 437212 AI765021 Hs.210775 ESTs	UDPGT	8.5
424717 H03754 Hs.152213 wingless-type MMTV integration site fami	wnt	8.4
450505 NM_004572 Hs.25051 plakophilin 2	TM	8.4
436396 Al683487 Hs.299112 Homo sapiens cDNA FLJ11441 fis, clone H	wnt	8.3
425695 NM_005401 Hs.159238 protein tyrosine phosphatase, non-receptor	Y_phosphatase	8.3
60 447268 Al370413 Hs.36563 Homo sapiens cDNA: FLJ22418 fis, clone	Ribosomal_S8	8.2
400195 0	TM	8.1 9.1
424906 Al566086 Hs.153716 Homo sapiens mRNA for Hmob33 protein,	IM · TAI	8.1 8.1
438202 AW169287 Hs.22588 ESTs 439759 AL359055 Hs.67709 Homo sapiens mRNA full length insert cDN	· TM TM	8.0
CF 100.00	TM,Fz,Frizzled	8.0
OD 453102 NM_007197 Hs.31664 frizzled (Dresophila) homolog 10 424001 W67883 Hs.137476 KIAA1051 protein	TM	8.0
442655 AW027457 Hs.30323 ESTs	TM	7.8
445657 AW612141 Hs.279575 ESTs	7tm_1	7.8
426320 W47595 Hs.169300 transforming growth factor, beta 2	SS,TGF-beta	7.8
70 412170 D16532 Hs.73729 very low density lipoprotein receptor	TM,ldl_recept_b,EGF	7.6
436476 AA326108 Hs.53631 ESTs	TM	7.6
414132 Al801235 Hs.48480 ESTs	TM	7.6
437789 Al581344 Hs.127812 ESTs, Weakly similar to AF141326 1 RNA	TM	7.6
450192 AA263143 Hs.24596 RAD51-interacting protein	TM TM	7.6
75 408826 AF216077 Hs.48376 Homo sapiens clone HB-2 mRNA sequence		7.5 7.4
413627 BE182082 Hs.246973 ESTs	TM LIM homanhov	7.4 7.4
446293 A1420213 Hs.149722 ESTs	LIM,homeobox TM,7tm_1	7.3
409242 AL080170 Hs.51692 DKFZP434C091 protein 450262 AW409872 Hs.271166 ESTs, Moderately similar to ALU7_HUMA	TM	7.3
80 450262 AW409872 Hs.271166 ESTs, Moderately similar to ALUT_HUMA 80 451659 BE379761 Hs.14248 ESTs, Weakly similar to ALUB_HUMAN A	TM	7.3
444342 NM_014398 Hs.10887 similar to tysosome-associated membrane		7.2
429126 AW172356 Hs.99083 ESTs	7tm_1	7.1
421464 AA291553 Hs.190086 ESTs	TM	7.0
420352 U79734 Hs.97206 huntingtin interacting protein 1	TM	7.0

	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiet	TM	7.0
	415138	C18356	Hs.78045	tissue factor pathway Inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	6.9
	429418	AJ381028	Hs.99283	ESTs	AAA	6.9
-	409178	BE393948	Hs.50915	kallikrein 5	SS,trypsin	6.9
5	425905	AB032959	Hs.161700	KIAA1133 protein	IM	6.9
	428532	AF157326	Hs.184786	TBP-interacting protein	TM	6.9
	433426	H69125	Hs.133525	ESTs	TM	6.9
	448674	W31178	Hs.154140	ESTs	TM	6.8
10	432415	T16971	Hs.289014	ESTs	TM	6.7
10	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6 6.6
	438394	8E379623	Hs.27693	CGI-124 protein	pro_isomerase	6.6
	452097 453745	AB002364 AA952989	Hs.27916 Hs.63908	ADAM-TS3; a disintegrin-like and metal Homo sapiens HSPC316 mRNA, partial cd	Reprolysin TGFb_propeptide	6.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	filament	6.6
15	452281	T93500	Hs.28792	ESTs	TGF-beta	6.5
13	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum	SS,trypsin	6.5
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
	434149	Z43829	Hs.19574	ESTs. Weakly similar to katanin p80 subun	pkinase,fn3	6.5
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,7tm_2	6.4
20	409517	X90780	Hs.54668	troponin I, cardiac	Y_phosphatase	6.4
~0	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein p	TM	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS	6.4
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fis, clone	TM	6.4
	424153	AA451737	Hs.141496	MAGE-like 2	TM	6.4
25	441081	Al584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
	443539	AI076182	Hs.134074	ESTs	TM	6.4
	418384	AW149266	Hs.25130	ESTs	TM	6.3
	425371	D49441	Hs.155981	mesothelin	SS	6.3
	449048	245051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	6.3
30	437117	AL049256	Hs.122593	ESTs	TM	6.3
	453370	Al470523	Hs.182356	ESTs, Moderately similar to translation init	ABC_tran	6.3
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
	452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E	TM	6.2
25	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	TM	6.2
35	436281	AW411194	Hs.120051	ESTs	TM	6.1
	415139	AW975942	Hs.48524	ESTs	TM	6.1
	449448	D60730	Hs.57471	ESTs	TM	6.1
	457979	AA776655	Hs.270942	ESTs	TM	6.1
40	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	SS,EGF,tsp_3	6.0
40	421502	AF111855	Hs.105039	solute carrier family 34 (sodium phosphate)	TM	6.0
	412733	AA984472	Hs.74554	KIAA0080 protein	C2 SS	6.0
	422095 418845	A1868872 AA852985	Hs.288966 Hs.89232	ceruloplasmin (ferroxidase) chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0 6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain	TM,disintegrin,Reprolysin	5.9
45	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
75	453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
	417866	AW067903	Hs.82772	*collagen, type XI, alpha 1*	TSPN,Collagen,COLFI	5.9
	430291	AV660345	Hs.238126	CGI-49 protein	TM	5.9
	405547	#(NOCAT)	. 101200120	0	TM,ABC_membrane	5.9
50	435793	AB037734	Hs.4993	ESTs	TM	5.8
	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	TM	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N	TM	5.7
	452971	AI873878	Hs.91789	ESTs	TM	5.7
55	428927	AA441837	Hs.90250	ESTs ·	TM	5.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	TM	5.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sap	TM	5.7
	447078	AW885727	Hs.301570	ESTs	kazal	5.6
60	421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid	TM	5.6
OU	432030	AI908400	Hs.143789	ESTs 4B	SS	5.6
	443270	NM_004272 U80034	Hs.9192	Homer, neuronal immediate early gene, 18	TM	5.5
	411096		Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	5.5 5.5
	419558 427386	AW953679 AW836261	Hs.278394 Hs.177486	ESTs amyloid bela (A4) precursor protein (protea	SS TM	5.5
65	427961	AW293165	Hs.143134	ESTs	TM	5.5
05	407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	ras,TM	5.5
	414315	Z24878	110.10010	gb:HSB65D052 STRATAGENE Human sk	TM	5.5
	441645	Al222279	Hs.201555	ESTs	SS	5.5
70	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanoga	TM	5.4
	441433	AA933809	Hs.42746	ESTs	TM	5.4
	445495	BE622641	Hs.38489	ESTs	LLWEQ,ENTH	5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone N	Glycos_transf_2	5.4
	442611	BE077155	Hs.177537	ESTs	TM	5.4
75	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	XIink,CUB	5.4
	419948	AB041035	Hs.93847	NADPH oxidase 4	TM	5.3
	427718	AI798680	Hs.25933	ESTs	histone	5.3
	453867	AI929383	Hs.108196		TM	5.3
00	408298	AI745325	Hs.271923	ESTs; Moderately similar to IIII ALU SUB	Glycos_transf_2,DSPc	5.3
80	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P	TM	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	TM	5.3
	449532	W74653	Hs.271593	ESTs	TM	5.3
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone	TM,EGF,fn3	5.3
	418379	AA218940	Hs.137516 .	fidgetin-like 1	AAA	5.2

	416530	U62801	Hs.79361	kallikreln 6 (neurosin, zyme)	TM,trypsin	5.2
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	TM	5.2
	406367	#(NOCAT)	115.12401	nyposiciosi protesti i Ca 10014	proteasome,trypsin	5.2
5	442500	AI819068	Hs.209122	ESTs	SS	5.2
9						
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	TM	5.2
	419140	Al982647	Hs.215725	ESTs	TM	5.2
	417791	AW965339	Hs.111471	ESTs	Ald_Xan_dh_C	5.1
10	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J1	TSPN,Folate_carrier	5.1
10	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegan	TM	5.1
	428093	AW594506	Hs.104830	ESTs	TM .	5.1
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8; feta	TM	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
	404939		***************************************	0	TM	5.0
15	447020	T27308	Hs.16986	hypothetical protein FLJ11046	TM	5.0
~~	410824	AW994813	Hs.33264	ESTs	TM	5.0
	417423	AA197341	Hs.111164	ESTs	TM	5.0
		AI904743		hypothetical protein FLJ10292	TM	5.0
	421477		Hs.104650			
20.	443555	N71710	Hs.21398	ESTs, Moderately similar to GNPI_HUMA	Glucosamine_iso	5.0
20'	424539	L02911	Hs.150402	activin A receptor, type I	SS,Activin_recp,pkinase	4.9
	416565	AW000960	Hs.44970	ESTs	TM.	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ty	SS	4.9
	408938	AA059013	Hs.22607	ESTs	TM	4.9
~~	436754	Al061288	Hs.133437	ESTs, Moderately similar to gonadotropin i	TM	4.9
25	409049	A1423132	Hs.146343	ESTs	TM	4.9
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	4.8
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed ce	TM	4.8
	428555	NM_002214	Hs.184908	integrin, beta 8	SS,integrin_B	4.8
30	452909	NM_015368	Hs.30985	pannexin 1	TM	4.8
50		W15267				4.8
	449535		Hs.23672	low density lipoprotein receptor-related pro	SS,ldl_recept_a,EGF	
	452232	AW020603	Hs.271698	ESTs	TM	4.8
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N	Cadherin_C_term	4.7
25	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha polype	TM,neur_chan	4.7
35	433330	AW207084	Hs.132816	ESTs	TM	4.7
	443933	AI091631	Hs.135501	Homo saplens two pore potassium channel	TM	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM	4.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	4.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA,DEAD,helicase_C	4.7
40	429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.7
	434988	Al418055	Hs.161160	ESTs	TM	4.6
	406400	#(NOCAT)		0	trypsin,TM	4.6
•	428301	AW628666	Hs.98440	ESTs	TM	4.6
	446254	BE179829	Hs.179852	Homo saplens cDNA FLJ12832 fis, clone N	TM	4.6
45	459574	AI741122		Homo sapiens cDNA FLJ 1232 fis, clone N	TM	4.6
73			Hs.101810			
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	TM	4.6
	435244	N77221	Hs.187824	ESTs	pkinase,fn3	4.6
	404996	#(NOCAT)	II- OFOOOF	0	Peptidase_C1	4.6
50	407905	AW103655	Hs.252905	ESTs	SS,Ephrin	4.6
30	441675	AI914329	Hs.5461	ESTs	TM	4.6
	420276	AA290938	Hs.190561	ESTs, Highly similar to mosaic protein LR1	TM,fn3,ldl_recept_a	4.5
	422529	AW015128	Hs.256703	ESTs	TM	4.5
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM	4.5
	457465	AW301344	Hs.195969	ESTs	Pribosyltran	4.5
55	418848	A1820961	Hs.193465	ESTs ·	TM,pkise	4.5
	447499	AW262580	Hs.147674	KIAA1621 protein	TM ·	4.5
	432731	R31178	Hs.287820	fibronectin 1	SS	4.5
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone H	Nucleoside_tra2	4.4
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	TM	4.4
60	409092	AI735283	Hs.172608	ESTs	TM	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
	453331	A1240665	Hs.8895	ESTs	TM	4.4
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	4.4
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
65	453279	AW893940		ESTs	TM	4.4
05			Hs.59698			4.4
	409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM,EGF,Idi_recept_a	
	431708	Al698136	Hs.108873	ESTs	TM	4.4
	433906	Al167816	Hs.43355	ESTs	TM	4.4
70	441423	Al793299	Hs.126877	ESTs	TM	4.4
70	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	TM	4.3
	412078	X69699	Hs.73149	paired box gene 8	TM	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
	448390	AL035414	Hs.21068	hypothetical protein	TM	4.3
	453628	AW243307	Hs.170187	ESTs	TM	4.3
75	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM	4.3
, 0	413775	AW409934	Hs.75528	nucleolar GTPase	MMR_HSR1	4.3
		AI805416	Hs.213897	ESTs	TM	4.3
	451592 419311		na.∠1303/	gb:nv66a12.s1 NCI_CGAP_GCB1 Homo s	TM	4.3
		AA689591	Un 24000			
80	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	TM	4.2
OU	428679	AA431765	11- 054005	gb:zw80c03.s1 Soares_testis_NHT Homo s	TM	4.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prote	TM	4.2
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P	TM	4.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	TM	4.2
	406671	AA129547	Hs.285754 .	met proto-oncogene (hepatocyte growth fac	F-actin_cap_A	4.2
				·		

		.5.				
	431750	AA514986	Hs.283705	ESTs	TM	4.2
	449554	AA682382	Hs.59982	ESTs	TM	4.2
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HP	SEA	4.1
_	433929	Al375499	Hs.27379	ESTs	TM	4.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN A	TM	4.1
	444381	BE387335	Hs.283713	ESTs	TM	4.1
	415539	AI733881	Hs.72472	BMPR-lb; bone morphogenetic protein rec	TM	4.1
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, long	TM	4.1
	453293	AA382267	Hs.10653	ESTs	TM	4.1
10	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	TM	4.1
•	429628	H09604	Hs.13268	ESTs	TM	4.1
	440452	Al925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retina	TM	4.1
	425322			protein kinase; DNA-activated; catalytic po	TM	4.1
15		U63630	Hs.155637		TM	4.1
IJ	417300	AI765227	Hs.55610	solute carrier family 30 (zinc transporter), m		
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM	4.1
	452834	AI638627	Hs.105685	ESTs	kinesin	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	PI-PLC-X,PI-PLC-Y	4.0
20	412314	AAB25247	Hs.250899	heat shock factor binding protein 1	TM	4.0
20	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulating c	TM	4.0
	- 450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	ribonuc_red	4.0
0.5	417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 prolein	TM	4.0
25	445941	AI267371	Hs.172636	ESTs _,	TM,lectin_c	4.0
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	lipocatin	4.0
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	TM	4.0
	418301	AW976201	Hs.187618	ESTs	TM	4.0
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	TGF-beta,Myc_N_term	4.0
30	408684	R61377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
	414869	AA157291	Hs.72163	ESTs	TM	4.0
	420281	Al623693	Hs.191533	ESTs	Cation_efflux	3.9
	416658	·U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	EGF,TB	3.9
	411274	NM_002776	Hs.69423	kallikrein 10	trypsin,TM	3.9
35	437222	AL117588	Hs.299963	ESTs	TM	3.9
	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	TM,cadherin,	3.9
	430634	AI860651	Hs.26685	ESTs	TM	3.9
	415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fis, clone H	NAP_family	3.9
	420179	N74530	Hs.21168	ESTs	TM	3.8
40	451250	AA491275	Hs.236940	Homo sapiens cDNA FLJ12542 fis, clone N	TM	3.8
•••	429496	AA453800	Hs.192793	ESTs	TM	3.8
	421764	Al681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM	3.8
	447197	R36075	110.00012	gb:yh88b01.s1 Soares placenta Nb2HP Hom	TM,SDF	3.8
	422939	AW394055	Hs.98427	ESTs .	TM	3.8
45	414737	Al160386	Hs.125087	ESTs	TM	3.8
73	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SS, trypsin	3.8
	425247		Hs.155324			3.7
	424433	NM_005940		matrix metalloproteinase 11 (stromelysin 3) ESTs	SS,Peptidase_M10 TM	3.7
		H04607	Hs.9218			3.7
50	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	
50	407792	AJ077715	Hs.39384	putative secreted ligand homologous to fix1	SS	3.7
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkise,pkinase	3.7
	434836	AA651629	Hs.118088	ESTs	TM	3.7
	439810	AL109710	Hs.85568	EST	TM	3.7
55	418693	Al750878	Hs.87409	thrombospondin 1	SS.EGF,TSPN	3.7
22	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
	436304	AA339622	Hs.108887	ESTs	TM	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transloco	, TM	3.7
	453468	W00712	Hs.32990	DKFZP566F084 protein	TM	3.6
60	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	M 000 000	3.6
UU	411402	BE297855	Hs.69855	NRAS-related gene	CSD,ras,CSD	3.6
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
	400296	AA305627	Hs.139336	ATP-binding cassette; sub-family C (CFTR	ABC_tran	3.6
	407340	AA810168	Hs.232119	ESTs	TM	3.6
65	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
65	438279	AA805166	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM	3.6
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	AAA AAA	3.6
	441111	A1806867	Hs.126594	ESTs	· TM	3.6
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM	3.6
70	409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
70	425441	AA449644	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone N	Aa_trans	3.6
	428137	AA421792	Hs.170999	ESTs	AAA	3.6
	433692	Al805860	Hs.208675	ESTs, Weakly similar to neuronal thread pr	TM	3.6
	438689	AW129261	Hs.250565	ESTs	TM	3.6
7.	443341	AW631480	Hs.8688	ESTs	TM	3.6
75	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-synt_D.PH	3.6
	414343	AL036166	Hs.75914	coated vesicle membrane protein	TM	3.5
	414812	X72755	Hs.77367	monokine induced by gamma interferon	SS,1L8	3.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-indu	· TM	3.5
~~	415786	AW419196	Hs.257924	ESTs	TM	3.5
80	427177	AB006537	Hs.173880	interleukin 1 receptor accessory protein	TM,ig	3.5
	427687	AW003867	Hs.112403	ESTs	7tm_1	3.5
	444619	BE538082	Hs.8172	ESTs	TM ⁻	3.5
	447336	AW139383	Hs.245437	ESTs	AhpC-TSA	3.5
	412519	AA196241	Hs.73980 .	troponin T1, skeletal, slow	TM	3.5
			•	•		

	44.0700	AD02700E	11	144.44004	***	
	418792	AB037805 AA081395	Hs.88442	KIAA1384 protein	TM	3.5
	408031	L24498	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone N	TM	3.5
	416892 418793	AW382987	Hs.80409	growth arrest and DNA-damage-inducible,	TM EGF	3.5
5	448089	A1467945	Hs.88474	prostaglandin-endoperoxide synthase 1 (pro	SS	3.5 3.5
,	422278	AF072873	Hs.173696	ESTs ESTs	TM,Fz,Frizzled	3.5
	442133	AW874138	Hs.114218 Hs.129017	ESTs	TM	3.5
	410908	AA121686	Hs.10592	ESTS	GTP_EFTU	3.5
	452198	AI097560	Hs.61210	ESTs	TM	3.5
10	408730	AV660717	Hs.47144	DKFZP586N0819 protein	pkinase	3.4
10	436488	BE620909			TM	3.4
	409745	AA077391	Hs.261023	hypothetical protein FLJ20958 gb:7B14E12 Chromosome 7 Fetal Brain cD	TM	3.4
	445870	AW410053	Hs.13406	syntaxin 18	TM	3.4
	451743	AW074266	Hs.23071	ESTs	TM	3.4
15	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with G	TM	3.4
13	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	SS	3.4
	412848	AA121514	Hs.70832	ESTs	TM	3.4
	413625	AW451103	Hs.71371	ESTs	filament	3.4
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like repeat d	SS	3.4
20	422972	N59319	Hs.145404	ESTs	TM	3.4
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4; MAP kinas	DSPc,Rhodanese	3.4
	450377	AB033091	Hs.24936	ESTs	TM	3.4
	443475	AI066470	Hs.134482	. ESTs	TM	3.4
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	TM,pkise,ig,SRF-TF	3.4
25	409744	AW675258	Hs.56265	Homo sagiens mRNA; cDNA DKFZp586P	TM	3.4
23	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
	404440		1 55.120042	0	TM,neur_chan	3.4
	417412	#(NOCAT) X16896	Hs.82112	interleukin 1 receptor, type 1	SS,TIR,ig	3.4
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	wnt	3.4
30	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	SS	3.4
50	421013	M62397	Hs.1345	mutated in colorectal cancers	TM .	3.4
	427072	H38046	110.1040	gb:yp58c10.r1 Soares fetal liver spleen 1NF	Ribosomal_L22e	3.4
	433703	AA210863	Hs.3532	nemo-like kinase	pkinase	3.4
	434294	AJ271379	Hs.21175	ESTs	TM	3.4
35	444188	Al393165	Hs.19175	ESTs	TM	3.4
-	446109	N67953	Hs.145920	ESTs	TM	3.4
	400881	1101000		0	Asparaginase_2	3.3
	450236	AW162998	Hs.24684	KIAA1376 protein	TM	3.3
	418836	AI655499	Hs.161712	ESTs	TM	3.3
40	437951	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone N	TM	3.3
	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone	TM	3.3
	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	m	3.3
	410060	NM_001448	Hs.58367	glypican-4	SS	3.3
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapi	TM	3.3
45	429609	AF002246	Hs.210863	cell adhesion molecule with homology to L	TM,fn3,ig	3.3
	413289	AA128061	Hs.114992	ESTs	TM	3.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	3.3
	401435	#(NOCAT)-		0	TM	3.3
	420072	AW961196	Hs.207725	ESTs	TM	3.3
50	421426	AA291101	Hs.33020	Homo sapiens cDNA FLJ20434 fis, clone K	TM	3.3
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, core	SS	3.3
	443295	AI049783	Hs.241284	ESTs	TM	3.2
	453116	AI276680	Hs.146086	ESTs	Ribosomal_L5_C	3.2
	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related acid	TM	3.2
55	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus recepto	TM	3.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9,	asp,Glyco_hydro_18	3.2
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated glyco	ТМ	3.2
	425159	NM_004341	Hs.154868	carbamoyl-phosphale synthetase 2, aspartat	TM	3.2
CO	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMA	carb_anhydrase	3.2
60	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase kin	TM	3.2
	411248	AA551538	Hs.69321	KIAA1359 protein	TM	3.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-	SS,IL8	3.2
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	ŢΜ	3.2
65	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	SS	3.2
65	444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
	434163	AW974720	Hs.25206	ESTs	TM	3.2
	421991	NM_014918	Hs.110488	KIAA0990 protein	SS	3.2
70	409589	AW439900	Hs.256914	ESTs	TM	3.2
70	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731	TM	3.2
	414661	T97401	Hs.21929	ESTs	TM	3.2
	437537	AA758974	Hs.121417	ESTs, Weakly similar to unnamed protein p	TM	3.2
	439702	AW085525	Hs.134182	ESTs	A2M	3.1
75	420552	AK000492	Hs.98806	hypothetical protein	TM	3.1
13	441028	A1333660	Hs.17558	ESTs	ICE_p20,CARD	3.1
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin indu	TM CC Rembesia	3.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	SS,Bombesin	3.1
	441859	AW194364	Hs.128022	ESTs, Wealdy similar to FIG1 MOUSE FIG	TM SS Eabda	3.1
80	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMA	SS,Ephrin	3.1
οU	447866	AW444754	Hs.211517	ESTs	homeobox	3.1
	419978	NM_001454	Hs.93974	forkhead box J1	Fork_head	3.1
	446219	AI287344	Hs.149827	ESTs	MIP	3.1
	448428	AF282874 AW753085	Hs.21201	nectin 3; DKFZP566B0846 protein gb:PM1-CT0247-151299-005-a03 CT0247	TM,ig TM	3.1 3.1
	407615	K441 20003		•	1 00	3.1
				209		

	410518	AW976443	Hs.285655	ESTs	RasGEF,PH,RhoGEF	3.1
	418396	A1765805	Hs.26691	ESTs	TM	3.1
	427855	R61253	Hs.98265	ESTs	TM	3.1
	429272	W25140	Hs.110667	ESTs	TM	3.1
5						3.1
)	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	
	414774	X02419	Hs.77274	plasminogen activator, urokinase	SS,kringle,trypsin	3.1
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	TM	3.1
	420062	AW411096	Hs.94785	hypothetical protein LOC57163	TM	3.1
	428698	AA852773	Hs.297939	ESTs; Weakly similar to neogenin [H.saple	TM	3.1
10	427051	BE178110	Hs.173374	ESTs	TM	3.1
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic diffe	SS	3.1
	452906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibitor, da	TM	3.1
	429419	AB023226	Hs.202276	KIAA1009 protein	TM	3.1
					TM	3.1
15	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisia		
15	406137	#(NOCAT)		0	TM	3.1
	424800	AL035588	Hs.153203	MyoD family Inhibitor	TM	3.1
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	TM	3.1
	420392	Al242930	Hs.97393	KIAA0328 protein	SS	3.1
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone	voltage_CLC,CBS	3.1
20	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone	Glyco_hydro_2	3.1
LU	449802		Hs.23984	hypothetical protein FLJ20147	TM	3.1
		AW901804				3.0
	450506	NM_004460	Hs.418	fibroblast activation protein; alpha	SS.Peptidase_S9	
	433849	BE465884	Hs.280728	ESTs	TM	3.0
~ -	411984	NM_005419	Hs.72988	signal transducer and activator of transcript	SH2,STAT	3.0
25	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	TM	3.0
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033	TM	3.0
	409757	NM_001898	Hs.123114	cystatin SN	SS,cystatin	3.0
	418727	AA227609	Hs.94834	ESTs	TM	3.0
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	TM	3.0
30	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatidat	TM	3.0
50				ESTs	SS	3.0
	432358	AI093491	Hs.72830		BTB	3.0
	416896	AI752862	Hs.5638	KIAA1572 protein		
	447312	A1434345	Hs.36908	activating transcription factor 1	TM	3.0
	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone P	TM	3.0
35	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltran	SS	3.0
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.0
	401197	#(NOCAT)		0	arf,Ets	3.0
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	TM	3.0
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	TM,FG-GAP	3.0
40	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	RGS	3.0
70	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypotheti	TM	3.0
					TM	3.0
	426882	AA393108	Hs.97365	ESTs SALASSIA		
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone M	TM	3.0
4	439444	A1277652	Hs.54578	ESTs	TM	3.0
45	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	TM	3.0
	444895	A1674383	Hs.301192	EST cluster (not in UniGene)	TM,ASC	3.0
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone	TM	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone N	TM,7tm_1	3.0
	434241	AF119913	Hs.283607	hypothetical protein PRO3077	SS	3.0
50					TM	3.0
50	424962	NM_012288	Hs.153954	TRAM-like protein		3.0
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU7_HUMA	TM	
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	TM	3.0
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.0
	407872	AB039723	Hs.40735	frizzied (Drosophila) homolog 3	TM,7tm_2,Fz,Frizzled	3.0
55	442577	AA292998	Hs.163900	ESTs	TM	3.0
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB5	TM	3.0
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	3.0
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cd	TM	3.0
	457590	Al612809	Hs.5378	spondin 1, (f-spondin) extracellular matrix	SS	3.0
60	418946	AI798841	Hs.132103	ESTs	TM	3.0
JU					TM,SPRY,7tm_1	3.0
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDN	INFOLKTION T	J.U
	TABLE 1	58: rique Eos probese	et identifier numb	ner		
	rkey. U	udag Eng highesi	er iochwich minn	/GI		

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087
	409073	109851_1	AA063458 AA063018 AI444822
	409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	410008	116812_1	AA075952 BE142525 BE142527
75	414147	1421271	BE091634
	414315	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
	416120	1571266_1	H46739 H51513 H19779
	419311	183793_1	AA689591 AW974261 AA236240 A1077451 AA631399 AW974262
	419546	185766_1	AA244199 AA244272 H57440
80	422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
	427072	274884_1	H38046 W69645 AA397968 H38047
	428679	294049_1	AA431765 AA432015
	438993	467651_1	AA328995 AA854879 AI926361
	447197	711623_1	R36075 AI366546 R36167

TABLE 15C:
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

5

	Pkey	Ref	Strand	Nt_position
	400881	2842777	Minus	91446-91603,92123-92265
10	401197	9719705	Plus	176341-176452
	401435	8217934	Minus '	54508-55233
	404440	7528051	Pius	80430-81581
	404939	6862697	Plus	175318-175476
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
15	405547	1054740	Plus	124361-124520,124914-125050
	406137	9166422	Minus	30487-31058
	406367	9256126	Minus	58313-58489
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Primekey
Ex. Accn: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title **25** .

Prot. Dom.: Predicted protein domain structure

30 ratio: ratio tumor vs. normal tissues

	Pkey	Ex. Acon	UG ID	Title	Prot. Dom.	ratio
	430691	C14187	Hs.103538	ESTs	CTADT.	34.9
35	432938	T27013	Hs.3132	steroidogenic acute regulatory protein Matrix metalloprotease 1 (interstitial collag	START SS.Peptidase_M10	28.0 22.3
33	418007	M13509 Al796330	Hs.83169 Hs.207461	ESTs	33,Fepauase_m10	10.8
	451181 452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		10.0
	407638	AJ404672	Hs.288693	EST		9.3
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
40	426890	AA393167	Hs.41294	ESTs		9.1
-10	421155	H87879	Hs.102267-	lysyl oxidase	SS,Lysyl_oxidase	8.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	taminin_EGF	7.6
	453866	AW291498	Hs.250557	ESTs		7.6
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
45	418738	AW388633	Hs.6682	solute carrier family 7, member 11		7.2
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA	7.0
	449579	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
	424586	NM_003401	Hs.150930	X-ray repair complementing defective repa		6.7
	445891	AW391342	Hs.199460	ESTs		6.2
50	424717	H03754	Hs.152213	wingless-type MMTV integration site famil	wnt	6.1
	452705	H49805	Hs.246005	ESTs		6.1
	421285	NM_000102		cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
	408562	A1436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote		5.3
55	420159	A1572490	Hs.99785	ESTs		5.3 5.2
22	451105	A1761324	11- 440043	gb:wi60b11.x1 NCI_CGAP_Co16 Homo s		5.2 5.0
	409049 448674	AI423132 W31178	Hs.146343 Hs.154140	ESTs ESTs	TM	5.0 5.0
	423811	AW299598	Hs.50895	homeo box C4	1 (44	4.9
	427469	AA403084	Hs.269347	ESTs		4.9
60	447033	Al357412	Hs.157601	EST - not in UniGene	PH	4.9
00	424433	H04607	Hs.9218	ESTs	•••	4.9
	448811	AI590371	Hs.174759	ESTs	TM	4.8
	444330	AI597655	Hs.49265	ESTs		4.8
	409041	AB033025	Hs.50081	KIAA1199 protein		4.7
65	418735	N48769	Hs.44609	ESTs		4.5
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	4.5
	430073	U86136	Hs.232070	telomerase-associated protein 1	WD40	4.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
70	422260	AA315993	Hs.105484	ESTs; Weakly similar to LITHOSTATHIN		4.4
70	421110	AJ250717	Hs.1355	cathepsin E	SS,asp	4.3
	445676	Al247763	Hs.16928	ESTs	F-1	4.2
	430704	AW813091	11. 440050	gb:RC3-ST0186-240400-111-d07 ST0186	Epimerase	3.8 3.8
	414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.0 3.7
75	438078	A1016377	Hs.131693 Hs.206892	ESTs		3.7 3.7
15	434032 445657	AW009951 AW612141	Hs.279575	ESTs ESTs	7tm_1	3.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	701(_1	3.5
	455666	BE065813	1 13.07 7 03	gb:RC2-BT0318-110100-012-a08 BT0318		3.5
	448844	AI581519	Hs.177164	ESTs		3.5
80	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induced g	SS	3.5
30	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	TM -	3.4
	458123	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004		3.4
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMA		3.4
	424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3

	424639	AI917494	Hs.131329	ESTs		3.3
	414083	AL121282	Hs.257786	ESTs		3.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2
5	428927 406129	AA441837	Hs.90250	ESTs 0	TM,cNMP_binding	3.1 3.1
,	452699	#(NOCAT) AW295390	Hs.213062	ESTs	tationar _baraing	3.1
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	homeobox	3.1
	428976	AL037824	Hs.194695	ras homolog gene family, member I	ras	3.1
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone H	wnt	3.0
10	454077	AC005952	Hs.37062	Insulin-like 3 (Leydig cell)	SS,Insulin,pkinase	3.0
	404253	#(NOCAT)		0	histone	2.9
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	2.9
	429597	NM_003816		a disintegrin and metalloproteinase domain	TM	2.9
1.5	413289	AA128061	Hs.114992	ESTs		2.9
15	429703	T93154	Hs.28705	ESTS		2.9 2.8
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fis, clone N		2.8
•	424796 424086	AW298244 Al351010	Hs.293507 Hs.102267	ESTs lysyl oxidase ·	Lysyl_oxidase	2.8
	408427	AW194270	Hs.177236	ESTs	2101/20/10000	2.7
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain		2.7
	446999	AA151520	Hs.279525	hypothetical protein PRO2605		2.7
	428819	AL135623	Hs.193914	KIAA0575 gene product		2.7
	422956	BE545072	Hs.122579	ESTs		2.7
0.5	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-0		2.7
25	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.6
	420380	AA640891	Hs.102406	ESTs	TM energin	2.6 2.6
	428651	AF196478	Hs.188401	annexin A10	TM,annexin EGF,Idl_recept_b	2.6
	417849 453700	AW291587 AB009426	Hs.82733 Hs.560	Nidogen 2 apollpoprotein B mRNA editing enzyme, ca	TM .	2.6
30	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone		2.6
50	448756	AI739241	Hs.171480	ESTs		2.6
	425087	R62424	Hs.126059	ESTs		2.5
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kelch	2.5
	443211	Al128388	Hs.143655	ESTs		2.5
35	415263	AA948033	Hs.130853	ESTs	histone	2.5
	432867	AW016936	Hs.233364	ESTs	GSHPx	2.5
	438639	A1278360	Hs.31409	ESTs		2.5 2.5
	455386	AW935875	11- 00000	gb:QV3-DT0019-120100-055-d06 DT0019	TM,SEA	2.5 2.5
40	419092 452055	J05581 AJ377431	Hs.89603 Hs.293772	mucin 1, transmembrane ESTs	TW,OLA	2.5
40	402000	M377431	113.233112			
45	CAT numbe	: ue Eos probese r: Gene cluste Genbank acce	r number		•	
50	Pkey 430704 451105 455386 455666 458123	CAT Number 322217_1 859083_1 1287756_1 1349545_1 479942_1	AW813091 / AI761324 AV AW935875 I BE065813 B	AW206655 AA484440 W880941 AW880937 3E069116 BE160251 E065788 BE065889 BE065832 AA853877 D44747		•
	TARIF 460			•		
55	Ref: Seque hum Strand: Ind	ue number com nce source. The an chromosom icates DNA stra	he 7 digit num e 22" Dunham and from which	an Eos probeset bers in this column are Genbank Identifier (GI) numbers , et al. (1999) <u>Natura</u> 402:489-495 n exons were predicted	, "Dunham I, et al." refers to the pu	blication entitled "The DNA sequence of
60	Nt_position:	Indicates nuc	leotide positio	ns of predicted exons		
OU	Pkey	Ref	Strand	Nt_position		
	404253	9367202	Minus	55675-56055		
	406129	9160131	Plus	2567-3056		
	400120	0.00.0.	* 1.00	200. 0000		•
65	Table 17A i "average" o 2.5.	ists about 183 varian cancer l	genes up-regu evel was set t	itated in endometrioid-type ovarian cancer compared to the 75th percentile amongst various endometrioid-type	normal adult lissues. These were s e ovarian cancers, and the tumor/no	elected as for Table 14A, except that the rmal tissue ratio was greater than or equal to
						•
70			UP-REGULAT	'ED GENES, ENDOMETRIOID OVARIAN CANCER VEI	RSUS NORMAL ADULT TISSUES	
	Pkey: Prim					
		Exemplar Acce	ssion			
	UG ID: Uni					
75	Title: UniG		1-i- di			
75		Predicted pro tumor vs. norm				
	ratio: ratio	tuittor vs. nom	iai ussue			
	Pkey	Ex. Accn	UGID	Title	Prot. Dom.	ratio
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanom		38.9
80	435094	Al560129	Hs.277523	EST		28.8
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252 similar to SR		24.1
						00.0
	428187	AI687303	Hs.285529	ESTs		23.9
	428187 449034	A1624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapi	man property and	19.9
	428187	A1624049	Hs.285529 7 Hs.31664		TM,Fz,Frizzled	

	412925	AI089319	Hs.179243	ESTs		15.7
	438817 447033	AI023799	Hs.163242	ESTs EST - not in UniGene	PH	13.6 13.5
	433222	Al357412 AW514472	Hs.157601 Hs.238415	ESTs, Moderately similar to ALU8_HUMA	rn	13.1
5	422956	BE545072	Hs.122579	ESTs		12.9
	450451	AW591528	Hs.202072	ESTs		11.9
	453964	Al961486	Hs.12744	ESTs	homeobox	11.5
	442438 431989	AA995998 AW972870	Hs.291069	gb:os26b03.s1 NCI_CGAP_Kid5 Homo sa ESTs	SS	11.4 10.3
10	413623	AA825721	Hs.246973	ESTs	33	9.7
	440901	AA909358	Hs.128612	ESTs		9.6
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6
	421478	AI683243	Hs.97258 Hs.21814	ESTs . class II cytokine receptor ZCYTOR7	SS,Tissue_fac	9.3 9.2
15	448706 410566	AW291095 AA373210	Hs.43047	Homo sapiens cDNA FLJ 13585 fis, clone P	33,113305_145	8.7
	438993	AA828995		Integrin; beta 8	SS,integrin_B	8.7
	427121	Al272815	Hs.173656	KIAA0941 protein	C2,	8.4
	420610 427356	AI683183 AW023482	Hs.99348 Hs.97849	distal-less homeo box 5 ESTs	homeobox	8.1 8.0
20	446577	AB040933	Hs.15420	KIAA1500 protein		8.0
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	carb_anhydrase	7.5
	448112	AW245919	Hs.301018	ESTs, Weakly similar to ALUB_HUMAN	101334 M 1	6.9
	451106	BE382701 Al672096	Hs.25960 Hs.9012	N-myc ESTs	HLH,Myc_N_term	6.6 6.3
25	449433 453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
	434636	AA083764	Hs.241334	ESTs		6.1
	453688	AW381270	Hs.194110	Homo saplens mRNA; cDNA DKFZp434C	Mariana	5.9
	422805 400292	AA436989 AA250737	Hs.121017 Hs.72472	H2A histone family; member A BMPR-lb; bone morphogenetic protein rec	histone	5.8 5.7
30	443179	AI928402	Hs.6933	Homo sapiens cDNA FLJ12684 fis, clone N		5.6
	418134	AA397769	Hs.86617	ESTs		5.5
	452249	BE394412	Hs.61252	ESTs	homeobox	5.5 5.5
	409269 413335	AA576953 AI613318	Hs.22972 Hs.48442	Homo sapiens cDNA FLJ13352 fis, clone O ESTs	TM,UPF0016	5.4
35	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
	428029	H05840	Hs.293071	ESTs		5.3
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitami	p450	5.3 5.2
	409094 432938	AW337237 T27013	Hs.3132	gb:xw82f01.x1 NCI_CGAP_Pan1 Homo sa steroidogenic acute regulatory protein	START	5.1
40	410102	AW248508	Hs.279727	ESTs;	SS	5.1
	447835	AW591623	Hs.164129	ESTs		5.1
	438202 423992	AW169287 AW898292	Hs.22588 Hs.137206	ESTs Homo sapiens mRNA; cDNA DKFZp564H		5.0 5.0
	425905	AB032959	Hs.161700	KIAA1133 protein	TM	5.0
45	452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9
	430691 441675	C14187 Al914329	Hs.103538 Hs.5461	ESTs ESTs		4.8 4.7
	425695	NM_005401		protein tyrosine phosphatase, non-receptor	Band_41,Y_phosphatase	4.6
50	440340	AW895503	Hs.125276	ESTs	T14	4.5
50	428579 444783	NM_005756 AK001468	Hs.184942 Hs.62180	G protein-coupled receptor 64 ESTs	TM PH	4.5 4.4
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMA		4.4
	413395	AI266507	Hs.145689	ESTs		4.3
55	415263	AA948033	Hs.130853	ESTs glutamate decarboxylase 1 (brain, 67kD)	histone pyridoxal_deC	4.2 4.2
55	413988 452030	M81883 AL137578	Hs.75668 Hs.27607	Homo saplens mRNA; cDNA DKFZp564N	pyriddxas_deC	4.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069		4.1
•	446431	R45652	Hs.153486	ESTs		4.1
60	434891 415139	AA814309 AW975942	Hs.123583 Hs.48524	ESTs ESTs	G-patch	4.0 4.0
00	453197	A1916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A	Ораши	4.0
	447112	H17800	Hs.7154	ESTs		3.9
	420633	NM_014581		odorant-binding protein 28	TM,lipocalin	3.9
65	459574 415138	Al741122 C18356	Hs.101810 Hs.78045	Homo saplens cDNA FLJ14232 fis, clone N tissue factor pathway Inhibitor 2 TFPI2	Kunitz_BPTI,G-gamma	3.9 3.9
05	414083	AL121282	Hs.257786	ESTs	Manager 11/0 Security	3.7
	442006	AW975183	Hs.292663	ESTs		3.7
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma Homo sapiens mRNA for Hmob33 protein,	Thymosin	3.7 3.7
70	424906 456662	AI566086 NM_002448	Hs.153716 Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
. •	429125	AA446854	Hs.271004	ESTs		3.6
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related pro	eu 10	3.6
	458861	A1630223 AA084248	Hs.85339	gb:ad06g08.r1 Proliferating Erythroid Cells G protein-coupled receptor 39	PHD	3.5 3.5
. 75	418506 423123	NM_012247		SELENOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
	437960	A1669586	Hs.222194	ESTs	•	3.4
	400298	AA032279	Hs.61635	STEAP1	TM	3.4 3.4
	407162 408621	N63855 A1970672	Hs.142634 Hs.46638	zinc finger protein chromosome 11 open reading frame 8; feta		3.3
80	445829	AI452457	Hs.145526	ESTs		3.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	T14	3.3
	457979 402606	AA776655 #(NOCAT)	Hs.270942	ESTs	TM	3.3 3.2
	426471	M22440	Hs.170009 .	transforming growth factor, alpha	SS,EGF	3.2

	430294	AI538226	Hs.135184	ESTs	polyprenyl_synt	3.2
	448027	A1458437	Hs.177224	ESTs		3.2
	432619	AW291722	Hs.278526	related to the N terminus of tre	TBC	3.2
_	413627	BE182082	Hs.246973	ESTs		3.2
5	441377	BE218239	Hs.202656	ESTs		3.2
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone N		3.2
	433527	AW235613	Hs.133020	ESTs	714	3.2
	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.2
10	419807	R77402	11- 00404	gb:yi75f11.s1 Soares placenta Nb2HP Hom	hamaahan	3.1
10	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	homeobox	3.1
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N	zf-C2H2	3.1 3.1
	450480	X82125 AA255920	Hs.25040 Hs.88095	zinc finger protein 239 ESTs	ZI-OZNZ	3.1
	420149 413415	AA829282	Hs.34969	ESTs	_	3.1
15	438966	AW979074	113.34303	gb:EST391184 MAGE resequences, MAGP		3.1
10	431041	AA490967	Hs.105276	ESTs	Oxysterol_BP	3.1
	415245	N59650	Hs.27252	ESTs	OXJStatol_Di	3.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6	kinesin	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422		3.0
20	448816	AB033052	Hs.22151	KIAA1226 protein		3.0
	447866	AW444754	Hs.211517	ESTs	homeobox	3.0
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2		3.0
	406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
0.5	433426	H69125	Hs.133525	ESTs :	TM	3.0
25	420440	NM_002407		mammaglobin 2	Uteroglobin .	3.0
	420181	Al380089	Hs.158951	ESTs		3.0
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro		2.9
	452055	Al377431	Hs.293772	ESTs	20 01 10 0	2.9
30	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolas	C2,PLA2_B	2.9
30	415125	AF061198	Hs.301941	Homo sapiens mRNA for noreplnephrine tr	TM,SNF	2.9
	412708 451389	R26830 N73222	Hs.106137 Hs.21738	ESTs KIAA1008 protein	TM,7tm_2,Rho_GDI	2.9 2.9
	423337	NM_004855		axin 2 (conductin, axil)	DIX.RGS	2.9
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase	DIAINGG	2.9
35	428054	A1948688	Hs.266619	ESTs		2.9
55	448243	AW369771	Hs.77496	ESTs		2.9
	425723	NM_014420		dickkopf (Xenopus laevis) homolog 4	SS	2.9
	432415	T16971	Hs.289014	ESTs		2.9
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)		2.9
40	400195			0		2.9
	449874	AA135688	Hs.10083	ESTs		2.8
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	Hydrolase	2.8
	428093	AW594506	Hs.104830	ESTs		2.8
15	409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
45	424169	AA336399	Hs.153797	ESTs	mito_carr	2.8
	409638	AW450420	Hs.21335	ESTs		2.8
	440048	AA897461	Hs.158469	ESTs, Wealdy similar to envelope protein [2.8
	426890	AA393167	Hs.41294	ESTS		2.8 2.8
50	452771 422505	T05477 AL120862	Hs.124165	gb:EST03366 Fetal brain, Stratagene (cat93 ESTs; (HSA)PAP protein (programmed ce		2.8
50	416624	H69044	113.12.1100	gb:yr77h05.s1 Soares fetal liver spleen 1NF	zf-C3HC4	2.8
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.7
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone	****	2.7
	447342	Al199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM		2.7
55	421247	BE391727	Hs.102910	general transcription factor IIH, polypeptid		2.7
	419752	AA249573	Hs.152618	ESTs		2.7
	410658	AW105231	Hs.192035	ESTs		2.7
	437698	R61837	Hs.7990	ESTs		2.7
60	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) f		2.7
60	438689	AW129261	Hs.250565	ESTS		2.7
	439876 428479	AI376278	Hs.100921 Hs.184572	ESTs, Weakly similar to ALU7_HUMAN A	SCAN pkinase	2.7
		Y00272		cell division cycle 2, G1 to S and G2 to M ESTs	pkinase	2.7 2.7
	436406 437938	AW105723 AI950087	Hs.125346	ESTs; Weakly similar to Gag-Pol polyprote		2.7
65	437336	AA320068	Hs.93701 .	Homo sapiens mRNA; cDNA DKFZp434E		2.7
00	434836	AA651629	Hs.118088	ESTs		2.7
	448404	BE089973	113.110000	ab:RC6-BT0709-310300-021-G07 BT0709		2.7
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	WD40	2.7
	409757		Hs.123114	cystatin SN	SS,cystatin	2.6
70	443775	AF291664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7tm_1	2.6
	427961	AW293165	Hs.143134	ESTs	•	2.6
	426668	AW136934	Hs.97162	ESTs '		2.6
	424717	H03754	Hs.152213	wingless-type MMTV Integration site fami	wnt	2.6
75	434669	AF151534	Hs.92023	core histone macroH2A2.2	histone,A1pp,DUF27	2.6
75	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor 2	SS,TM,PTN_MK	2.6
	451009	AA013140	Hs.115707	ESTs		2.6
	429774	AI522215	Hs.50883	ESTs	pkinase	2.6
	439951	AI347067	Hs.124636	ESTs	TM	2.6
80	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	AIRS,formyl_transf	2.5
ov	416806 420900	NM_000288 AL045633	Hs.79993 Hs.44269	peroxisomal biogenesis factor 7 ESTs	WD40 Ald_Xan_dh_C	2.5 2.5
	420900 457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	Oihydroorolase	2.5
	457030 459583	AI907673	(13,11,000)	gb:IL-BT152-080399-004 BT152 Homo sa	Surjutostado	2.5
	440870	A1687284	Hs.150539 .	Homo sapiens cDNA FLJ13793 fis, clone T	PAX	2.5
	7.0070			O 1 A		

	446693 407289 400882	AW750373 AA135159	Hs.42315 Hs.203349	Homo sapiens cDNA FLJ1303 Homo sapiens cDNA FLJ1214 0	9 fis, clone M	тм	2.5 2.5 2.5					
5	431322 424081 451996	AW970622 NM_006413 AW514021 #(NOCAT)	Hs.139120 Hs.245510	gb:EST382704 MAGE reseque ribonuclease P (30kD) ESTs 0	ences, MAGK		2.5 2.5 2.5 2.5					
10	403381 419488 418882	AA316241 NM_004996	Hs.90691 Hs.89433	nucleophosmin/nucleoplasmin ATP-binding cassette, sub-fam	3 ily C (CFTR	SS TM,ABC_membrane	2.5 2.5					
	TABLE 17B: Picey: Unique Eos probeset Identifier number CAT number: Gene cluster number Accession: Genbank accession numbers											
15	Pkey CAT Number Accession											
20	409094 416624 419807 431322 437938	1099611_1 1604694_1 188252_1 331543_1 44573_2	AW337237 AW861642 AW861655 AW858008 AW857990 AW858007 H69044 T47567 H75691 T50292 R77402 AA260988 R06794 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AU950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 AJ251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AU820501 AU820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AJ219788 AA884444 N92578 F13493 AA927794 AJ560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AU890387 AJ950344 AJ741346 AJ689062									
25		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251674 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513995 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005										
30	438966 438993 442438 448404 449034	467436_1 467651_1 542469_1 761515_1 794817_1	AA999074 AA834841 AA828650 AA828995 AA834879 Al926361 AA999978 AB1616584 R61781 T77332 F07756 F08149 F07647 BE089973 Al498612 AW805032 Al624049 AW117770 Al858360									
35	452771 458861	930983_1 798085_1	T05477 T0785 Al630223 Al65									
40	TABLE 17C: Pksy: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495 Strand: Indicates DNA strand from which exons were predicted NL_position: Indicates nucleotide positions of predicted exons											
45	Pkey 400882 402606 403381	Ref 2842777 9909429 9438267	Minus Minus	Nt_position 110431-110708 81747-82094 26009-26178								
50	Table 18 lists lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesels on the Affyrnetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4,											
55	and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.											
60	TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES Pkey: Primekey Ex. Accn: Exemplar Accession UG ID: UniGene ID Title: unigene ID											
65	Pkey 428579 436982	Ex. Accn NM_005756 AB018305	UG ID Hs.184942 Hs.5378	Title G protein-coupled receptor 64 spondin 1, (f-spondin) extracellular m	aat	ratio 30.5 29.4						
70	427585 423739 418007 438993 428664 439820	D31152 AA398155 M13509 M73780 AK001666 AL360204	Hs.179729 Hs.97600 Hs.83169 Hs.52620 Hs.189095 Hs.283853	collagen; type X; alpha 1 (Schmid mc ESTs Matrix metalloprotease 1 (interstitial integrin; beta 8 stmilar to SALL1 (sal (Drosophila)-lik Homo sapiens mRNA full length inse	:	27.0 22.7 20.6 16.7 16.5 16.5						
75	400289 421155 431989 426635 424581	X07820 H87879 AW972870 BE395109 M62062	Hs.2258 Hs.102267 Hs.291069 Hs.129327 Hs.150917	Matrix Metalloproteinase 10 (Stromo lysyl oxldase ESTs ESTs catenin (cadherin-associated protein	lysin	16.2 16.1 15.9 15.7						
80	424361 428976 416209 439706 452055 410102 428392	AL037824 AA236776 AW872527 AI377431 AW248508 H10233	Hs.194695 Hs.79078 Hs.59761 Hs.293772 Hs.279727 Hs.2265	ras homolog gene family, member I MAD2 (milotic arrest deficient, yeast ESTs ESTs; secretory granule, neuroendocrine p	, h rotei	15.1 15.0 14.7 13.2 12.5						
					215							

	402606	44424200	II- ocrea	hunghalian	44.5
	443715	AA434329 Al583187	Hs.36563	hypothetical protein FLJ22418 cyclin E1	11.5 10.7
	433496	AF064254	Hs.9700 Hs.49765	VLCS-H1 protein	10.6
	418601	AA279490	Hs.86368	calmegin	10.3
5	409269	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fis,	10.1
_	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	9.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	9.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.7
10	429782	NM_005754		Ras-GTPase-activating protein SH3-domain	9.5
10	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	9.4
	435509	AI458679	Hs.181915	ESTs	9.3 9.0
	408908 433764	BE296227 AW753676	Hs.48915 Hs.39982	serine/threonine kinase 15 ESTs	9.0
15	445413	AA151342	Hs.12677	CGI-147 protein	8.7
13	438078	Al016377	Hs.131693	ESTs	8.6
	447342	Al199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFA	8.1
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	7.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	7.5
20	426320	W47595	Hs.169300	transforming growth factor, beta 2	7.5
	424001	W67883	Hs.137476	KIAA1051 protein	7.4
	458861	NM_007358	Hs.31016	DNA-BINDING PROTEIN M96	7.3
	425465	L18964	Hs.1904	protein kinase C; lota	7.2
25	425776	U25128	Hs.159499	parathyroid hormone receptor 2	7.1
25	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum com	7.0
	409178	BE393948	Hs.50915	kallikrein 5	6.8 6.6
	433159 410530	AB035898 M25809	Hs.150587 Hs.64173	kinesin-like protein 2 ESTs, Highly similar to VAB1	6.5
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose Induc	6.5
30	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	6.4
-	425371	D49441	Hs.155981	mesothelin	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	6.4
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	6.3
35	420440	NM_002407	Hs.97644	mammaglobin 2	6.2
	457030	Al301740	Hs.173381	dihydropyrimidinase-like 2	6.2
	415139	AW975942	Hs.48524	ESTs	6.1
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	6.0
40	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	6.0 6.0
40	437960 410555	A1669586 U92649	Hs.222194 Hs.64311	ESTs a disintegrin and metalloproteinase doma	5.9
	433447	U29195	Hs.3281	neuronal pentraxin II	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1	5.9
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.9
45	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	5.8
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	5.6
5 0	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232	5.6
50	424539	L02911	Hs.150402	activin A receptor, type I	5.5
	441645	Al222279 ·		ESTs	5.5
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.4
	426514 425154	BE616633 NM_001851	Hs.301122	bone morphogenetic protein 7 (osteogenic collagen, type IX, alpha 1	5.4 5.4
55	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.3
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
	452930	AW195285	Hs.194097	ESTs	5.2
	431130	NM_006103		epididymis-specific; whey-acidic protein	5.1
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	5.1
60	432158	W33165	Hs.55548	ESTs, Weakly similar to unknown protein	5.0
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.0
	443268	A1800271	Hs.129445	hypothetical protein FLJ12496	4.9
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	4.9
65	418882	NM_004996		ATP-binding cassette, sub-family C (CFTR	4.8
05	428555 427528	NM_002214 AU077143		integrin, beta 8 minichromosome maintenance deficient (S.	4.8 4.7
	406400	AA343629	Hs.179565 Hs.104570	kallikrein 8 (neuropsin/ovasin)	4.7
	439024	R96696	Hs.35598	ESTs	4.6
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.6
70	448027	AI458437	Hs.177224	ESTs	4.6
	404996	NM_001333		Cathepsin L2	4.6
	443933	AI091631	Hs.135501	ESTs	4.5
	409459	D86407	Hs.54481	. low density lipoprotein receptor-related	4.4
7-	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	4.3
75	423123	NM_012247		SELENOPHOSPHATE SYNTHETASE	4.3
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	4.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.1
	420736	A1263022	Hs.82204	ESTs	4.1
80	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.1 4.0
30	414343 450654	AL036166 AJ245587	Hs.75914 Hs.25275	coated vesicle membrane protein Kruppel-type zinc finger protein	4.0
	445808	AV655234	Hs.298083	ESTs	3.9
	417389	BE260964	Hs.82045	Midkine (neurite growth-promoting factor	3.9
	425247	NM_005940		matrix metalloproteinase 11 (stromelysin	3.8

	430634	A1860651	Hs.26685	ESTs	3.8
	431846	BE019924	Hs.271580	Uroplakin 1B	3.7
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.7 3.7
5	407792 420585	AI077715 AW505139	Hs.39384 Hs.279844	putative secreted ligand homologous to f	3.7
5	407756	AA116021	Hs.38260	hypothetical protein FLJ10033 ubiquitin specific protease 18	3.6
	411773	NM_006799		protease, serine, 21 (testisin)	3.6
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.5
	431958	X63629	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
10	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.5
	422278	AF072873	Hs.114218	ESTs	3.5
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.4
1.5	408730	AV660717	Hs.47144	DKFZP586N0819 protein	3.4
15	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
	421841	AA908197	Hs.108850	KIAA0936 protein	3.3
	439864	AI720078	Hs.291997 Hs.203845	ESTs	3.3 3.2
	456546 410687	A1690321 U24389	Hs.65436	ESTs, Weakly similar to TWIK-related acl lysyl oxidase-like 1	3.2
20	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.2
	420552	AK000492	Hs.98806	hypothetical protein	3.1
	421991	NM_014918		KIAA0990 protein	3.1
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	3.1
	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.1
25	411789	AF245505	Hs.72157	Homo saplens-mRNA; cDNA DKFZp564I19	3.1
	434241	AF119913	Hs.283607	hypothetical protein PRO3077	3.1
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosy	3.1
	409533	AW969543	Hs.21291	mitogen-activated protein kinase kinase	3.1
30	416391	Al878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
30	412604	AW978324 NM_001490	Hs.47144	DKFZP586N0819 protein	3.1 3.0
	425851 431259	NM_006580		glucosaminyl (N-acetyl) transferase 1, c claudin 16	3.0
	418557	BE140602	Hs.246645	ESTs	3.0
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.0
35	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
	457590	AI612809	Hs.5378	spondin 1, (f-spondin) extracellular mat	2.9
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
40	417315	AI080042	Hs.180450	ribosomal protein S24	2.9
40	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.musculus	2.9
	442295	A1827248	Hs.224398	ESTs	2.9 2.9
	428248 403019	A1126772 AA834626	Hs.40479 Hs.66718	ESTs RAD54 (S.cerevisiae)-like	2.8
	436252	AI539519	Hs.120969	Homo sepiens cDNA FLJ11562 fis	2.8
45	419488	AA316241		nucleophosmin/nucleoplasmin 3	2.8
. •	434288	AW189075	Hs.116265	ESTs	2.7
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	2.7
	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.7
50	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fis, clone NT	2.7
50	453779	N35187	Hs.43388	ESTs	2.7
	433068	NM_006456		sialyltransferase	2.7
	426841	AI052358 AK000530	Hs.193726 Hs.193326	ESTs fibroblast growth factor receptor-like 1	2.7 2.7
	428778 451346	NM_006338		glioma amplified on chromosome 1 protein	2.6
55	443883	AA114212	Hs.9930	serine (or cysteine) proteinase Inhibito	2.6
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.6
	447149	BE299857	Hs.328	TAR (HIV) RNA-binding protein 2	2.6
	433656	AW974941	Hs.292385	ESTs	2.6
~ 0	408210	N81189	Hs.43104	ESTs	2.6
60	430651	AA961694	Hs.105187	kinesin protein 9 gene	2.5
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.5
	421802	BE261458	Hs.108408	CGI-78 protein	2.5 2.5
	446211 404029	AI021993 W72881	Hs.14331 Hs.266470	S100 calcium-binding protein A13 protocadherin beta 2	2.5
65	453012	T95804	Hs.31334	putative mitochondrial outer membrane pr	2.5
	419981	AA897581	Hs.128773	ESTs	2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	419220	AA811938	Hs.291759	ESTs	2.5
7 0	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.4
70	406850	AI624300	Hs.172928	collagen, type I, alpha 1	2.4
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.4
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevislae) 3-like	2.4
	409956	AW103364 W25945	Hs.727 Hs.18745	H.sapiens activin beta-A subunit (exon 2 ESTs	2.4 2.4
75	407584 448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4
, 5	440120	W 141053	13.33 [33	Edia, righty anima to Account 200 a boot 2	2.7

Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was applicated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER UG ID: UniGene ID

Title: UniGene Title 5 % tumors: percent of tumors detected expressing gene

	Single genes		
	UGID	Title	% tumors
	Hs.5378	spondin 1, (f-spondin) extracellular matrix protein	77
10	Hs.12844	EGF-like-domain 6	86
	Hs.151254	kallikrein 7 (chymotryptic; stratum comeum)	66
	Hs.97644	mammaglobin 2	73
	Hs.155981	mesothelin (cytokine)	57
	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	21
15	Hs.50915	kallikrein 5	27
_	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
	Hs.79361	kallikrein 6 (neurosin, zyme)	38
	Hs.83169	MMP 1 (Interstitial collagenase)	23
	Hs.72026	protease, serine, 21 (testisin)	16
20	Hs.39384	putative secreted ligand homologous to fix1	46
	Hs.2719	epididymis-specific; whey-acidic protein type; four-disulfide core	91
	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
	Hs.1584	cartilage oligomeric matrix protein	25
	Hs.169300	TGF beta 2	21
25	Hs.2250	leukemia inhibitory factor (cholinergic differentiation factor)	23
	Exemplary (Combinations:	
		EGF-like-domain 6 + mammaglobin 2	93
		kallikrein 7 + mesothelin	71
30		mammaglobin 2 + bone morphogenic protein 7	88
_		EGF-like-domain 6 + bone morphogenic protein 7	91
		kallikrein 7 + bone morphogenic protein 7 + testisin	75
		kallikrein 7 + mammaglobin 2 + mesothelin	84
		mammaglobin 2 + bone morphogenic protein 7 + TGF beta 2	91
35		EGF-like-domain 6 + bone morphogenic protein 7 + MMP 1	95

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 probesels such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 95th percentile value amongst various non-malignant lissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant lissues was subtracted from 40 both the numerator and the denominator before the ratio was evaluated.

Tables 20B-24B list accession numbers for Pkey's lacking UnigenelD's for tables 20A-24A. For each probeset is listed a gene cluster number from which oligonucleolides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarly using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 45

Tables 20C-24C list genomic positioning for Pkey's lacking Unigene ID's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:

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TABLE 20A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: UniGene title
Pred. Protein Dom.: Predicted protein domain 55

R1: Ratio of tumor to normal body tissue

60	Pkey	ExAccn	UniGene ID	Unigene Title	Pred. Protein Dom.	R1
•	421296	NM_002666		perilipin	perilipin,SS	32.5
	453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	26.5
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	26.3
65	446374	AA329256	Hs.24756	ESTs. Moderately similar to al		22.6
00	441021	AW578716	Hs.7644	H1 histone family, member 2		22.3
	409518	BE384836	Hs.3454	KIAA1821 protein	SS	21.3
	413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	21.2
	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
70	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase, SS, Ets	20.7
, 0	422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
	429556	AW139399	Hs.98988	ESTs	SS,pkinase,PMP22_Claudin	20.1
	436485	X59135	Hs.156110	immunoglobulin kappa constant	SS,ig,SS	19.9
	423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
75	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	19.4
	422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40.SS	19.3
	420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	18.5
	441356	BE384381	Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ank	18.5
	424659	AW891298	Hs.331601	Homo sapiens, Similar to cyste	SS,Fork_head	18.4
80	439924	Al985897	Hs.125293	ESTs	SS	18.1
••	458814	A1498957	Hs.170861	ESTs, Weakly similar to Z195_H	SS,TM,ldl_recept_a,ldl_re	17.5
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF, RhoGAP, PH, C2	17.2
	439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin, SS, TM, PDZ, WD	16.9
	432945	AL043683	101	hypothetical protein FLJ10803	SS	16.8
	.02010					

	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	16.8
	438424	Al912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	16.7
	409435	AI810721	Hs.95424	ESTs	SS .	16.4
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2
5						16.0
5	421612	AF161254	Hs.106196	8D6 antigen	Idl_recept_a,SS,TM	
	456177	NM_012391		prostate epithelium-specific E	Ets,SAM_PNT	15.7
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
	432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	15.5
• •	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	15.5
10	401278			Target Exon	Band_41	15.4
	444804	A1084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
	410259	AK000337	Hs.61485	hypothetical protein	GFO_IDH_MocA,GFO_IDH_MocA	15.4
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	15.1
	423081	AF262992	Hs.123159	sperm associated antigen 4	TM	14.9
15	421495	Al583067	Hs.149152	ESTs, Weakly similar to RHOP M		14.7
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rm,SS	14.7
	413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	14.6
	406901	M14624	1101100200	gb:Human 4-beta-galactosyltran	antiminate objection	14.6
	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
20			Hs.5074	similar to S. pombe dim1	DIM1,SS	14.5
20	436186	BE390717	115.3014			14.4
	455557	AW995839	11- 07070	gb:QV4-BN0044-110200-108-h07 B	Metallophos	
	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	14.2
	421489	Al922821	Hs.32433	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
25	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
25	435017	AA336522	Hs.12854	angiotensin II, jype I recepto		14.0
	446572	AV659151	Hs.282961	ESTs		13.9
	434068	AA977935	Hs.127274	ESTs	SS	13.7
	432481	AW451645	Hs.151504	Homo saplens cDNA FLJ11973 fis	SS,Collagen,COLFI,TSPN	13.7
	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS_Peptidase_C2	13.6
30	421182	AA284855	Hs.104480	ESTs	SS,Topoisomerase_I,Topois	13.3
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
	456642	AW451623	Hs.109752	putative c-Myc-responsive	00,000.0	13.3
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657	SQS_PSY	13.2
		AW449612	Hs.152475	ESTs	SS S	13.1
35	430178				Sec7,PH	12.9
33	430399	Al916284	Hs.199671	ESTs	Georgen	
	436725	BE045223	Hs.136912	hypothetical protein MGC10796	CO THE CONTRACTOR COLO	12.9
	410219	T98226 .	Hs.171952	occludin -	SS,TM,Occludin,BIR	12.7
	442620	C00138	Hs.8535	Homo saplens mRNA for KIAA1668	SS,RNA_poLK	12.7
40	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	425018	BE245277	Hs.154196	E4F transcription factor 1	zf-C2H2,LIM,SS,Exo_endo_p	12.6
	423801	NM_015071	Hs.132942	GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	417826	T85105	Hs.15471	ESTs	SS,cadherin,Cadherin_C_te	12.6
	409261	BE315042	Hs.19210	hypothetical prolein MGC11308		12.6
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin,SS,TM,cadherin	12.6
45	411570	BE144584	Hs.314341	ESTs		12.5
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12,4
	441805	AA285136	Hs.301914	neuronal specific transcriptio	LIM,SS,LIM	12.3
	402365			Target Exon	SS,SS,TM,ig	12.2
50	414371	Al905865		thymosin, beta 4, X chromosome	Thymosin	12.2
• •	446780	R31107		gb:yh61g01.s1 Soares placenta		12.1
	428782	X12830	Hs.193400	Interleukin 6 receptor	SS,TM,fn3,ig,SS,TM	12.1
	427695	R88483	Hs.172862	intron of Bicaudal D homolog 1	CO!, in oligio e!	12.1
		100400	113.112002	C11002253*:gi[129091]sp[P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
55	400460	A A 04 000C	Hs.204918		SS,TM	12.0
"	407341	AA918886		ESTs, Weakly similar to ALU8_H	SS S	11.9
	424049	AB014524	Hs.138380	KIAA0624 protein		
	422872	BE326786	Hs.187646	ESTs	TM	11.9
	450800	BE395161	Hs.1390	proteasome (prosome, macropain	SS NAME AND ADDRESS OF THE PARTY OF THE PART	11.8
60	428648	AF052728	Hs.188021	potassium voltage-gated channe	cNMP_binding	11.7
60	432329	NM_002962		S100 calclum-binding protein A	S_100,efhand,SS,efhand,S_	11.7
	417061	A1675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis	CTF_NFI	11.6
	451195	U10492	Hs.438	mesenchyme homeo box 1	homeobox,SS	11.5
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.5
	426500	NM_014638	Hs.170156	KIAA0450 gene product	SS	11.4
65	433124	U51712	Hs.13775	hypothetical protein SMAP31		11.4
	444001	Al095087	Hs.152299	ESTs, Moderately similar to S6		11.4
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	11.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (hom	SS	11.3
	411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans,SS,TM	11.2
70	404438	0,000	110.00010	Target Exon	101/202110/00// 111	11.2
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
	406230		191	Target Exon	sopritages	11.2
	432125	A18/079567	Hs.183006	Homo sapiens cDNA FLJ12300 fis	Band_41,ERM	11.2
		AW972667			DOMEST INCIDEN	11.1
75	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_H	TO CO Chara tract 42 COLF	
13	400206	0056-5	11- 00100-	Eas Control	SS,SS,Glyco_tranf_43,COLF	11.1
	450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.0
	407605	W03512	Hs.6479	hypothetical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	11.0
	432143	AL040183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	10.9
0.0	446839	BE091926	Hs.16244	mitatic spindle coiled-coil re	Troponin,SS,glycolylic_en	10.8
80	443559	Al076765	Hs.269899	ESTs, Moderately similar to AL	SS,TM,B!R,UQ_con	10.8
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 L		10.8
	409557	BE182896	Hs.211193	ESTs		10.8
	435158	AW663317	Hs.65588	DAZ associated protein 1	rm,SS,rm	10.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
					210	

219

	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	10.6
	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	10.6 10.5
	416819 419341	U77735	Hs.80205 Hs.118888	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra SS,TM,UPF0016	10.5
5	444359	N71463 Al697160	Hs.143594	ESTs, Weakly similar to ALU1_H ESTs, Weakly similar to HS4L_H	55,1111,011.0010	10.5
9	404333	71037 100	113.140034	C7001735*:gi[7768636 db] BAA95	vwd	10.5
	401210		•	C12000519:gi 7710046 ref NP_05	*	10.5
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	10.4
10	401594			NM_024817:Homo saplens hypothe		10.3
10	441790	AW294909	Hs.132208	ESTS	OO OO OACO OAND	10.3 10.3
	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP SS	10.3
	438185 432031	Y19188 AF039196	Hs.320461 Hs.272367	ESTs hairless protein (putative sin	JmjC	10.2
	410471	T88872	115.212501	gb:yd31a12.s1 Soares fetal liv	jiigo	10.1
15	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	10.1
	417371	N74613	Hs.269149	ESTs		10.0
	428167	AA770021	Hs.16332	ESTs .	SS,ig,fn3	10.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis	5 100 04D 01V	10.0
20	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	10.0 9.9
20	425863 442739	U43604 NM_007274	Hs.159901	Human unidentified mRNA, parti cytosolic acyl coenzyme A thio	Acyl-CoA_hydro,SS,TM	9.9
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P,GDC-P	9.9
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	9.8
~~	445625	BE246743		hypothetical protein FLJ22635	SS,TM .	9.8
25	435339	AI358300		ESTs ~	SS,ras	9.8 9.8
	407235	D20569	Hs.169407 Hs.98502	SAC2 (suppressor of actin muta	SS,TM,Ribosomal_S13,Galac SS	9.8
	428758 401349	AA433988	HS.900UZ	CA125 antigen; mucin 16 inositol polyphosphate-1-phosp	33	9.7
	437915	A1637993	Hs.202312	Homo sapiens clone N11 NTera2D		9.7
30	424511	BE300512	Hs.193557	ESTs, Moderately similar to AL		9.7
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
	405143			NM_013432*:Homo sapiens nuclea	ank,SS,TM,CPSF_A	9.6
	427497	AW139476	Hs.31240	ESTs	00	9.6 9.6
35	420423	AAB27718	Hs.88218	ESTs	SS ldh,ldh_C,SS,ldh	9.6
33	431512 450052	BE270734 Al681298	Hs.2795 Hs.236524	lactate dehydrogenase A ESTs	zf-C3HC4,zf-B_box	9.5
	412738	N34731	Hs.74562	slah binding protein 1; FBP in	homeobox	9.5
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.5
40	451165	Al340575	Hs.286084	MRIP-1 protein		9.5
40	411450	H49619	Hs.127301	ESTs	SS,pkinase	9.5 9.5
	405371	1140422	Hs.285737	NM_005569*:Homo saplens LIM do Homo saplens cDNA: FLJ20895 fi	pkinase,LIM,PDZ SS,G6PD,Glucosamine_iso,G	9.5
	435782 416866	N49433 AA297356	Hs.80324	serine/threonine protein phosp	Metallophos, Metallophos	9.4
	405474	777237555	113.00024	NM_001093*:Homo sapiens acetyl	CPSase_L_chain,biotin_lip	9.4
45	412837	AI922293	Hs.58389	hypothetical protein MGC4090		9.3
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.3
	431081	AA491594	Hs.75813	polycystic kidney disease 1 (a	SS,TM	9.3
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,late_protein_L2,SS,GS	9.2 9.2
50	427435 407688	AW938739 W25317	Hs.115412 Hs.37616	hypothetical protein FLJ13881 Human D9 splice variant B mRNA	SS	9.2
50	407507	U73799	115.01010	gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
	400833	0.0.00		C11000890:gi[3746443 gb]AAC639	SS,TM,7tm_1	9.2
	422064	AW452589	Hs.335742	ESTs	TM	9.2
55	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2 9.2
55	451752 432931	AB032997 AF174487	Hs.293753	KIAA1171 protein Bcl-2-related ovarian killer p	TBC,SS,TM,pkinase,laminin	9.1
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	9.1
	427397	AJ929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	9.1
	405159			ENSP00000243337*:CDNA FLJ13984		9.1
60	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45,	CDC45	9.1
	407058	X94563	Un 20400	gb:H.sapiens dbl/acbp gene exo	SS SS,TM,UPAR_LY6,toxin,SS,T	9.0 9.0
	448045 400772	AJ297436	Hs.20166	prostate stem cell antigen NM_003105*:Homo sapiens sortil	ldi_recept_a,fn3,ldi_rece	9.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp5	spectrin,SH3,PH,CH	9.0
65	414391	BE409872		gb:601299655F1 NIH_MGC_21 Homo		9.0
	447867	A1525268	Hs.164303	ESTs	TM	9.0
	422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	9.0
	454319	AW247736		ESTs, Weakly similar to T32527	SS	8.9 8.9
70	428781 408645	AF164799 AW245738	Hs.193384 Hs.109274	putatative 28 kDa protein hypothetical protein MGC4365	SS,TM	8.9
70	429527	AA454184	Hs.289014	ESTs	00,111	8.9
	406651	A1559224		gb:tq32c02.x1 NCI_CGAP_Ut1 Hom		8.9
	430893	BE502068	Hs.282067	ESTs		8.8
76	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
75	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	8.8 8.8
	432211 421694	BE274530 BE387430	Hs.273333 Hs.106880	hypothetical protein FLJ10986 bystin-like	•	8.8
	421694 453683	AL079854	Hs.118598		SS	8.8
	456741	W37608	Hs.184492		SS,pkinase	8.7
80	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fi		8.7
	415898	Z43379	Hs.177193			8.7
	456977	AK000252			SS,TM,transmembrane4	8.7 8.7
	439632 431462	AW410714 AW583672			SS	8.7
	731702	F-111000012		O Pop		
					220	

	400128			Eos Control	TM,E1-E2_ATPase,HMA,Hydro	8.7
	438582	AI521310	Hs.283365	ESTs, Weakly similar to ALU5_H	SS	8.7
	450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4	CNES A) helianne C CC	8.7 8.7
5	410855 415126	X97795 D60945	Hs.66718	RAD54 (S.cerevisiae)-like gb:HUM141D04B Clontech human f	SNF2_N,helicase_C,SS SS,TM	8.7
,	418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.6
	431157	AI823969	Hs.132678	ESTs	SS.MAPEG.SS.MAPEG	8.6
	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	8.6
	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	8.6
10	432343	NM_002960		S100 calcium-binding protein A	S_100,SS,efhand,S_100,efh	8.6
	458440	Al095468	Hs.135254	Homo sapiens clone 1 thrombosp		8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
	452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6 8.6
15	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF SS,ras	8.6
13	420836 455588	AW958453 AI129903	Hs.204959 Hs.74669	hypothetical protein FLJ14886 vesicle-associated membrane pr	synaptobrevin,SS,TM	8.5
	431974	AW972689	Hs.200934	ESTs	bZIP	8.5
	410720	AF035154	Hs.65756	regulator of G-protein signall	RGS,G-gamma,DEP,SS,RGS,DI	8.5
	449751	AW207115	Hs.25555	ESTs	**************************************	8.5
20	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
	405557			Target Exon	Els,SAM_PNT	8.5
	443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	8.5
	428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
25	421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,mm,PDZ	8.4
25	401885	41000107	11 407075	Target Exon	kinesin,SS,TM	8.4
	449382	A1650407	Hs.197875	ESTs .	SS,rm,zf-RanBP	8.4 8.4
	432862 441363	AW004958 AW450211	Hs.236720 Hs.126825	amnionless protein ESTs, Weakly similar to A46302	SS,MATH,zf-TRAF,zf-C3HC4 SS,TM,HSP20,7tm_1	8.4
	407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,ig,SS,G_glu_transpept	8.4
30	425380	AA356389	Hs.32148	AD-015 protein	SS,TM,LRR,P,Peptidase_S8	8.4
~ • •	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis	SS,SAM,SS,TM,7tm_1	8.4
	424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ10967 fis		8.3
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length		8.3
25	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.3
35	404365			Target Exon	SS	8.3
	424310	AA338648	Hs.50334	testes development-related NYD	SS,TM	8.3
	401935	A A 04 20 4C		Target Exon	PH SS,myb_DNA-binding,myb_DN	8.3 8.3
	434796 423098	AA812046 AA321980	Hs.204682	ESTs ESTs	55,myo_ONA-binding,myo_DN	8.3
40	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
10	457082	AA470687	Hs.104772	ESTs	SS	8.2
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.2
	402445			Target Exon	fn3,SS,TM,BNR	8.2
	422078	AW872378	Hs.120170	hypothetical protein FLJ21415	SS	8.2
45	418361	AW505368	Hs.12460	gb:UI-HF-BN0-alu-d-03-0-UI.r1		8.2
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	8.2
	403885	414/070000	11-007000	Target Exon	TM, Sulfate_transp, STAS, HM	8.2 8.2
	450029 452512	AW073380 AW363486	Hs.267963 Hs.337635	hypothetical protein FLJ10535 ESTs	SS,Pyridox_oxidase,zf-C2H SS	8.2
50	420138	BE268854	Hs.177729	ESTs	SS	8.2
50	439788	N71241	Hs.119275	ESTs	UQ_con	8.2
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.2
	449656	AA002008	Hs.188633	ESTs	PIP5K	8.1
	452295	BE379936	Hs.28866	programmed cell death 10	SS,serpin	. 8.1
55	448650	AW769385	Hs.204891	ESTs	SS,IL8	8.1
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine pro .	KH-domain	8.1
	444406	Al147237		immunoglobulin heavy constant	SS	8.1
	437215	AL117488		Human clone 23564 mRNA sequenc	SS CO THE DIV DOZ DED Cirk and	8.1
60	408891 400409	NM_006577	rts.204204	ESTs, Highly similar to beta-1 Homo sapiens winged helix/fork	SS,TM,DIX,PDZ,DEP,Disheve SS	8.1 8.0
00	443801	AF153341 AW206942	Hs.253594	Intron of: trichorhinophalang	GATA	8.0
	425281	AA444390	Hs.155482	hydroxyacyl glutathione hydrol	lactamase_B,SS	8.0
	458216	AW024282	Hs.104938	hypothetical protein MGC15906		8.0
	401507	************		C15000810*:gi[11131272[sp]P793		8.0
65	401180			eukaryotic translation elongat	SS,TM,ion_trans,IQ	8.0
	454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
	444014	AI095718	Hs.135015	ESTs		8.0
	412128	AW894709		gb:CM1-NN0032-020500-212-d05 N	SCAN,zf-C2H2,KRAB	7.9
70	408363	NM_003389		coronin, actin-binding protein	WD40	7.9
70	425694 425263	U51333 NM 001107	Hs.159237 Hs.155419	hexokinase 3 (white cell) BCL2-interacting killer (apopt	hexokinase,hexokinase2,he SS,TM,TspO_MBR	7.9 7.9
	425263 447045	AW392394	13.100419	sorting nextn 17	SS,1M,1SPO_MBR SS,1F-2B,PP2C	7.9
	457613	AA598869	Hs.173770	ESTs		7.9
	410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	7.9
75	402545			Target Exon	•	7.9
-	454246	AW245185	Hs.6996	ESTs		7.9
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	7.9 .
	443678	AW009605	Hs.231923	ESTs	SS	7.9
90	404676	4)500000		Target Exon		7.9
80	406649	Al569392	Un 204400	gb:tn86a02.x1 NCI_CGAP_Ut2 Hom	Fork hand CS Fork hand	7.9 7.9
	420230 413534	AL034344 BE146961	Hs.284186	forkhead box C1 gb;QV4-HT0222-011199-019-b12 H	Fork_head,SS,Fork_head SS,TM	7.8
	413534	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2,SS,TM	7.8
	410839	NM_006849		protein disulfide isomerase	thiored,Rho_GDl,gntR,SS,T	7.8
					221	
					441	

221

	444046	AI360834	Hs.135094	ESTs .	SS,GTP_EFTU,EFG_C,GTP_EFT	7.8
	439501	AF086321	Hs.287452	Homo sapiens cDNA FLJ11760 fis	TM	7.8
	415441	R13977	Hs.9634	ESTS	SS	7.8 7.8
5	450461 448993	8E408081 Al471630	Hs.46736	hypothetical protein FLJ23476 KIAA0144 gene product	33	7.8 7.8
•	400923			Target Exon	SS,TM,DUF289	7.8
	440546	AJ491994		gb:to07g09.x1 NCI_CGAP_Ut2 Hom	SS,HATPase_c	7.8
	419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
10	451721	NM_006946		spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	7.8
10	458834 422633	Al566883 X56832	Hs.196446 Hs.118804	ESTs enclase 3, (beta, muscle)	enolase,SS,TM,kinesin,FHA	7.8 7.7
	438452	Al220911	Hs.288959	hypothetical protein FLJ20920	SS	7.7
	421445	AA913059	Hs.104433	Homo sapiens, done IMAGE:4054	asp,SS,TM,ion_trans,K_tet	7,7
1.5	434743	AI363410		ribosomal protein S18	SS,TM	7.7
15	450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.7
	442394 434333	R62926 AA186733	Hs.285193 Hs.292154	ESTs stromal cell protein		7.7 7.7
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	VHL,TM	7.7
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	7.7
20	444670	H58373	Hs.332938	hypothetical protein MGC5370	SS,zf-RanBP,MDM2	7.7
	449495	A1652833	11- 000007	gb:wb22c11.x1 NCI_CGAP_GC6 Hom	SS CONTRACTOR OF CASE	7.7
	444607 449125	AW405635 Al671439	Hs.293687 Hs.196029	ESTs Homo sapiens mRNA for KIAA1657	SS,PI-PLC-X,PH,PI-PLC-Y,C TIMP	. 7.7 7.7
	447151	Al022813	Hs.92679	Homo saplens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	. 7.6
25	448626	W27670	Hs.55613	hypothetical protein FLJ22531		7.6
	430432	AB037758	Hs.241419	KIAA1337 protein	TM,Patched,TM	7.6
	401822	*1400744		C17001422:gi 2695866 emb CAA75		7.6
	428909	Al190714 BE257293	Hs.98945 Hs.76366	ESTs	SS,hormone_rec,zf-C4	7.6 7.6
30	414534 421620	AA446183	Hs.91885	BCL2-antagonist of cell death ESTs, Weakly similar to 155214	55,101110116_1ec;21-C4	7.6 7.6
50	441650	Al261960	Hs.132545	ESTs	SS,TM,KOW	7.6
	442232	Al357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
35	400286	DEFFOCAL	11- 2072C	C16000922:gi[7499103[pirl[T209	TM,ABC_tran,ABC_membrane	7.5
55	452833 417390	BE559681 AA196552	Hs.30736 Hs.85852	KIAA0124 protein hypothetical protein MGC3169	WD40	7.5 7.5
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,Integrin_B,	7.5
	450716	T57758	Hs.10255	ESTs		7.5
40	407435	AF211976		gb:Homo sapiens LENG9 mRNA, pa		7.5
40	413956	AI821351	Hs.193133	ESTs. Weakly similar to ALU7_H	00.0444-1 00.044	7.5
	427899 406495	AA829286	Hs.332053	serum amyloid A1 Target Exon	SS,SAA_proteins,SS,SAA_pr	7.5 7.5
	430387	AW372884	Hs.240770	nuclear cap binding protein su	SRCR,TM,Acetyltransf rm,SS,TM,rrm	7.5 7.5
	408601	U47928	Hs.86122	protein A	SS,7tm_1,SS,ig,WD40,zf-UB	7.5
45	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763	SS,ras	7.4
	409832	AW963293		gb:EST375366 MAGE resequences,	SS	7.4
	448043	A1458653	Hs.201881	ESTs	PHD Systemia CS Pastidose 1447	7.4
	421148 420970	AF008936 AA305079	Hs.102178 Hs.1342	syntaxin 16 cytochrome c oxidase subunit V	Syntaxin,SS,Peptidase_M17 COX58	7.4 7.4
50	419295	BE397712	Hs.144027	ESTs	myb_DNA-binding,myb_DNA-b	7.4
	448330	AL036449		ESTs	,	7.4
	419639	AK001502	Hs.91753	hypothetical protein		7.4
	431488	AB037785	Hs.257594	KIAA1364 protein	SS,CH,LIM,SS	7.4 7.4
55	456487 448615	AF064804 Al910868	Hs.212957	suppressor of Ty (S.cerevisiae ESTs	SS	7.4 7.4
	427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	7.4
	441076	N49809	Hs.11197	Homo saplens, clone IMAGE:3343	•	7.4
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	7.4
60	411448	AA178955	Hs.271439	ESTs, Weakly similar to 138022	rm,PDZ	7.4 7.4
ر٥٥	442318 425055	Al792199 AW961959	Hs.96940	ESTs ESTs	SS,zf-C2H2	7.4 7.4
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	SS,TM,transmembrane4	7.4
	403748			Target Exon	TM	7.4
65	447282	A1989963	Hs.197505	ESTs	TM	7.3
65	422305	A1928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.3
	416472 427273	AA180756 AW139032	Hs.340316 Hs.107376	ESTs, Moderately similar to AL hypothetical protein DKFZp434N	zf-C2H2 SS,SS,TM	7.3 7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
	447859	AK002194	Hs.19851	peroxisomal biogenesis factor	0. · _0/	7.3
70	432747	NM_014404		calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
	405727	AJ219282	Hs.2186	eukaryotic translation elongat	SS,G-gamma	7.3
	404199	BE391690	He oner	ENSP00000211797*:Helicase SKI2 hypothetical protein FLJ20917	SS,RasGAP,PH,SS,PHD SS,PWWP,Exonuclease,lipoc	7.3 7.2
	445434 428550	AW297880	Hs.9265 Hs.98661	ESTs	SS,homeobox,homeobox	7.2
75	454718	AW815144	. 10.50001	gb:QV4-ST0212-120100-075-d10 S	SS,ATP-synt_ab,ATP-synt_a	7.2
	407686	AW901268	Hs.126043	chromosome 21 open reading fra	SS,TM,ISK_Channel	7.2
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Ho	serpin	7.2
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	7.2
80	407581 430746	R48402 AW977370	Hs.173508 Hs.222012	P3ECSL ESTs	SS,TM,7tm_1 SS	7.2 7.2
00	402651	Vital Ial	1 13.2220 12	NM_000721*:Homo sapiens calciu	ion_trans	7.2 7.2
	407323	AA181183	Hs.143504	gb:zp57c02.s1 Stratagene endot	SS,Ribosomal_S4e,ubiquiti	7.2
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
	434035	Al762074	Hs.204769	ESTs, Weakly similar to T28770	SS,TM	7.2
					222	

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	400419	AF084545		Target	EGF,ig,lectin_c,sushi,Xii	7.2
	424241	AW995948	Hs.182339	Homo saplens pyruvate dehydrog	SAM_PNT	7.2
	445837	Al261700		ESTs		7.2
_	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.1
5	421879	AW959607		gb:EST371677 MAGE resequences,	00 514504 00051	7.1
	418285	H68616	Hs.293756	ESTS	SS,EMP24_GP25L	7.1 7.1
	442893 437829	H78133	Un 402024	gb:yu86c11.s1 Soares fetal liv ESTs		7.1
	457629	A1358522 BE464016	Hs.103834 Hs.238956	ESTS	SS,zf-C2H2,mm	7.1
10	433396	AI742071	Hs.133205	ESTs	SS,TM	7.1
	415595	R54144	Hs.278707	chromosome 21 open reading fra	SS	7.1
	436629	AA861011	Hs.249795	ESTs	TM	7.1
	414593	BE386764		gb:601273249F1 NIH_MGC_20 Homo		7.1
1.5	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
15	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	7.1
	405247	00000010		Target Exon	SS	7.1 7.1
	455778	BE088746	U- 12720	gb:CM2-BT0693-210300-123-d09 B	WD40	7.1
	431005 435717	AA490544 AF227905	Hs.127269 Hs.105794	ESTs, Weakly similar to T02345 UDP-glucose:glycoprotein gluco	Glyco_transf_8	7.1
20	405113	MF221300	115.100754	Target Exon	SS	7.1
20	428070	T63918	Hs.182313	retinol-binding protein 2, cel	lipocalin,lipocalin,WD40	7.1
	429029	AA443443	Hs.85524	for muscle specific ring finge	SS	7.1
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	7.0
	412970	AB026436	Hs.177534	dual specificity phosphatase 1	Rhodanese, DSPc, SS, DSPc	7.0
25	438701	AA937112	Hs.207788	ESTs	TM,sushi	7.0
	454756	AW819273		gb:CM2-ST0284-061299-046-a12 S		7.0
	401264	11114 4076 1	11- 040000	C18000090*:gi 6678656 ref NP_0	SS,laminin_Nterm,laminin_	7.0
	408080	AW149754	Hs.248652 Hs.86947	ESTs, Weakly similar to T00273	SS disintagrin Reprolysin Pe	7.0 7.0
30	418641 431402	BE243136 AA743534	Hs.250861	a disintegrin and metalloprote ESTs	disintegrin,Reprolysin,Pe	7.0
50	423790	BE152393	. 10.2000,1	gb:CM2-HT0323-171199-033-a08 H	SS	7.0
	450688	AW272352	Hs.60450	ESTs	TM	7.0
	405928			Target Exon	SS,cystatin,Coprogen_oxid	7.0
~ ~	454438	AA224053		cell division cycle 27	SS,TM,SPRY,7tm_3,ANF_rece	7.0
35	407281	Al307226	Hs.164421	ESTs	SS TO THE TOTAL TO	6.9
	423386	AW136098	Hs.314081	ESTS	SS,WD40,EPO_TPO	6.9
	459360	BE384526	Hs.25734 Hs.95744	gb:601277913F1 NIH_MGC_20 Homo hypothetical protein similar t	ank TM	6.9 6.9
	420187 431549	AK001714 AA507036	Hs.170673	ESTs	ank,TM	6.9
40	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		6.9
	454577	AW809272		gb:MR4-ST0118-040100-034-c08_1		6.9
	438118	AW753311		ESTs	SS,lipocalin	6.9
	416233	AA176633		gb:zp13g01.s1 Stratagene fetal		6.9
AE	417012	N38970	Hs.194214	ESTs	00 #1.	6.9
45	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin PAF-AH_lb,Lipase_GDSL,\$\$,	6.9 6.9
	439963 418416	AW247529 U11700	Hs.6793 Hs.84999	platelet-activating factor ace ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	6.9
	404956	011700	113.04333	C1003210*:gi[6912582]ref]NP_03	PI3_PI4_kinase,PI3K_C2,PI	6.9
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	SS	6.9
50	438525	AW368528	Hs.100855	ESTs	SS	6.9
	400906			C18000324:gi 12229928 sp Q9PTW		6.9
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA13	SS	6.8
	406834	Al318680		gb:ta49g09.x1 NCI_CGAP_Lu25 Ho	00.00	6.8
55	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	SS,COesterase,SS,COestera	6.8 6.8
33	424198 445873	AB029010 AA250970	Hs.143026 Hs.251946	KIAA1087 protein poly(A)-binding protein, cytop	SS,TM,Na_Ca_Ex,Calx-beta, SS,PABP,rm,pkinase,14-3-	6.8
	439605	AF086431	Hs.22380	ESTs	SS,TM	6.8
	432284	AA532807	Hs.105822	ESTs	SS,TM,pkinase	6.8
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035		6.8
60	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin,SS,TM	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	PHD,Virus_HS,SS,ICin_chan	6.8
	400205	414400000		NM_006265*:Homo sapiens RAD21 ESTs	SS	6.8 6.8
65	434315 418184	AW196608 AA367375		Homo sapiens cDNA FLJ14015 fis		6.8
05	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		6.7
	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.7
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	6.7
	429712	AW245825	Hs.211914	ENSP00000233627°:NADH-ubiquino	oxidored_q6,SS,TM,rrm	6.7
70	456886	AW089093	Hs.144996	ESTs, Weakly similar to 138022		6.7
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	6.7
	434000	BE002846	Hs.112964	ESTS	CC protocomo	6.7 6.7
	432530	AF131786	Hs.278303	Homo sapiens clone 25220 mRNA	SS,proteasome	6.7
75	436141 441794	AA970001 AW197794	Hs.150319	Homo sapiens, cione IMAGE:3610 ESTs	SS,TM	6.7
15	450287	AW291483	Hs.255909	ESTs		6.7
	441523	AW514263		ESTs, Weakly similar to ALUF_H	SS	6.7
	452798	Al918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
00	451937	AF119664	Hs.27299	transcriptional regulator prot	SS,integrin_B,fn3,Calx-be	6.7
80	421417	AA291004	Hs.326088	ESTs		6.7
	440317	BE561888	i . 400-00	gb:601346093F1 NIH_MGC_8 Homo	eminates 1 2 CC TH 1 DD	6.7
	421321 444004	NM_005309 AW452054	Hs.103502 Hs.161139	glutamic-pyruvate transaminase ESTs	aminotran_1_2,SS,TM,LRR	6.7 6.7
	444904 449730	R72290	Hs.117557	ESTs, Weakly similar to 138022	RasGAP,thyroglobulin_1,Ri	6.7
	710100					
				•	223	

	450622	AI660285	Hs.58210	ESTs, Highly similar to ITH4_H	SS,TM,vwa	6.7
	425424	NM_004954		ELKL motif kinase	pkinase,KA1,UBA,SS	6.7
	435864	AL036499	Hs.188491	ESTs	CO homoshow LIDEO160 DUE22	6.7 6.7
5	410397 454262	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23 SS,TM,voltage_CLC,CBS	6.7 6.7
5	453023	AW612232 AW028733	Hs.254835 Hs.31439	ESTs serine protease Inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	6.6
	419157	AA234540	Hs.23871	ESTs	pkinase	6.6
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214	SS,cadherin,crystall	6.6
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis	SS,adh_short,Transglutami	6.6
10	456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS	· - · · ·	6.6
	411490	R39474		gb:yh95b09.r1 Soares placenta	SS	6.6
	455885	BE153524		gb:PM0-HT0339-241199-002-C03 H	SS,pkinase	6.6
	438857	Al627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.6
1.5	420307	AW502869	Hs.66219	ESTs	SS,TM	6.6 6.6
15	453496	AA442103 AA234822	Hs.33084	solute carrier family 2 (facil	sugar_tr,SS,TM	6.6
	419182 406301	AAZ340ZZ	Hs.66147	ESTs Target Exon	SS,TM,ion_trans,ion_trans TM	6.6
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.6
	448980	AL137527	Hs.289038	hypothetical protein MGC4126		6.6
20	454095	AW178110	Hs.191705	gb:IL3-HT0061-010999-013-H04 H	SS,TM,homeobox,trypsin,PD	6.6
	459702	A1204995		gb:an03c03.x1 Stratagene schiz	•	6.6
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1,SS,TM	6.6
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	6.6
25	404149		11 000-10	C6002509*:gi 5031885 ref NP_00	SS,TM,kringle	6.6
25	418576	AW968159	Hs.302740	Epithelial calcium channel 2,	SS,TM	6.6 6.6
	421363	NM_001381		docking protein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	. 6.6
	458919 427502	Al681567 Al811865	Hs.13349 Hs.7133	KIAA0756 protein Homo saplens, clone IMAGE:3161	TM SS,TM,ABC_tran,Glyco_tran	6.5
	412289	AW935967	Hs.170162	KIAA1357 protein	SS	6.5
30	447105	AW377610	Hs.11123	DKFZP564G092 protein	SS,TM	6.5
50	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	6.5
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	6.5
	420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
	431849	A1670823	Hs.85573	hypothetical protein MGC10911	SS,TM	6.5
35	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF,SS	6.5
	437662	AA765387		ESTs	WD40,RCC1,SPRY	6.5
	436543	NM_002212	Hs.5215	Integrin beta 4 binding protei	elF6	6.5
	405375	A A ACCOED	U= 440400	CX000741*:gi 4885461 ref NP_00	SS,TM	6.5 6.5
40	430116 406109	AA465350	Hs.119400	ESTs Target Exon	SS,TM,adh_short	6.5
70	414871	BE549179	Hs.29008	gb:601078714F1 NIH_MGC_12 Homo		6.5
	440656	Al979248	Hs.148221	ESTs		6.5
	438951	U51336	Hs.6453	Inositol 1,3,4-triphosphale 5/	SS,oxidored_nitro,SS	6.5
	405376			Target Exon	SS,TM	6.5
45	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fi	SS	6.5
	400500			Target Exon		6.5
	408294	BE141732		gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	6.5
	447904	AW206303	11- 074000	ESTs	66	6.4 6.4
50	439211 426828	AI890347 NM_000020	Hs.271923 Hs.172670	Homo sapiens cDNA: FLJ22785 fi activin A receptor type II-lik	SS pkinase,Activin_recp,SS,T	6.4
50	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.	SS,TM	6.4
	442146	R52599	1.0.10001	gb:yg81g01.r1 Soares infant br	TM	6.4
	425041	Al377150	Hs.150914	ESTs	SS	6.4
~ ~	457584	AA147979	Hs.285005	mitochondrial import receptor	Josephin	6.4
55	435449	AA682379	Hs.303460	EST		6.4
	406284			Homo sapiens mRNA full length		6.4
	425944	AK000664	Hs.164256	hypothetical protein FLJ20657	OC TH	6.4 6.4
	453367	AW732847 U66048	Hs.70573 Hs.92683	PKCI-1-related HIT protein Homo sapiens clone 161455 brea	SS,TM	6.4
60	419725 412452	AA215731	NS.52003	suppression of tumorigenicity	SS	6.4
00	421273	AJ245416	Hs.103106		Sm,SS,tRNA-synt_1,GST_C,G	6.4
	432746	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1BD	6.4
	429398	AA452239		KIAA0970 protein		6.4
	404430			C8000066*:gij10432395[emb]CAC1	SS	6.4
65	427339	A1734109	Hs.97984	SRY (sex determining region Y)		6.4
	436389	AI811706		CHMP1.5 protein		6.4
	428890	AA525226	Hs.303293	ESTs, Moderately similar to 15	20	6.4
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS bounds 2 bounds	6.4
70	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase hormone_rec,zf-C4,SS,TM,h	6.4 6.4
70	423847 408493	U16997 BE206854	Hs.133314 Hs.46039	RAR-related orphan receptor C phosphoglycerate mutase 2 (mus	PGAM,BRCT,RNA_pol_L	6.4
	439569	AW602166	Hs.222399	CEGP1 protein	CUB,EGF,SS	6.4
	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.4
	444550	BE250716	Hs.87614	ESTs	SS	6.4
75	407198	H91679		gb:yv04a07.s1 Soares fetal liv	BIR	6.4
-	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.4
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.3
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
80	400137	A18/0742F0	Un £3300	Eos Control	SS	6.3 6.3
ου	408784 435028	AW971350 AW193035	Hs.63386 Hs.187370	ESTs ESTs		6.3
	435026	A1467908	Hs.8882	ESTs	SS,TM,7tm_1	6.3
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.3
	436050	AI057205	Hs.14584	ESTs		6.3

	403672			C4001244:gi[539933[pir][A61275	tubulin,TM	6.3
	448269	BE622358	Hs.61260	hypothetical protein FLJ13164		6.3
	430217	N47863	Hs.180450	ribosomal protein S24	Ribosomal_S24e	6.3
5	426675 423510	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2 Trehalase	6.3 6.3
5	428573	AB000824 AA430651	Hs.129712 Hs.209249	trehalase (brush-border membra ESTs	Helidiase	6.3
	457052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
	445099	BE163341	110.47 000	gb:QV3-HT0458-230200-099-b01 H		6.3
	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	6.3
10	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657	SS,TM,sugar_tr	6.3
	427880	AA436011	Hs.98187	ESTs		6.3
	426722	U53823	Hs.171952	occludin	Occludin,SS,TM,BIR	6.3
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase SS	6.2 6.2
15	431161 413055	AA493591 AV655701	Hs.75183	gb:nh01a12.s1 NCI_CGAP_Thy1 Ho cytochrome P450, subfamily IIE	p450	6.2
13	431250	BE264649	Hs.251377	taxol resistance associated ge	p430	6.2
	406373	DC204043	113.231011	Target Exon	SS,TM,vwa,FG-GAP,integrin	6.2
	403003			NM_024944*:Homo sapiens hypoth	TM	6.2
•	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Ho	SS	6.2
20	406299			Target Exon	44	6.2
	439327	AF086141	Hs.50760	ESTs, Highly similar to BimL (SS	6.2
	414246	BE391090	Hs.280278	EST	SS	6.2 6.2
	427812	AA770424	Hs.98162	ESTs		6.2
25	420926 443766	AA830402 N91071	Hs.221216 Hs.109650	ESTs .	UQ_con	6.2
23	431082	AA491600	13.103030	gb:ne80a11.s1 NCI_CGAP_Ew1 Hom		6.2
	420530	Al218431		coagulation factor VIII-associ		6.2
	407360	X13075		gb:Human 2a12 mRNA for kappa-i		6.2
••	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)		6.2
30	409946	AW162263	Hs.312468	ESTs, Weakly similar to ALUC_H	RasGAP,C2,PH,BTK	6.2
	413272	AA127923	11- 447000	ESTs	SS	6.2
	445050	AW205483	Hs.147260	ESTs	SS,trypsin,kringle,fn2,EG	6.2 6.2
	458130 449940	AA115811 AW291126	Hs.6838 Hs.187520	ras homolog gene family, membe Homo sapiens, clone IMAGE:3834	ras,arf SS,zf-C2H2	6.2
35	440390	AW207385	Hs.36475	KIAA0493 protein	COLL CELLE	6.2
55	423106	N52572	Hs.13702	ESTs, Moderately similar to AL	•	6.2
	402501			sperm specific antigen 2	ig,MHC_I,SS	6.1
	431470	AA832417	Hs. 139650	ESTs	SS,ig,pkinase,LRR,LRRCT	6.1
40	416597	H66891		gb:yr71c03.r1 Soares fetal liv		6.1
40	412122	AW852707		G-rich RNA sequence binding fa	SS,WD40	6.1
	415056	AB004662	Hs.77867	adenosine A1 receptor	7tm_1,SS,TM	6.1 6.1
	400358 405473	AF181286		Homo saplens mutant dystrophin NM_001093*:Homo saplens acetyl	CPSase_L_chain,biotin_lip	6.1
	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	6.1
45	422262	AL022315	Hs.113987	tectin, galactoside-binding, s	Gal-bind_lectin	6.1
	401121			C12001638*:gij7291960 gb AAF47	_	6.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	TM	6.1
	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796	bZIP_Maf,SS,P5CR,EF1BD	6.1
50	456021	BE246628	Hs.250726	gb:TCBAP1D5030 Pediatric pre-B	SS,TM,SS	6.1 6.1
30	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	6.1
	410082 450593	AA081594 AF129085	Hs.158311 Hs.25197	Musashi (Drosophila) homolog 1 STIP1 homology and U-Box conta	SS,HECT,phoslip TPR,SS,TM,Rhomboid,lactam	6.1
	437050	AA766420	113.23131	ESTs	SS	6.1
	458835	AI868753	Hs.76372	ESTs	SS	6.1
55	412777	Al335773		ESTs		6.1
	454364	BE263928	Hs.323806	gb:601191272F1 NIH_MGC_7 Homo	\$S,TM	6.1
	448877	AI583696	Hs.253313	ESTs		6.1
	413045	X92121	Hs.75180	protein phosphatase 5, catalyt	Metallophos, TPR	6.1
60	408054	AW816490	Hs.8102	ESTs	terromousbased CC TM	6.1 6.1
60	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me gb:zq75h01.r1 Stratagene hNT n	transmembrane4,SS,TM	6.1
	415870	AA199830 H15578	Hs.21017	ESTs		6.1
	438723	M34429	110.21017	gb:Human PVT-IGLC fusion prote		6.1
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.0
65	406575			Target Exon	SS,pkinase,pkinase_C,RFX_	6.0
	401488			Target Exon	Glyco_hydro_1	6.0
	437650	AA814338	Hs.292297	ESTs	aldages DAC DE bind DU	6.0 6.0
	439827	AA846538	Hs.187389	ESTs membrane-spanning 4-domains, s	pkinase,DAG_PE-bind,PH SS,TM	6.0
70	456373 454513	BE247706 BE159271	Hs.89751 Hs.109731	gb:MR0-HT0407-180100-004-h05 H	33,1W	6.0
7.0	414944	C15044	113.103701	gb:C15044 Clontech human aorta	SS,TM	6.0
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobro	Cys_knot,vwc	6.0
	401215			C12000457*:gi]7512178[pir][T30	trypsin,SS,TM	6.0
75	408117	AL138255		ESTs, Weakly similar to 138022	SS,zf-C3HC4,BIR	6.0
	426357	AW753757		gb:RC3-CT0283-271099-021-a08 C	SS aliana	6.0
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytop	SS,pkinase .	6.0 6.0
	400389	AL135841		olfactory receptor, family 2,	7tm_1,SS,TM,CSD	6.0
80	447128 431297	Al271898 AA651771	Hs.3076	cyclin K ESTs		6.0
50	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p .	PARP,PARP_reg,SS,TM,Pepti	6.0
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.0
	453101	AW952776		ESTs	TM	6.0
	407383	AA532576		ESTs, Moderately similar to AL	SS,Patatin,ank	6.0
					225	

	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	SS,SS,TM,ig	6.0
	459111	AU077013	Hs.28757	transmembrane 9 superfamily me	EMP70	6.0
	405770			NM_002362:Homo sapiens melanom	MAGE	6.0
_	415611	T26376		gb:AB123C11R Infant brain, LLN	SS,TM,mm,sushi	6.0
5	453413	AJ003294		gb:AJ003294 Selected chromosom	SS,Folate_carrier	6.0
	424415	NM_001975		enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	5.9
	426048	AI768853	Hs.134478	ESTs	TM	5.9
	435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	5.9
10	439469	W69836	11. 007004	gb:zd48a02.r1 Soares_fetal_hea	SS,pkinase,C2,pkinase_C,D	5.9
10	445664	AW968638	Hs.237691	ESTs, Weakly similar to KIAA06	THEODR OIL D. Law.	5.9
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	TM,CDP-OH_P_transf	5.9
	452113	AI859393	Un 22046	gb:wm11a02.x1 NCI_CGAP_Ut4 Hom	actin	5.9 5.9
	449101	AA205847	Hs.23016	G protein-coupled receptor	7tm_1,SS,TM	5.9
15	437640	AA764893	Hs.272155	ESTs, Weakly similar to 138022	CC Papildoca #/10 homopovi	5.9
1.3	400748 442370	AI143593	Hs.129419	NM_022122:Homo sapiens matrix ESTs	SS,Peptidase_M10,hemopexl	5.9
	442419	AI749893	Hs.270532	ESTs, Weakly similar to 138022	Adaptin_N,Alpha_adaptinC2	5.9
,	439986	AW750272	Hs.128608	ESTs	SS,TM,ISK_Channel	5.9
	407553	Z11168	110.120000	gb:H.sapiens 5HT1A receptor re	SS,TM	5.9
20	431424	AI222969		ESTs	SS	5.9
	442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spe	PDEase	5.9
	457845	H93040	Hs.297729	ESTs	SS,TM,WD40	5.9
	446912	Al347650	Hs.128521	ESTs, Moderately similar to AL	SS	5.9
~ ~	451381	BE241831	Hs.172330	hypothetical protein MGC2705	SS,Ribosomal_L28e	5.9
25	416024	AW886484	Hs.343522	ATPase, Ca transporting, plasm	E1-E2_ATPase,Hydrolase,Ca	5.9
	446329	NM_013272		solute carrier family 21 (orga	kazal,OATP_N,OATP_C	5.9
	431321	AW136372		acid phosphatase, prostate	SS,TM,acid_phosphat	5.9
	420039	NM_004605		sulfotransferase family, cylos	Sulfotransfer, SS, DAGKc	5.9
20	428223	AA424313	Hs.98402	ESTs	HECT	5.9
30	433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	5.9
	450251	BE080483	11 07000	gb:QV1-BT0630-280200-086-a05 B	SS	5.9
	408511	AW206404	Hs.27268	ESTs	00.0110	5.9
	414348	AF041430	Hs.75922	brain protein 13	SS,SH3	5.9
35	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL CRSnap Labele	5.9 5.8
55	412173 404001	T71071		gb:yc50b05.r1 Stratagene liver Target Exon	CPSase_L_chain	5.8
	445263	H57646	Hs.42586	KIAA1560 protein	SS	5.8
	441583	AI791499	Hs.205742	ESTs, Weakly similar to ALUA_H	33	5.8
	430168	AW968343	113.2037 42	DKFZP434I1735 protein	SS,TM,efhand,efhand	5.8
40	454682 ·	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	5.8
. •	453829	AL138200		gb:DKFZp547N052_r1 547 (synony	SS,TM,ATP-synt_C,Galactos	5.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G	SS	5.8
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	5.8
٠	451045	AA215672		gb:zr96e09.s1 NCI_CGAP_GCB1 Ho	SS,Peptidase_C1,zf-C2H2	5.8
45	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis	SS,TM	5.8
	455679	BE066529		gb:RC3-BT0333-300300-017-a12 B	UBX	5.8
	457125	AW444451	Hs.134812	ESTs	SS	5.8
	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.8
50	421707	NM_014921		lectomedin-2	Latrophilin,OLF,7tm_2,Gal	5.8
50	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	5.8
	414347	BE275835	U- 200207	gb:601121639F1 NIH_MGC_20 Homo	SS	5.8
	439910	H66765 AW664971	Hs.339397	ESTS	SS LIM	5.8 5.8
	410382 426391	AW161050	Hs.259546 Hs.169611	ESTs second milochondria-derived ac	SS	5.8 5.8
55	423358	AI815474	Hs.343866	gb:au47f10.y1 Schneider fetal	SS	5.8
33	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fi	Peplidase_M1	5.8
	402189	1111017201	110.001.00	ENSP00000247423*:D-siglec prec	. opaca.o	5.8
	439949	AW979197	Hs.292073	ESTs, Weakly similar to ALU7_H		5.8
	457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	5.8
60	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	5.8
	411602	L01406	Hs.767	growth hormone releasing hormo	7tm_2,HRM	5.8
	433357	T05639		gb:EST03528 Fetal brain, Strat	SS	5.8
	404311			Target Exon	TM	5.8
~~	428092	AW879141		ESTs	SS,TM	5.8
65	452620	AA436504	Hs.119286	ESTs	SS	5.8
	401938			Target Exon	SS,PHD,proteasome	5.7
	407202	N58172	Hs.109370	ESTs	SS,F5_F8_type_C,pkinase,E	5.7
	458882	R34993	Hs.226666	ESTs, Moderately similar to 15	SS,CRAL_TRIO,PKI	5.7
70	452357	AI638176	Hs.283865		SS,TM,SS,TM	5.7
70	452625	AA724771	Hs.61425	ESTs CGI-69 protein	mito_carr,SS,TM	5.7 5.7
	430281 430490	A1878842 AW902951	Hs.237924 Hs.301723	Homo saplens cDNA FLJ12974 fis	TM	5.7 5.7
	450122	BE313765	Hs.343443	ESTs, Weakly similar to 138022	SS,TM,Y_phosphalase,LON,A	5.7
	450801	AI739013	Hs.203348	ESTs	SS,TM,Hint,HH_signal	5.7
75	413413	D82520	Hs.132390	zinc finger protein 36 (KOX 18	SS,rm,DUF185	5.7
	445631	AK001822	52000	Homo sapiens cDNA FLJ10960 fis		5.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	5.7
	423139	AW402725	Hs.288560	hypothetical protein FLJ21106	-	5.7
••	426221	AB007881		KIAA0421 protein	PI3_PI4_kinase,FATC,SS,TM	5.7
80	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS pro		5.7
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	5.7
	446596	AW204515		ESTs, Weakly similar to G01025		5.7
	432353		Hs.274411	SCAN domain-containing 1	SCAN	5.7
	427625	AF008216	Hs.285013	putative human HLA class II as		5.7
					206	

	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
	418087	AA961613	Hs.127838	ESTs		5.7
	432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
-	433943	AA992805	Hs.44865	lymphoid enhancer-binding fact		5.7
5	414274	AW300961	Hs.334684	Homo sapiens, clone IMAGE:4127	SS,Vps26,Acyl-CoA_dh	5.7
	431328	AA502999	Hs.291591	ESTs		5.7
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.7
	430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH	5.6
10	419516	H82550		ATP-binding cassette, sub-fami	SS,TM,ABC_tran,ABC_membra	5.6
10	413564	BE260120	•	gb:601146990F1 NIH_MGC_19 Homo	00714	5.6
	415958	H10942		gb:ym06c11.r1 Soares infant br	SS,TM	5.6
	401402	DE200407	Lin 94.446	Target Exon	SS,DIX,PDZ,DEP,Dishevelle	5.6 5.6
	456145	BE299427	Hs.21446 Hs.341906	KIAA1716 protein ESTs		5.6 5.6
15	431536 456266	AL133066 L29073	Hs.198726	-	TM,SAM_decarbox,SS,pkinas	5.6
13	435800	AI248285	Hs.118348	cold shock domain protein A ESTs	CSD,homeobox,SS,TM,7tm_2, TM,ECH,chromo	5.6
	449285	AI912702	Hs.139135	ESTs	t micor nomonto	5.6
	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	5.6
	417442	AA199940	Hs.124039	ESTs		5.6
20	405931	, - 1, 000 10		Target Exon		5.6
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 H	SS	5.6
	446931	AJ348856	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho		5.6
	446548	AI769392	Hs.200215	ESTs	SS,TM,Ribosomal_S25,sugar	5.6
~ ~	401984			C17000146*:gij2143629 plr A57	pkinase,SS,TM,P2X_recepto	5.6
25	404066			Target Exon	SS,tRNA-synt_2b,HGTP_anti	5.6
	418363	AA218628	Hs.202977	ESTs .		5.6
	458198	AJ286100		ESTs		5.6
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	SS,TM,GNS1_SUR4,SS,TM,Rho	5.6
20	432328	Al572739	Hs.195471	6-phosphofructo-2-kinase/fruct	PGAM,6PF2K	5.6
30	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.6
	415514	F11301 .	Hs.138329	ESTs	SS,TM	5.6
	426208 429367	AI370379 AB007867	Hs.132216 Hs.278311	ESTs plexin B1	SS,TM Sema,PSI,TIG,SS,TM,TIG,Se	5.6 5.6
	405939	ABOUTOUT	HS.270311	Target Exon	35111a,F31,11G,33,1141,11G,36	5.6
35	457331	AV647405	Hs.18443	aldehyde dehydrogenase 8 famil	GTP_EFTU	5.6
J J	438705	AI049624	Hs.283390	ESTs. Weakly similar to 210926	SS,E2F_TDP,E2F_TDP	5.6
	428624	Al125222	Hs.98712	hypothetical protein DKFZp434H	SS,TM;ras,MSP_domain	5.6
	419389	A1074951	Hs.319095	ESTs	SS,DPPIV_N_term	5.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	5.6
40	408015		-Hs.244349	epidermal differentiation comp		5.6
	413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.5
	452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.5
	434357	. AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.5
15	455274	BE151622		gb:PM0-HT0302-271099-001-a08 H	SS,TM,RNA_pol_L	5.5
45	453904	AW003821		ESTs		5.5
	424624	AB032947	Hs.151301	Ca2+dependent activator protei	Fork_head	5.5
	426576	AA381720	11- 27404	gb:EST94853 Activated T-cells	vwa,Integrin_A,FG-GAP	5.5
	440682	AW362152	Hs.27181	nuclear receptor binding facto	cc	5.5 5.5
50	419125 450207	AA642452 T87615	Hs.130881 Hs.14716	B-cell CLL/lymphoma 11A (zinc ESTs	SS	5.5
50	405211	101013	113.14710	C7000900:gi 4508027 ref NP_003	SS	5.5
	413937	H65775	Hs.207915	ESTs		5.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regula	WD40, Clathrin, Clathrin_pr	5.5
	412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.5
55	446536	W74413	Hs.15251	hypothetical protein	SS	5.5
	451117	AA015752	Hs.205173	ESTs		5.5
	409547	AW409885	Hs.335877	Homo sapiens, clone MGC:4558.	TM	5.5
	412673	AL042957	Hs.31845	ESTs	•	5.5
CO	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	5.5
60	449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
	403938		11. 400	Target Exon	Ephrin	5.5
	441197 455604	BE244638	Hs.166	sterol regulatory element bind	HLH	5.5 5.5
	457468	BE011183 AW971345	Hs.292715	gb:PM3-BN0218-100500-003-d09 B ESTs		5.5
65	447677	Al419235	Hs.344456	gb:tf21d02.x1 NCI_CGAP_Bm23 H	SS,zf-C2H2,SCAN,SCAN,zf-C	5.5
00	415473	R39986	Hs.12778	ESTs	TM,ion_trans	5.5
	408422	AW977031	Hs.143554	ESTs, Highly similar to B45036		5.5
	442780	AI017521		ESTs	SS,TM,7tm_1	5.5
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-fami	ABC_tran,SRP54,SS,TM,ECH	5.5
70	439422	AW452791	Hs.249625	ESTs	SS,TM	5.5
	423479	NM_014326	Hs.129208	death-associated protein kinas	pkinase	5.5
	459558	AI539821	Hs.298799	ESTs, Weakly similar to 210926	SS	5.5
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	SS,TM,tubulin	5.5
75	420894	AA744597	Hs.88854	ESTs	SS,ank	5.5
75	404710	1170707	U. 40740	C9001584:gi[7499208[pir][T2099	V phosphotone (-2 to 1444)	5.5
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	5.5 5.5
	448387	A1874402	Hs.292590	ESTS		5. 5 5.5
	419541 449686	AW749617 AW072813	Hs.280776 Hs.270868	tankyrase, TRF1-interacting an ESTs, Moderately similar to At.		5.5 5.5
80	426315	AA854219	Hs.348137	Homo saplens, clone IMAGE:3542	SS,crystall	5.5 5.5
-	451312	A1769831	Hs.337054	ESTs	SS	5.5
	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
	446790	AW452105		ESTs	SS,zf-C2H2	5.5
	448682	T09471	Hs.250820	hypothetical protein FLJ14827		5.5
					227	

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022	SS	5.5
	411219	AW832917		gb:QV2-TT0003-161199-013-h06 T	20	5.5
	439742 432004	A1827721	Hs.284298	Homo sapiens mRNA full length	SS SDCE SS	5.5 5.5
5	402916	BE018302	Hs.2894	placental growth factor, vascu ENSP00000202587*:Bicarbonate t	PDGF,SS HCO3_cotransp,SS	5.5 5.5
9	405346			Rag C protein	RCC1	5.5
	415976	R43144	Hs.21919	ESTs	TM	5.4
	435064	T70740	Hs.31433	ESTs	SS,MDM2	5.4
4.0	440024	AA969333	Hs.160098	ESTs		5.4
10	431525	AA506656	Hs.6185	KIAA1557 protein		5.4
	458644	AW270149		ESTs, Moderately similar to GG		5.4
	410895	AW809679		gb:MR4-ST0124-261099-015-f05 S		5.4
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	66	5.4
15	413034	BE392896	Hs.129126	Homo sapiens, clone MGC:10992,	SS DSPc,Rhodanese,SS,TM	5.4 5.4
13	444664 443887	N26362 NM_004729	Hs.11615	map kinase phosphatase-like pr Ac-like transposable element	zf-BED	5.4 5.4
	445871	Al702901	Hs.145582	ESTs, Weakly similar to FOR4 M	SS,TM,efhand,efhand	5.4
	411992	AW816214	Hs.143055	ESTs	SS,TM	5.4
	458341	AW373583	Hs.221994	gb:QV4-BT0534-281299-053-e08 B	·	5.4
20	451677	AA059222	Hs.33538	ESTs, Weakly similar to oxygen		5.4
	432656	NM_000246	Hs.3076	MHC class II transactivator	LRR	5.4
	417739	Z43995		gb:HSC1QB121 normalized infant	SS,ArfGap,vwa,TSPN,fn3,Co	5.4
	424618 446847	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	5.4 5.4
25 ·	436094	T51454 Al798701	Hs.82845	Homo sapiens cDNA: FLJ21930 fi ESTs	SS,TM,BNR,fn3,Id1_recept_	5.4
40	433168	AI085436		gb:ow84g06.s1 Soares_fetal_liv	SS,TM,PID	5.4
	417359	T99264	Hs.191117	ESTs	30,1114.12	5.4
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.4
	435154	AA668764	Hs.301637	ESTs	SS,TM	5.4
30	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	5.4
	444064	W85970	Hs.16292	ESTs	SS,TM,Dihydroorotase	5.4
	415970	H23333	Hs.29002	KIAA1706 protein	0011 00	5.4
	445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	SS,sushi,SS	5.4
35	421542 459704	AA411607	Hs.118964 Hs.274441	ESTs, Weakly similar to KIAA11	SS,SS	5.4 5.4
55	402285	AA719572	NS.27444 I	Homo sapiens mRNA; cDNA DKFZp4 sclerostin	SS,TM	5.4 5.4
	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	5.4
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,ras	5.4
	417516	AA203473	Hs.81529	ESTs	TM	5.4
40	423233	BE048021	Hs.11067	ESTs, Highly similar to T46395		5.4
	420733	AW291446	Hs.88651	ESTs	SS	5.4
	404807			Target Exon	UPF0027	5.4
	436483	AJ272063	Hs.283010	vanilloid receptor subtype 1	SS,TM,ank,ion_trans,SS,TM	5.4
45	425316	AA354977	Hs.99010	ESTs, Moderately similar to T1	SS,pkinase,ig	5.4 5.4
40	425565 413341	AA359485 H78472	Hs.173084 Hs.191325	gb:EST68511 Fetal lung II Homo ESTs, Weakly similar to T18967		5.4
	401203	11/04/2	115.131525	Target Exon	filament	5.4
	422452	AL110255	Hs.116808	Homo saplens mRNA; cDNA DKFZp5	SS,asp,PGAM	5.4
	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	SS,TM	5.4
50	428501	AL041162	Hs.98587	ESTs	TM	5.4
	439695	W28548	Hs.285050	ESTs	TM,ion_trans.K_tetra,Kv2c	5.3
	417514	AA203445	Hs.325819	ESTs		5.3
	441358 401722	AW173212		ESTs Target Exon	TM,PLAT,SS	5.3 5.3
55	408905	AV655783	Hs.661	Target CAT	144-151,00	5.3
-	454453	AW752781	1.0.001	hypothetical protein FLJ12614		5.3
	410312	AW850953	Hs.75350	gb:IL3-CT0220-150200-068-A11 C	Vinculin	5.3
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	· 5.3
C O	458682	AV659151	Hs.282961	ESTs		5.3
60	411605	AW006831		ESTs	TM,synaptobrevin	5.3
	409164	AA706639	Un 224000	gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3 5.3
	438868 439034	AW246243	Hs.334800	hypothetical protein FLJ20974 gb:Homo sapiens full length in	filament, filament	5.3
	411426	AF075083 BE141714		gb:QV0-HT0101-061099-032-c04 H	SS	5.3
65	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A,	Glyco_hydro_38,SS,TM,Pept	5.3
••	438470	AW936329	Hs.227823	pM5 protein	SS,TM	5.3
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093		5.3
	430230	BE257724	Hs.236361	seb4D	rm,SS,2-Hacid_DH,WD40	5.3
70	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	5.3
70	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.3 5.3
	414927	T83587	Hs.186476	ESTs Target Exon	SS,Sulfatase SS	5.3 5.3
	404596 454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
	431627	AW609720		HSPC042 protein	- 21) 3.200 - 0.000 - 2	5.3
75	422379	AA932860	Hs.133864	ESTs		5.3
-	426765	AA743603	Hs.172108	nucleoporin 88kD	MAM33	5.3
	433325	AW206986	Hs.143905	ESTs	SS	5.3
	403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	5.3
9Λ	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755	SS,Transglutamin_C,Transg	5.3
80	405085	A A 777304	Un 201520	Target Exon ESTs, Weakly similar to ALUC_H	SS,SS,SNF2_N,helicase_C	5.3 5.3
	438080 439091	AA777381 AA830144	Hs.291530 Hs.135613	ESTs, Weakly similar to ALUC_H ESTs, Moderately similar to I3	KH-domain	5.3 5.3
	427326	Al287878	100013	gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	5.3
	427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.3
					220	

228

	421779	Al879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.3
	408270	AW177805	11- 040000	gb:IL3-HT0059-180899-007-B06 H		5.3 5.3
	418437 409879	AA771738 BE083422	Hs.348000 Hs.56851	ESTs, Moderately similar to AL hypothetical protein MGC2668	SS,TM	5.3
5	428304	AI743177	113.00001	ESTs	SS,TM	5.3
	418678	NM_001327		cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.3
	436540	BE397032 AA054477	Hs.14468	hypothetical protein MGC14226	SS,TM	5.2 5.2
	437161 400171	AAU54477	Hs.25391	ESTs ENSP00000211797:Helicase SKI2W	SS,TM SS,proleasome	5.2 5.2
10	431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28	o ipicus sum i	5.2
	402197			Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	5.2
	449514	AW970440 AW806859	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	5.2 5.2
	442472 409679	BE250521		gb:MR0-ST0020-081199-004-c03 S ras homolog gene family, membe	SS,TM,Inos-1-P_synth,Occl SS,homeobox,CUT	5.2
15	439150	AF086006		gb:Homo sapiens full length in	SS	5.2
	412934	BE011437		gb:CM4-BN0220-080500-170-f03 B		5.2
	435186 400668	AL119470		ESTs Target Exon	SS CARD,ICE_p20,SS,ICE_p20,I	5.2 5.2
	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.2
20	445904	AW449920	Hs.248855	ESTs	SS,homeobox	5.2
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	SS,TM,ank,Adap_comp_sub	5.2
	414551 432872	AI815639 AI908984	Hs.76394 Hs.279623	enoyl Coenzyme A hydratase, sh selenoprotein X, 1	ECH,Peptidase_U7,SS,TM DUF25,SS,Ribosomal_L3,PDZ	5.2 5.2
	419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metaltoph	5.2
25	407478	L77559		gb:Homo sapiens DGS-B partial		5.2
	457892	AA744389	Lin DOCOGA	gb:ny51e10.s1 NCI_CGAP_Pr18 Ho	CDESK BOALL	5.2
	457228 437536	U15177 X91221	Hs.206984 Hs.144465	Human cosmid CRI-JC2015 at D10 ESTs	6PF2K,PGAM SS,TM,Na_Ca_Ex	5.2 5.2
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN		5.2
30	431275	T56571	Hs.10041	ESTs	SS,HLH	5.2
	428021 422400	A1022287 AA974434	Hs.111991 Hs.128353	ESTs, Weakly similar to T33900 ESTs	SS	5.2 5.2
	446442	BE221533	Hs.257858	ESTs		5.2
2.5	415585	R59946	Hs.184852	KIAA1553 protein	SS	5.2
35	438429	D16918	Hs.12547	Homo sapiens cDNA: FLJ23388 fi	TM	5.2
	401677 405637			BAI1-associated protein 3 . Target Exon	SS,TM,zf-C2H2,kinesin,Vau	5.2 5.2
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.2
40	408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.2
40	452666 401553	AW194601	Hs.13219	ESTs Target Exon	PI-PLC-X,PI-PLC-Y,C2,PH	5.2 5.2
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	zf-CCHC	5.2
	453434	AJ271378	Hs.333243	ESTs		5.2
45	450351	BE547267	Hs.59791	hypothetical protein MGC13183	SS,TM	5.2
43	411456 445634	AW847588 AI624849	Hs.344612	gb:IL3-CT0213-161299-038-G09 C ESTs, Weakly similar to NEL1_H	SS,TM vwd	5.2 5.2
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC	THO	5.2
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fi	SS,TM,EPH_lbd,pkinase,fn3	5.1
50	416470	N90464	Hs.303023	bela tubulin 1, class VI	SS,tubulin,SS	5.1 5.1
50	432022 457579	AL162042 AB030816	Hs.272348 Hs.36761	Homo sapiens mRNA; cDNA DKFZp7 HRAS-like suppressor	TM	5.1 5.1
	438484	AW021671	Hs.293330	ESTs, Weakly similar to p40 [H		5.1
	422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158,ank	5.1
55	401724 438670	Al275803	Hs.123428	C16001374:g [6755086 ref[NP_03 ESTs	TM,PLAT,SS	5.1 5.1
	414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.1
	425098	AW295349	Hs.8038	ESTs	SS,TM	5.1
	431896 416732	AW297844 H81066	Hs.101428 Hs.285017	ESTs hypothetical protein FLJ21799	SS SS	5.1 5.1
60	404571			NM_015902*:Homo sapiens proges	HECT,zf-UBR1,PABP	5.1
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 po	SS	5.1
	426358	AA376438	Un 120064	gb:EST88856 HSC172 cells II Ho	TM SS TM toyogin bringle LIDA	5.1 5.1
	456767 412915	Al086412 AW087727	Hs.129064 Hs.74823	Homo sapiens chromosome 19, co NM_004541:Homo sapiens NADH de	SS,TM,trypsin,kringle,UPA	5.1
65	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	5.1
	415886	Z42737		gb:HSC0SE081 normalized infant	SS FAD avidence C FAD bladies	5.1
	401674 424266	AA337810	Hs.149152	C16001417*:gi[7500345 pir[]T21 ESTs, Weakly similar to RHOP M	FAD-oxidase_C,FAD_blnding	5.1 5.1
	455035	AW851734	1101110102	gb:MR2-CT0222-011199-007-e10 C		5.1
70	408567	S72921		ciliary neurotrophic factor	CNTF	5.1
	436616	AW799109	Hs.226755	ESTs ESTs	14-3-3	5.1 5.1
	409078 447976	AW327515 AW972653	Hs.293691	ESTs, Highly similar to CR2_HU		5.1
7.	457720	AA992835	Hs.186776	ESTs		5.1
75	400528	DE0/0444	Un 400045	NM_020975*:Horno sapiens ret pr	cadherin,pkinase,SS	5.1
	407757 452446	BE048414 AA086123	Hs.165215 Hs.297856	hypothetical protein MGC5395 ESTs	SS,EF1G_domain,GST_C,GST_ mm,NTF2	5.1 5.1
	450807	AI739262	,	gb:wi17b08.x1 NCI_CGAP_Co16 Ho		5.1
00	432540	Al821517	Hs.105866	ESTs	SS,TM	5.1
80	449324 426434	A1638706	Hs.2041	ESTs, Weakly similar to A47582	EGF,sushi,An_peroxidase,p	5.1 5.1
	426434 407652	M17755 W27953	Hs.292911	thyroid peroxidase ESTs, Highly similar to S60712	Troponin	5.1 5.1
	443952	Al149106		ESTs	SS,pkinase	5.1
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_H	SS,TM	5.1
					229	

	422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	5.1
	407143	C14076	Hs.332329	EST	SS,TM	5.1
	442296	NM_007275		lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.1
_	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	5.1
5	427336	NM_005658		TNF receptor-associated factor	MATH, SS, MATH, A2M_N, A2M, NT	5.1
	447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.1
	400863	A1604440	11- 470025	C11002296:gi]11692557[gb]AAG39	SS,TM	5.1
	409034 421696	Al684149 AF035306	Hs.172035 Hs.106890	hypothetical protein similar t Homo sapiens clone 23771 mRNA	SS	5.1 5.1
10	427587	BE348244	Hs.284239	ESTs, Weakly similar to 178885	SS,UDPGT	5.1 5.1
10	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	5.1
	454219	X75042	Hs.44313	v-rel avian reticuloendothelio	RHD,TIG	5.1
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.1
	435902	AA701867	Hs.297726	ESTs	co, m, co classifa coas	5.1
15	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_H	SS,fibrinogen_C,Rhodanese	5.1
	454923	AW897236		gb:CM0-NN0057-150400-335-c06 N	SS,Caldesmon	5.1
	440518	AA888046	Hs.233235	ESTs	SS,TM	5.1
	448237	A1471790	Hs.309386	ESTs	TM,Ribosomal_S7	5.1
	428924	AI016405	Hs.98959	ESTs, Weakly similar to JC5314	SS,TM,lectin_c	5.1
20	412081	Z24895	Hs.293818	gb:HSB67F122 STRATAGENE Human	SS,TM,SQS_PSY,GATA	5.1
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.1
	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	5.1
	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.0
25	417151	AA194055	Hs.293858	ESTs	PH Assessment of the second	5.0
25	408307	Al761786	Hs.204674	ESTs	Armadillo_seg	5.0 5.0
	404752	AA032155	Hs.61622	NM_024778:Homo saplens hypothe ESTs		5.0 5.0
	453126 413983	BE348384	Hs.279194	ESTs		5.0
	405366	DECHOOON	113.213134	NM_003371*:Homo saplens vav 2	SS	5.0
30	412425	AW949156		gb:QV4-FT0005-110500-205-b06 F	00	5.0
50	437036	AI571514	Hs.133022	ESTs	SS,TM,Glycos_transf_2	5.0
	448455	AI252625	Hs.269860	ESTs, Moderately similar to S6	SS,TM	5.0
	411413	BE379438	Hs.211573	heparan sulfate proteoglycan 2	ig.laminin_B.laminin_EGF,	5.0
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD,SS,HSF_DNA-bind,E2F_	5.0
35	424874	AA347951		Homo sapiens cDNA FLJ20812 fis	SS .	5.0
	408023	BE018269	Hs.279688	ESTs		5.0
	411758	AW860667		gb:QV0-CT0383-210400-204-d03 C	homeobox,homeobox	5.0
	410660	AI061118	Hs.65328	Fanconi anemia, complementatio		5.0
40	427411	AA402242		ESTs	00 TH 500 / 50004	5.0
40	437018	AA889078		ESTs	SS,TM,ERG4_ERG24	5.0
	427029	AA397596	11- 42540	ESTs	SS,ras SS	5.0 5.0
	452047 432093	N35953 H28383	Hs.43510	ESTs, Weakly similar to BOX B gb:yl52c03.r1 Soares breast 3N	Band_41,ERM	5.0
	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	5.0
45	441456	Al458911	Hs.127765	ESTs	•	5.0
	414356	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1	SS,TM	5.0
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.0
	436393	AW022213		ESTs	Galactosyl_T_2	5.0
50	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960		5.0
50	448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	00711	5.0
	428079	AA421020	Hs.208919	ESTs	SS,TM,trypsin	5.0
	421951	BE327432	Hs.109804	H1 histone family, member X	20.00	5.0 5.0
55	427204 409690	AA405404 W45393	Hs.215725 Hs.55888	ESTs activating transcription facto	SS,SS	5.0
33	436574	AW293527	Hs.126465	ESTs		5.0
	457761	AW401809	Hs.4779	KIAA1150 protein	SS.LIM.SS	5.0
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis	HMG_box	5.0
	445372	N36417	Hs.144928	ESTs	SS,PID,PDZ	5.0
60	440511	AF132959	Hs.7236	eNOS interacting protein	SS,TM,MAGE,Ribosomal_S17,	5.0
	424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama	5.0
	401539			NM_002675:Homo saplens promyel	zf-B_box,zf-C3HC4,SS	5.0
	417903	NM_002342		lymphotoxin bela receptor (TNF	TNFR_c6,SS	5.0
65	442451	AI498080	Hs.129616	ESTs	SS CO Coloba and	5.0
65	450536	AI699529	11. 400544	gb:tt17a02.x1 NCI_CGAP_GC6 Hom	SS,G-alpha,arf	5.0
	425169	AW292500	Hs.128514	ESTs	SS	5.0 5.0
	435262	AA677088	tin 12004	ESTs	CTO SETU CTO SETU DO CTO	5.0 5.0
	444855 433507	BE409261 AIB17336	Hs.12084 Hs.191791	Tu translation elongation fact ESTs	GTP_EFTU,GTP_EFTU_D3,GTP_ pkinase	5.0
70	433307	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.0
, ,	438395	AA017514	Hs.6211	methyl-CpG binding domain prot	MBD,zf-CXXC,SS,zf-CXXC	5.0
	446603	NM_014835		oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	400762			Target Exon		5.0
~~	440133	AI056255	Hs.133349	ESTs		5.0
75	445903	AI347487	Hs.132781	class I cytokine receptor	· SS,TM,EF1BD	5.0
	412940	BE295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	419269	AA235838		gb:zs41b04.s1 Soares_NhHMPu_S1	TM	5.0

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TABLE 20B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	
	408117	104000_1	AL138255 BE380045 AA047314 D82381 T18585 H64978 T10798
	408215	10478_1	BE614290 AA307674 N35629 AA338538 A1193603 AA781096 AI680061 AI613258 AW276647 BE221263 AI348910 AI985031 A1090078 AI359617
-			AA666391 Al160210 Al446461 Al355345 Al343638 Al343640 Al275091 M78746 AW262795 AW250002 AA503756 Al934519 AW272086 N26520
5			AA626639
	408270	1049980_1	AW177805 AW177816 AW177901 BE141597 BE141584 AW177822 AW177818 AW177899
	408294	1050553_1	BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
	408567	10663_1	S72921 NM_000614 X55889 X60542 X60477
10	409078	1098756_1	AW327515 AW327774 AW327571
10	409164	110421_1	AA706639 AA064707 AL036920 Al651598
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
	409832	115564_1	AW963293 AI866310 AA077791 AA362540
	410445	120374_2	AA199830 AI143895 AW961629 AA322482
1.5	410471	1204721_1	T88872 AW749857
15	410895	1226051_1	AW809679 AW809678 AW810113 AW810182 AW809900 AW809851 AW810110 AW810228 AW810342 AW810181 AW809632 AW809745
			AW810372 AW809681 AW809792 AW809806 AW810452 AW809675 AW809964 AW810033 AW810111 AW809846 AW809847 AW809717
	411219	1236055_1	AW832917 AW832913 AW832906 AW832788 AW832915 AW832776
	411298	1237955_1	AW835838 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835
20	***	4040040 4	AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
20	411426	1245515_1	BE141714 AW845993 AW845989 .
	411456	1246706_1	AW847588 AW847716 AW847664 AW847592
	411490	1247426_1	R39474 AW888420 R76943
	411605	125123_2	AW006831 AA678298 R12579 W86152 AI123683 AA699780 AI672156 BE092587 AA094230 AI633815 AA526153 W86151
25	411758	1256751_1	AW850667 AW850665
23	412091	1276564_1	R06185 AW891805 AW901802 AW901805 AM901805 AW901805 AW901
	412122	127838_2	AW852707 N57282 A725075 AI703492 AW612137 AI696372 AI879394 AI653605 W26914
	412128 412173	1278726_1	AW894709 N78140 T71071 AW902279 AW897608
	412475	1280870_1 1293726_1	17/17/1 AV932/27 AV93/905 AV9349156 AW949003 AW949008
30	412423	129707_1	AX315731 N48523 AA307559 AA130794 BE296746 BE378396 AA190411 AI904194 AA311805 AI356291 AA446714 AI818924 AI609152
30	412432	125/01_1	AW771476 BE298184 AA295023 AA130708 AI078381 AA114156 AI198283 AA215665 AI201085 AI694848 AI077572 AA102778 AW016425
			A1923123 AA577072 A1671
	412777	132672_1	A333573 A1288496 AA120880
	412934	1337389_1	BED11437 BED11402 BED11495 BED11428 BED11407 BED11421 BED11406
35	413272	135718_1	AA127923 AA127846 AA534131 N53566 AA533669 AW511251 A1174441 AA127875 A1685293 AA127913 N72525 AW770386 N69010 AW070312
33	413272	100710_1	H80275 H80289 AA972923
	413534	1375357_1	BE146961 BE146780 BE146788 BE146967 BE146774 BE146963 BE146907
	413564	1376722_1	BE260120 BE148538
	414347	1437406_1	BE275935 BE390063 BE388764 BE409101
40	414371	14388_8	A1905865 BE294801 BE562308 BE297957 AW157051 A1815883 AW162529 BE439610 AW157225 AW157210 AW162675 AW161998 A1816168
,,,	11.01.		AW162599 AI816004 AI815820 AW162158 AW162339 M17733 AW157639 AI879416 BE258811 AW157436 AW162433 AW161633 AW162155
			AW157410 AW157269 AW162
	414391	1441921_1	BE409872 BE281460
	414413	1443696_1	BE294877 BE294759
45	414593	1464909_1	BE386764 BE387560
	414944	1509480_1	C15044 D80943 C15696
	415126	1523506_1	D60945 D61346 D81568 D80539 .
	415611	1540555_1	T26376 F12852 T75058
50	415886	1560411_1	Z42737 T08986 H07956
50	415958	1563222_1	H10942 Z42911 R60453
	416233	158010_1	AA176633 AW961842 AA309418
	416597		
		1603081_1	H66891 R98149 H68467
	417739	1696198_1	Z43995 R12357 R34740
55	418184	1696198_1 172744_1	Z43995 R12357 R34740 AA367375 AA486701 BE152479 BE152800 AW816961 AA214097
55	418184 418304	1696198_1 172744_1 173658_2	Z43995 R12357 R34740 AA367375 AA486701 BE152479 BE152800 AW816961 AA214097 AA215702 AA368006 AA215703 BE066555 BE006876
55	418184 418304 419269	1696198_1 172744_1 173658_2 183444_1	Z43995 R12357 R34740 AA367375 AA486701 BE152479 BE152800 AW816961 AA214097 AA215702 AA368006 AA215703 BE066555 BE006876 AA235838 BE180775
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	452113	899664_1	AND 2018 244000 HUSAN BESSON AWASSIN BEAUST AND 1200 BEAUSING MISSUN 10200 AND 110200 AN
65	453413	966269_1	AJ003294 AJ003315 AJ003293
00	453829	982731_1	AL138200 T71830 T71820
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            TABLE 20C:
            Pkey: Unique number corresponding to an Eos probeset
            Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted
10
            Nt_position: Indicates nucleotide positions of predicted exons
15
                                                            Nt position
                                            Strand
                                                            35559-36295
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                                            Plus
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                                            Minus
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                            6981824
                                            Plus
                                                            472381-472528,474170-474277,475328-475542,475878-476000
                            8118719
             400668
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20
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            400748
                                            Plus
                            8131616
                                                            7235-7605
             400762
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                                                            34896-35021,41078-41197
187599-188138
21575-22330
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                            8131629
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            400833
                            8705148
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                            9798616
                                            Plus
25
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                            9966290
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                                                            94518-94659
57211-57525
150981-152128
            400923
                            7637836
                                            Minus
            401121
401180
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9438648
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                                            Minus
                            9743387
                                                            172961-173056,173868-173928
            401203
                                            Minus
30
                                                            166969-167133,169760-169877,171563-171733
103739-103919
                            7712287
9858408
                                            Plus
            401210
             401215
                                            Plus
                            9797154
                                                            130810-130927,133367-133504
            401264
                                            Plus
             401278
                            9799936
                                                            98428-98573
                                            Plus
             401349
                            9930791
                                            Plus
                                                            72440-73030
35
            401402
401488
                            7710964
                                                            75730-76077
                                            Plus
                            7341775
                                                            54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
                                            Plus
                            7534110
                                                            71055-71259
             401507
                                            Plus
             401539
                            8072433
                                            Minus
                                                            62028-62608
83990-84161
             401553
                            8099284
                                            Minus
                                                            83990-84161
7997-8170
139786-138927,139157-139298,139440-139599,139960-140159
62856-63086,63603-63884
14386-144054
40
             401594
                            7230963
                                            Plus
             401674
                            7689903
             401677
                            9965537
                                            Minus
                            7656694
                                            Plus
             401722
             401724
                            7656694
                                            Plus
                                                            150063-150241
45
                                                            88400-89959
148234-148321,150365-150559
46329-46473
             401822
                            6730824
                            8140731
3808091
            401885
401935
                                            Plus
                                            Plus
                            6102666
                                                            151891-152032
             401938
                                            Plus
             401984
                            4454511
                                                            103825-104024
50
             402189
                            8576043
                                            Minus
                                                            128318-129601
                            8576113
                                                            199466-199585
             402197
                                            Plus
             402285
                            2689079
                                            Minus
                                                            92386-92634
             402365
                            9454515
                                            Minus
                                                            70928-71185
            402445
402501
                            9796614
9797862
                                            Plus
                                                            90925-91064,91172-91331
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                                                            8601-8876
                                            Plus
             402545
                            9838114
                                                            48547-48678,50604-50737,51384-51467
                                            Minus
                                                            174215-174380
361-474,541-687
            402651
402916
                            7960391
7406502
                                            Plus
                                            Minus
                            5441423
                                                            79403-79560,79712-80021
             403003
                                            Minus
60
                                                            122884-123018,123134-123283,123372-123695,123779-123940,124059-124256 96600-96881,96951-97280,97393-97594
             403128
                            7331426
                            7283286
7658423
             403672
                                            Minus
             403748
                                                            129503-130344
                                            Minus
             403885
                            7710403
                                                            53259-53524
                                             Minus
                                                            48636-48822
137995-138317
71040-71288
             403938
                            7711795
65
            404001
404066
                            8655948
3367505
                                             Minus
                                             Minus
             404149
                            7534008
                                             Plus
                                                             121831-121951,124044-124150
                                                            121531-121531,124044-124150
1669-2740
149189-149303
137948-138024,138111-138300
50151-50319,50859-51098
             404199
                            6010176
                                             Minus
             404311
404333
                            8570412
                                            Minus
70
                            9802821
                                             Minus
             404365
                             9964977
                                             Plus
             404430
                             7407979
                                             Plus
                                                             42921-43109
                                                            63413-63553
112450-112648
             404438
                            6984205
                                             Plus
                            7249169
             404571
                                             Minus
75
                                                             104807-105043
             404596
                             9958262
                                             Minus
                                                            56167-56342,58066-58189,58891-59048,60452-60628
45190-45339,47509-47622,48137-48264,48805-48946,50073-50345,51467-51588
             404676
                             9797204
                                             Minus
             404710
404752
                             9801097
                                             Minus
                             7109522
                                                             120168-120326
                                             Minus
             404807
                             4165210
                                                             124246-124422
                                             Minus
80
             404956
                            7387343
8072509
                                                            55883-56203
44045-44230
             405085
405113
                                             Minus
                             8096927
                                                             170073-170894
                                             Plus
                             9438278
                                                             5894-5983,7355-7427
             405143
                                             Plus
             405159
                             9966252
                                                             79659-79804
```

	405211	6692345	Minus	31340-32609
	405247	7249301	Minus	65578-65778,68088-68234
•	405346	2981263	Plus	101982-102171
_	405366	2182280	Plus	22478-22632
5	405371	2078469	Minus	47657-47766,48461-48596
	405375	1552539	Pius	11646-12050,12207-12485
	405376	1552533	Plus	28875-29099
	405473	8439781	Plus	153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-
				165259,165868-166003,167375-167552,169252-169364,171127-171281
10	405474	8439781	Plus	172005-172175
	405557	1621108	Plus	39883-40047
	405637	6289229	Plus	189852-189978
	405770	2735037	Plus	61057-62075
	405928	7717155	Minus	2923-3209
15	405931	6758795	Minus	148233-148705
	405939	6758795	Plus	170500-170654
	406109	9127147	Minus	58328-58485
	406230	4760409	Plus	71716-72515
~~	406284	7549620	Plus	74002-74199
20	406299	5686278	Minus	35655-36119
	406301	8575868	Plus	57291-57494
	406373	9256130	Plus	188922-189152
	406495	7711328	Minus	174661-174978
25	406575	7711679	Plus	142034-142473
25				

Table 21A lists about 933 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0, the "average" ovarian cancer level was set to the 95th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst variou non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). The predicted 30 protein domains are noted.

TABLE 21A: 35 Pkey: Unique Eos probeset identifier number ExAcon: Exemplar Accession number, Genbank accession number UG ID: Unigene number Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

40

	Pkey	ExAcon	UGID	Title	Pred. Protein Dom.	R1
	407223	H96850		gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	58.9
	421296	NM_002666	Hs.103253	perilipin	perilipin.SS	47.6
45	430281	A1878842	Hs.237924	CGI-69 protein	mito_carr,SS,TM	46.7
	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldi_recept_a,trypsi	41.0
	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	37.1
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	35.6
	438424	Al912498	Hs.25895	hypothetical protein FLJ14996	SS.TM	35.3
50	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS	34.4
• •	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS.TM.zf-DHHC	33.9
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS.PAS.HLH	32.5
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	30.5
	452849	AF044924	Hs.30792	hook2 protein	bZIP.SS.AhpC-TSA	29.6
55	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	28.2
	416819	U77735	Hs.80205	pim-2 oncogene	pkinase,SS,TM,OTU,K_tetra	27.9
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	27.7
	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	27.5
	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	27.2
60	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS.PWWP.Exonuclease.lipoc	26.8
•	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	26.5
	419451	Al907117	Hs.90535	syntaxin binding protein 2	Sec1,SS,TM	25.1
	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG, SS, TM, MAPEG	25.1
	407893	BE408359	Hs.43621	Homo saplens, Similar to hypot	SS,SS,arf,ras,fn3,ras	25.0
65	412674	X04106	Hs.74451	catpain 4, small subunit (30K)	efhand,SS,CAP_GLY	24.4
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	24.3
	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	24.0
	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	23.1
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	23.0
70	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	23.0
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	22.4
	427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	22.2
	407117	AA146625		gb:zo71c07.s1 Stratagene pancr	SS	21.3
	402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	20.8
75	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase, SS, TM	20.7
	422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.6
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	20.1
	453157	AF077036	Hs.31989	DKFZP586G1722 protein	SS, Tropomyosin	20.0
	422179	AF091619	Hs.112667	dynein, axonemal, intermediate	WD40,SS	20.0
80	419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	19.5
	416893	AA455588	Hs.62406	hypothetical protein FLJ22573	SS,rrm,SS	19.2
	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	19.1
	411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	18.9
	422305	A1928242	Hs.293438	ESTs, Highly similar to AF1984	SS	18.8
			•	* *		

	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS	18.6
	406663	U24683		immunoglobulin heavy constant	SS.	18.5
	429712	AW245825	Hs.211914	ENSP00000233627":NADH-ubiquino	oxidored_q6,SS,TM,rrm	18.5
_	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	GST_C,GST_N,Tropornyosin,S	18.4
5	447151	AI022813	Hs.92679	Homo sapiens done CDABP0014 m	SS,TM,LRR,aminotran_1_2	18.4
	413343	8E392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	18.2
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	17.7
	427721	AI582843	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	17.6
10	443780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	17.2
10	421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a,SS,TM	17.1 16.7
	444607	AW405635	Hs.293687	ESTs	SS,PI-PLC-X,PH,PI-PLC-Y,C SS	16.6
	406621	X57809	Hs.181125	immunoglobulin lambda locus		16.6
	443496 440104	AJ006973 AA132838	Hs.9482	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxygenase SS,DS	16.3
15	427640	AF058293	Hs.239894 Hs.180015	hypothetical protein MGC2803 D-dopachrome tautomerase		16.2
IJ	445625	BE246743	ns.100015	hypothetical protein FLJ22635	MIF, Late_protein_L2, SS, GS SS, TM	16.1
	443625 427461	AA531527	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	15.9
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
	409017	T86957	Hs.272299	hypothetical protein RP4-622L5	SS,TM	15.6
20	428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	15.5
20	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	15.5
	400460	DLZJUUTU	113.37770	C11002253*:gi[129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	15.4
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	15.4
	406918	M88357	113.00020	gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	15.4
25	435158	AW663317	Hs.65588	DAZ associated protein 1	mm,SS,mm	15.3
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	15.3
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	15.1
	402365	7		Target Exon	SS,SS,TM,ig	14.9
	450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	14.8
30	427502	AI811865	Hs.7133	Homo saplens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	14.6
	432872	A1908984	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	14.5
	416897	M78146	Hs.324700	hypothetical protein MGC2663	SS .	14.3
~ ~	447304	Z98883	Hs.18079	phosphalidylinositol glycan, c	SS,Peptidase_C2	14.2
35	431543	AW969619	Hs.259768	adenylate cyclase 1 (brain)	TM	14.0
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	14.0
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	13.8
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	13.8
40	412623	R28898	Hs.74170	metallothionein 1E (functional	SS,TM,metalthlo,DEAD,meta	13.7
40	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	13.5
	453367	AW732847	Hs.70573	PKCI-1-related HIT protein	SS,TM .	13.5
	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	13.2
	408724	AI685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	13.2
45	423464	NM_016240	Hs.128856	CSR1 protein	Collagen,SS	13.1
43	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	13.0
	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	12.9
	438857	AI627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	12.8
	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS SS TM:	12.8 12.6
50	427527	A1809057	Hs.153261	immunoglobulin heavy constant	SS,TM,ig	12.5
50	430168 437543	AW968343 H16443	Us 7447	DKFZP434I1735 protein glutamate receptor, ionotropic	SS,TM,efhand,efhand SS,TM,lig_chan,ANF_recept	12.4
	413711	AW291765	Hs.7117 Hs.75486	heat shock transcription facto	NA,SS,E2F_TDP	12.3
	422625	AW504698	Hs.155976	cultin 48	SS,SS,Cullin,Cullin	12.2
	443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	Exostosin, SS, TM	12.1
55	407143	C14076	Hs.332329	EST	SS,TM	12.1
-	424707	BE061914	Hs.10844	Homo sapiens cDNA FLJ14476 fis	SS,SS,TM,Sema	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	12.0
	421572	· AA531607		hypothetical protein FLJ22678	SS,TM,TGF-beta,ASC	12.0
60	447946	AI566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	11.9
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	11.7
	427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	11.7
	427397	Al929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	11.7
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	11.7
65	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
	447451	Al379925	Hs.207525	ESTs	SS.pkinase,PH.pkinase_C	11.5
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,homeobox,UPF0160,DUF23	11.4
	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	11.3
70	419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	11.3
70	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	11.3
	422178	AL122083	Hs.112645	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	11.2
	450122	BE313765	Hs.343443	ESTs, Weakly similar to 138022	SS,TM,Y_phosphatase,LON,A	11.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	11.1
75	444744	BE394732	Hs.147562	ESTs	SS	10.9
75	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	10.9
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	10.9
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	10.8
	450593	AF129085	Hs.25197	STIP1 homology and U-Box conta	TPR,SS,TM,Rhomboid,lactam	10.7
80	406837	R70292	Hs.156110	immunoglobulin kappa constant C-type lectin-like receptor-1	SS lactin a SS TM	10.7 10.7
50	452434	D30934	Hs.29549	Homo sapiens, clone IMAGE:3940	lectin_c,SS,TM SS,TM,SS,TM,Peptidase_M22	10.7
	440150	AW975738	Hs.7001	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	10.6
	418641	BE243136 NM_004371	Hs.86947 He 75897	coatomer protein complex, subu	WD40,SS,WD40,Ribosomal_S2	10.6
	414313 420307	AW502869	Hs.75887 Hs.66219	ESTs	SS,TM	10.6
	420307	V11005003	110.002.10		00,	.0.0

	414918	Al219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	10.6
	446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	10.5
	419846	NM_015977	Hs.285681	Williams-Beuren syndrome chrom	SS,HLH,SS,TM,WD40	10.4
	453023					10.4
5		AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	
,	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	10.3
	431275	T56571	Hs.10041	ESTs	SS,HLH	10.3
	407241	M34516		gb:Human omega light chain pro	SS,ig,PH,ig,PH	10.3
	441238	Al372555	Hs.322456	hypothetical protein DKFZp761D	homeobox,SS,TM,Rho_GDI,th	10.3
	436325	AL390088	Hs.7393	hypothetical protein from EURO	SS,Synapsin_C,SS	10.3
10	435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	10.3
	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	10.3
	425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
	415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	Nol1_Nop2_Sun,SS,SNF2_N,h	10.2
15	414874	D26351	Hs.77515	inositol 1,4,5-triphosphale re	TM,RYDR_ITPR,ion_trans,MI	10.2
10	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
	434552	AA639618	Hs.325116		SS	10.2
				Homo sapiens, clone MGC:2962,		
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	SS	10.1
20	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	10.1
20	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU p	SS,F5_F8_type_C,EGF,TGT	10.1
	427672	AA356615	Hs.336916	death-associated protein 6	SS,BTB,abhydrolase_2,RasG	10.0
	423218	NM_015896	Hs.167380	BLu protein	zf-MYND,SS,TM,Glyco_hydro	10.0
	403028			Target Exon	SS,trefoil	10.0
	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	10.0
25	419823	AW271708	Hs.118918	-ESTs, Weakly similar to M2OM_H	SS,TM	10.0
	433886	AA613596	Hs.28412	ESTs	SS	9.9
	428092	AW879141		ESTs	SS,TM	9.8
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
	420423	AA827718	Hs.88218	ESTs	SS SINGING TO LINGING ITS	9.7
30	452302				SAND.SS	
20		AF173867	Hs.28906	glucocorticoid modulatory elem		9.7
	444681	AJ243937	Hs.288316	chromosome 6 open reading fram	notch,EGF,ank,GoLoco,SS,T	9.7
	414249	A1797994	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,ig,IRK,SS,TM,fn3,ig,R	9.6
25	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	9.6
35 ·	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	9.6
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc,TM	9.6
	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Glyco_hydro_31,G	9.5
	444633	AF111713	Hs.286218	iunctional adhesion molecule 1	ig,SS,TM,HLH	9.4
40	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	9.4
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	9.4
	400201	1142313	115.7 0003			9.4
		A14/04772C	11- 404047	NM_006156*:Homo sapiens neural	ubiquitin,SS,TM,Transglut	
45	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	9.4
45	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,nm,GA	9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinase,SS	9.4
	407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.4
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	9.4
50	411674	AW861123		gb:RC3-CT0297-120200-014-a05 C	SS	9.3
50	414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx,SS,ras,HLH	9.3
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	9.3
	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	9.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,histone	9.1
	412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	9.1
55	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GDSL,SS,	9.1
	412104	AW205197	Hs.240951	Homo saplens, Similar to RIKEN	SS,TM	9.1
	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran,SS	9.1
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	9.0
	418776	Al401004	Hs.88411	lymphocyte antigen 117	SS,TNF,TNF	9.0
60	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM,CaMBD,SK_channel,TM	9.0
00	419244	AJ436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE,SS,rrm,Ephrin	8.9
	451855	R54913	Hs.175804	ESTs	SS,TM,vwa	8.9
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogiuta · KIAA1319 protein	20G-Fell_Oxy,Glycos_trans	8.9
65	447374	AF263462	Hs.18376		SS,Myosin_tail,M	8.9
05	430167	Y08976	Hs.234759	FEV protein	Ets,SS,crystall	8.8
	409936	AK001691	Hs.57655	hypothetical protein FLJ 10829	SS,TM	8.7
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	8.7
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	8.7
5 0	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	8.7
70	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	8.7
	433333	Al016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	8.7
	423228	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	8.7
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	8.7
	420160	AI492840		ESTs	SS,TM ·	8.6
75	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	8.6
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphalase,fn3.iq,MAM,	8.6
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	SS	8.6
	418678	NM_001327	Hs.167379	cancer/lestis antigen (NY-ESO-	SS,TM,zf-C2H2	8.5
			Hs.278728	Rad and Gem-related 2 (rat hom		
80	458963	AI701393			ras,SS,Peptidase_M10,hemo	8.5
90	406868	AA505445	Hs.300697	immunoglobulin heavy constant	SS,TM,ig	8.3
	434105	AW952124	Hs.13094	presentlins associated rhombol	TM,Rhomboid,SS,TM	8.3
	421726	AK001237	Hs.319088	hypothetical protein FLJ10375	TM	8.3
	421707	NM_014921	Hs.107054	lectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
	453898	AW003512	Hs.232770	arachidonale lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	8.2
				226		

	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	8.2
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	8.2
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon,SS,Ribosomal_S2	8 <u>-1</u> ·
_	444341	AI142027	Hs.146650	ESTs	SS,TM,Reprolysin,Pep_M12B	8.0
5	413762	AW411479 ·	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	8.0
	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,pkinase,Activin_rec	8.0
	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697	SS,bZIP_Maf	8.0
	431493	AI791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	7.9
10	447598	AI799968	Hs.199630	ESTs	SS,TM	7.9
10	415758	BE270465	Hs.78793	protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
	457022	AW377258		gb:MR2-CT0222-261099-003-a10 C	SS,Ribosomal_L7Ae	7.8
	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr	7.8
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.8
1.0	441084	W24563	Hs.9911	hypothetical protein FLJ11773	SS,TM,hormone_rec,zf-C4	7.8
15	424443	Al751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	7.7
	424198	AB029010	Hs,143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Caix-beta,	7.6
	430513	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	7.6
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	7.6
20	432891	AF161483	Hs.279761	HSPC134 protein	SS,TM,ubiquitin,Transglut	7.5
20	432234	AA531128	Hs.115803	ESTs	SS	7.5
	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	7.5
	441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,7tm_1	7.5
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	7.5
0.5	418256	AW845318	Hs.12271	f-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
25	457274	AW674193	Hs.227152	-mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	7.5
	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q,Collagen,SS	7.4
	431934	AB031481	Hs.272214	STG protein	SS	7.4
20	418349	NM_001383	Hs.84183	diptheria toxin resistance pro	Diphthamide_syn,SS	7.4
30	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	7.3
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
	412841	AI751157	Hs.101395	hypothetical protein MGC11352	SS,TM	7.3
	418313	BE244231	Hs.84038	. CGI-06 protein	SS,wap	7.3
25	429367	AB007867	Hs.278311	plexin B1	Sema,PSI,TIG,SS,TM,TIG,Se	7.3
35	418837	U48263	Hs.89040	prepronociceptin	Opiods_neuropep,SS	7.2
	423015	U18548	Hs.123034	G protein-coupled receptor 12	TM	7.2
	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK,SS,TM	7.2
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	SS,TM,ACAT	7.2
40	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	7.2
40	446143	BE245342	Hs.306079	sec61 homolog	secy,SS,TM	7.2
	417704	NM_001747	Hs.82422	capping protein (actin filamen	Gelsolin, SS, Gelsolin	7.2
	440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	7.1
	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
15	438856	N40027	Hs.7473	ESTs	SS,TM,connexin	7.1
45	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase,pkinase	7.1
	418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	7.1
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevislae	S1,SH2,Ribosomal_L23,pkin	7.1
	421748	NM_014718	Hs.107809	KIAA0726 gene product	cadherin,TM,TPR	7.1
50	413837	AW163525	11 474004	titin-cap (telethonin)	SS,Methyltransf_3	7.0
50	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	pkinase,SS,UCH-2,UCH-1,rr	7.0
	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	7.0
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	7.0
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
55	428156	BE269388	Hs.182698	mitochondrial ribosomal protei	SS	7.0
55	459255	Al493244	Hs.239500	hypothetical protein MGC13114	SS	7.0
	441323	AA928413	Hs.159089	ESTs, Weakly similar to ALU7_H	SS,Peptidase_C1,zf-C2H2	6.9 6.9
	455928	BE170313	11- 005720	gb:QV4-HT0536-040500-193-g02 H	SS	6.9
	420856	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,ig,pkinase TM	6.9
60	421543	AK000519	Hs.105606 Hs.8186	hypothetical protein FLJ20512		6.9
OO	442296 445937	NM_007275		lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc GalactosyI_T_2,SS,TM,tsp_	6.9
•		AJ452943 AW629604	Hs.321231 Hs.167641	UDP-Gal:betaGlcNAc beta 1,4- g hypothetical protein from EURO	SS,TM,SS,TM,A2M,A2M_N,NTR	6.8
	439732		Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	GalactosyL_T_2,ig,SS,TM,A	6.8
	429542 420190	AF038660 AI816209	Hs.95867	hypothetical protein EST00098	SS,dynamin_2,dynamin,PH,G	6.8
65			ns.55007	syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	6.7
05	408215 410277	BE614290 R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	6.7
		AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
	419667		115.52200	ESTs	SS,TM	6.7
	448677 425228	A1560769 NM_005253	Hs.301612	FOS-like antigen 2	bZiP,SS	6.6
70	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
, 0	421864	BE387198	Hs.108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
		M69113	Hs.226795	glutathlone S-transferase pi	GST_C,GST_N,SS,efhand	6.6
	429962 406867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	6.6
	426068	AF029778	Hs.166154	lagged 2	DSL,EGF,vwc,granulin,SS,T	6.5
75	420000	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bl	6.5
, ,		AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,7tm_	6.5
	424681	NM_002342	Hs.1116	lymphotoxin beta receptor (TNF	TNFR_c6,SS	6.5
	417903	BE502835	Hs.15463	Homo sapiens, clone IMAGE:2959	SS,efhand	6.4
	423876	AA431176		ribosomal protein S15	TM,SS,TM,TPR,ras	6.4
80	433439	AW175787	Hs.133230	selenium binding protein 1	SS,RFX_DNA_binding	6.4
90	441379	BE614192	Hs.334841	melanoma-associated antigen re	SS,TM,RGS,DIX	6.4
	432968		Hs.279869	ESTs	fusion_gly,homeobox,TM	6.4
	456863	T16837	Hs.4241	macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
	432269	NM_002447 AW410656	Hs.2942 Hs.159161	Rho GDP dissociation inhibitor	Rho_GDI,homeobox,SS,Cytid	6.4
	425676	OCCUPATE	110.100101	THE GOT GISSOCIATION MINUSION	rate_continumentox,55,0ytt	U.4

	443420	R06846	Hs.191208	ESTs	SS	6.4
	436322	AL355092	Hs.120243	parvin, gamma	CH,SS,TM,CTF_NFI	6.4
	440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-El_box	6.4
_	447665	BE044245	Hs.30011	hypothetical protein MGC2963	SS,TM	6.3
5	431785	AA292385	Hs.268763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
	422714 434916	AB018335 AF161383	Hs.119387 Hs.284207	KIAA0792 gene product	DUF221,SS,TM,TGFb_propept TM	6.3 6.3
	414551	AI815639	Hs.76394	Homo saplens, Similar to RIKEN encyl Coenzyme A hydratase, sh	ECH.Peptidase_U7.SS.TM	6.3
	413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isodh,SS	6.3
10	458367	AA088470	Hs.83135	Homo saplens, Similar to RIKEN	SS,tRNA-synt_2d	6.3
	415010	NM_004203	Hs.77783	membrane-associated tyrosine-	pkinase,SS,PMP22_Claudin	6.3
	410076	T05387	Hs.7991	ESTs	SS	6.3
	412940	BE295701	Hs.819	homeo box 97	hameobox,SS,hameobox,home	6.2
15	440042	AI073387	Hs.133898	ESTs gb:TCBAP1D1053 Pediatric pre-B	SS SS	6.2 6.2
13	414023 414513	BE243628 AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	6.2
	446662	NM_013323	Hs.15827	sorting nexin 11	PX.SS	6.2
	409882	AJ243191	Hs.56874	heat shock 27kD protein family	HSP20,SS,TM,zf-C2H2,BTB,E	6.2
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin,SS,TM,G6PD,G6PD	6.2
20	447507	H59696	Hs.18747	POP7 (processing of precursor,	SS,TM,WD40,vwd,MAM,EPO_TP	6.2
	453447	AW771318	Hs.326586	hypothetical protein MGC11134	SS,TPR	6.1
	435968	AW161481 X14850	Hs.111577	integral membrane protein 3	TM histone,CBFD_NFYB_HMF,SS,	6.1 6.1
	424441 434558	AW264102	Hs.147097 Hs.39168	H2A histone family, member X 'ESTs	SS,TM,LRRCT,LRR	6.1
25	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	432183	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	6.0
	444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,syna	6.0
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	6.0
20	407704	BE315072	Hs.78768	malignant cell expression-enha	TM,MBOAT,SS,TM	6.0
30	453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN,SS	6.0
	439975 449514	AW328081 AW970440	Hs.6817 Hs.23642	inosine triphosphatase (nucleo protein predicted by clone 236	Ham1p_like,SS SS,PX,arf,lipocalin,PHD,z	6.0 6.0
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	6.0
	414362	Al347934	Hs.75932	N-ethylmalelmide-sensitive fac	NSF,SS,TM	6.0
35	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	427988	AA789333	Hs.181349	hypothetical protein 628	SS,SS	6.0
	423473	H49104	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,rrm,ENTH	6.0
	406773	AAB12424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.9 5.9
40	409938 424959	AW974648 NM_005781	Hs.153937	gb:EST386752 MAGE resequences, activated p21cdc42Hs kinase	SS,Adap_comp_sub,GYF pkinase,SH3	5.9 5.9
40	453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,ion_trans	5.9
	452094	AF049105	Hs.27910	centrosomal protein 2	bZIP,5_3_exonuclease,M,SS	5.9
	451524	AK001466	Hs.26516	hypothetical protein FLJ 10604	SS,SS,TM,pkinase,pkinase_	5.9
15	427438	AW328515	Hs.178011	hypothetical protein FLJ20257	SS,TM	5.9
45	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,PWWP,TSC22	5.9
	440511 417334	AF132959 AA337572	Hs.7236 Hs.157240	eNOS interacting protein hypothetical protein MGC4737	SS,TM,MAGE,Ribosomal_S17, SS,TM,ion_trans	5.9 5.9
	425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	5.8
	433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
50	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	TM,SET	5.8
	410239	AI568350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	5.8
	458060	R95860	Hs.293629	hypothelical protein MGC3121	SS SS TM I IM hamashay	5.8 5.8
	409591 409686	AA532963 AK000002	Hs.9100 Hs.55879	Homo sapiens cDNA FLJ13100 fis Homo sapiens mRNA; cDNA DKFZp4	SS,TM,LIM,homeobox SS,ABC_tran,SS,TM	5.8
55	450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran,SS,TM,HSP	5.8
	423612	NM_002067	Hs.1686	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	5.8
	422701	NM_014699	Hs.119273	KIAA0296 gene product	zf-C2H2,GST_C,PHD,SS,TM,H	5.8
	412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	5.8
60	436957	AA902488	Hs.122952	ESTs	SS,DAGKc,DAGKa,RA,DAG_PE-	5.8
.60	423158	H97991	Hs.193313	Target CAT cyclin-dependent kinase (CDC2-	MoaA_NifB_PqqE,SS,TM pkinase	5.8 5.8
	414788 420904	X78342 AL035964	Hs.77313 Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4,SS,DNA_	5.7
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA	pkinase	5.7
	420508	AJ270993	Hs.98428	homeo box B6	homeobox,SS,homeobox,home	5.7
65	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	5.7
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2	TM	5.7
	451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM SS	5.7 5.7
	453054 415117	AI878908 AF120499	Hs.31547 Hs.78016	Target CAT polynucleotide kinase 3'-phosp	Viral_helicase1.SS,Amino_	5.7 5.7
70	413163	Y00815	Hs.75216	protein tyrosine phosphalase.	fn3,ig,Y_phosphatase,SS,T	5.7
	425246	AI085561	Hs.155321	serum response factor (c-fos s	SRF-TF,flavodoxin,SS,TM,p	5.7
	433271	BE621697	Hs.14317	nucleolar protein family A, me	SS,TM	5.7
	448484	BE613340	Hs.334725	Homo saplens, Similar to RIKEN	TM,SS,TM,Kunitz_BPTI	5.7
75	449139	BE268315	Hs.23111	phenylalanine-IRNA synthetase-	neur,SS,zf-C2H2,DNase_II	5.7
75	449181 414457	X96783 AW514320	Hs.23179 Hs.76159	synaptotagmin V ATPase, H transporting, lysoso	C2,SS,TM,Y_phosphatase,Tr ATP-synt_C,SS,TM,pkinase	5.6 5.6
	414457 424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	5.6
	407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	5.6
80	413049	NM_002151	Hs.823	hepsin (transmembrane protease	trypsin,SS,TM,ATP1G1_PLM_	5.6
	454252	H50256	Hs.63236	ribosomal protein S15a	SS	5.6
	431787	AW972024	Hs.343661	ret finger protein	SS,WD40,pkinase	5.6
	431607 406782	AB033097 AA430373	Hs.183669	KIAA1271 protein gb:zw20f11.s1 Soares ovary tum	SS,TM . SS	5.6 5.6
	700102		•			0.0
				238		
				•		

					aa = 11	
	444364	AL137294	Hs.10964	hypothetical protein FLJ22351	SS,TM,pkinase	5.6
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	5.5
	443759	BE390832	Hs.134729	FXYD domain-containing ion tra	SS,TM,ATP1G1_PLM_MAT8,ATP	5:5 ·
_	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N,SS,thi	5.5
5	406673	M34996	Hs.198253	major histocompatibility compl	SS,TM,MHC_II_alpha,ig,SS,	5.5
	415351	U44755	Hs.78403	small nuclear RNA activating c	SS,TM,pkinase	5.5
	411030	BE387193	Hs.67896	7-60 protein	SS, Collagen, Collagen	5.5
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein	zf-C3HC4,SS,SNF2_N,helica	5.5
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA,SS,TM	5.5
10	437741	BE561610	Hs.5809	putative transmembrane protein	SS,TM,SS,TM,RA,VPS9,SH2	5.5
10		X55079				5.4
	421883		Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31,SS	
	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	5.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	5.4
1.0	457313	AF047002	Hs.241520	transcriptional coactivator	SS,rm,SS,Cytidylyltransf	5.4
15	428345	AI242431	Hs.118282	PAP-1 binding protein	SS,TM	5.4
	434845	BE267057	Hs.325321	hypothetical protein R32184_1	SS,TM,CH,calponin,ARID	5.4
	427162	AB011133	Hs.173864	KIAA0561 protein	SS,pkinase,PDZ,SS,SH2,Rho	5.4
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	SS,TM	5.4
	433676	AW371389	Hs.250173	hypothetical protein FLJ13158	SS	5.4
20	424373	AJ133798	Hs.146219	copine VII	C2,SS	5.4
20	423402	BE167615	Hs.141556	Homo sapiens cDNA FLJ12976 fis	SS	5.4
						5.4 5.4
	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	
	450184	W31096	Hs.237617	Homo saplens, clone IMAGE:3447	SS CUID CUID	5.3
25	431629	AU077025	Hs.265827	Interferon, alpha-inducible pr	pkinase,SH2,SH3	5.3
25	430413	AW842182	Hs.241392	.şmall inducible cytokine A5 (R	IL8,SS	5.3
	440333	A1378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	5.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	5.3
	412276	BE262621	Hs.73798	macrophage migration inhibitor	MIF,SS,TM,MIF,sugar_tr	5.3
	416181	AA174126	Hs.332163	ESTs	SS,TM,GalP_UDP_transf,Gal	5.3
30	440609	Al287585	Hs.7301	G protein pathway suppressor 2	SS,Acyt-CoA_dh,Acyt-CoA_d	5.3
-	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	5.2
	421139	AW953933	Hs.301372	KIAA1552 protein	SS,TM	5.2
		W16752	Hs.32981	sema domain, immunoglobulin do	SS,Sema,ig,PSI,SS,TM,G-al	5.2
	453449					
25	414411	X54079	Hs.76067	heat shock 27kD protein 1	HSP20,SS	5.2
35	440906	AW161556	Hs.240170	hypothetical protein MGC2731	SS,TM,Furin-like,pkinase,	5.2
	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	5.2
	439473	Al215529	Hs.144787	ESTs	SS	5.2
	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	5.2
	407191	AA608751		gb:ae56h07.s1 Stratagene lung	SS,Peptidase_C1	5.2
40	427515	T79526	. Hs.179516	Integral type I protein	EMP24_GP25L,SS	5.2
	405325		* ********	C14000786*:gij7023514[dbj BAA9	SS .	5.2
	434119	AF193844	Hs.3758	COP9 complex subunit 7a	SS	5.1
	413052	BE249841	110.07.00	gb:600942857F2 NIH_MGC_15 Homo	TM,SS,TM	5.1
		AF039916	Hs.12330		SS,TM,GDA1_CD39,SS,TM,pho	5.1
45	445109			ectonucleoside triphosphate di		
45	409323	H28855	Hs.53447	Homo sapiens mRNA; cDNA DKFZp7	TPR,SS,TM,pkinase,lg	5.1
	438707	L08239		amino acid system N transporte	SS,TM,ACAT,MBOAT,SS,TM,TB	5.1
	442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank,SS,TM,HHH,ig	5.1
	420372	AW960049	Hs.293660	Homo sapiens, done IMAGE:3535	SS	5.1
~ ^	436576	AI458213	Hs.77542	ESTs	SS,TM,7tm_1,DnaJ	5.1
50	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	AAA,DnaB,UPF0079,SS,Cys_k	5.1
	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	5.1
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase .	5.1
	425743	BE396495	Hs.159428	BCL2-associated X protein	Bcl-2,SS,ferritin,Bcl-2,e	5.1
	418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM,SS,TM,zf-UBP,UCH-2,UB	5.0
55	419238	AW959538	Hs.321214	hypothetical protein DKFZp564D	SS,TM,WH2	5.0
	441917	A1989925	Hs.24891	ESTs, Highly similar to unknow	SS,TM,Ammonlum_transp	5.0
	437617	At026701	Hs.5716	KIAA0310 gene product	SS,zf-C3HC4,Peptidase_M16	5.0
	412867	AU076861	Hs.74637	testis enhanced gene transcrip	UPF0005,SS,TM	5.0
			Hs.296200	hypothetical protein AF053356_	MSP_domain,SS,TM,CUB,NTR, .	5.0
60	419579 425824	W49529 Al939563	Hs.159589	ESTs, Moderately similar to RE	SS,PHD	5.0 5.0
00					SS,SS,TM,GDI,Sema,TIG,PSI	5.0 5.0
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysoso		
	436042	AF284422	Hs.119178	cation-chloride cotransporter-	SS,TM,aa_permeases,SS,TM,	5.0
	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD,SS,TM,REJ,PLAT,PK	5.0
c=	453350	Al917771	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	4.9
65	400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
	426811	BE259228	Hs.172609	nucleobindin 1	efhand,SS,TM,GFO_IDH_MocA	4.9
	421179	U72664	Hs.148495	proteasome (prosome, macropain	UIM,SS,TM,PMP22_Claudin,P	4.9
	429762	Al346255	Hs.216354	ring finger protein 5	SS,zf-C3HC4,Palm_thioest	4.9
	419250	AW770185		U5 snRNP-specific protein, 116	SS,TM,7tm_1,BAH,zf-CXXC,D	4.9
70	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.9
. •	442103	AA333367	Hs.8088	similar to S. cerevisiae Sec6p	SS	4.9
	414820	AA371931	Hs.77422	proteolipid protein 2 (colonic	SS	4.9
		AA454912	Hs.169407	SAC2 (suppressor of actin muta	SS,RasGEF,RA,RasGEFN,horm	4.9
	426347					
75	423880	BE278111	Hs.134200	DKFZP564C186 protein	UPF0120,SS,TM	4.9
75	429545	AI824164		lymphocyte antigen 6 complex,	SS,TM	4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N,SS,TM	4.9
	417080	BE392846	Hs.1063	small nuclear ribonucleoprotei	SS,S10_plectin	4.8
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.8
• •	410182	NM_001983	Hs.59544	excision repair cross-compleme	HHH,SS,SH3,ank	4.8
80	456062	A1866286	Hs.71962	ESTs, Weakly similar to B36298	SS	4.8
	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.8
	408985	BE267317	Hs.332040	hypothetical protein MGC13010	SS,TM,ACAT,LRR	4.8
	416976	BE243985	Hs.80680	major vault protein	Vault, SS,TM, kinesin, zf-C2	4.8
		AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.8
	436057	AND TOUR	113.3039	manapant migor esteroso	CHAM TOWNSHIP LINICIANS, TO	7.0

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	424501	Al470163	Hs.323342	actin related protein 2/3 comp	SS,HhH-GPD	4.8
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957	SS,EF1BD,P5CR	4.8
	432716	AI762964	Hs.205180	ESTs ,	SS,TM pkinase,SS,WD40	4.8 4.8
5	414460 443329	L00727 BE262943	Hs.898 Hs.9234	dystrophla myotonica-protein k hypothetical protein MGC1936	SS,TM,SS,TM,gpdh,gpdh_C	4.0
,	426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.7
	405356		1.0.110000	ENSP00000247029*:SEBOX.	SS,TM,hemopexin,Somatomed	4.7
	437118	AB037857	Hs.300591	CD9 partner 1	TM,ig,SS,TM	4.7
10	430609	AA302921	Hs.247362	dimethylarginine dimethylamino	SS,TM,GST_C,abhydrolase	4.7
10	447131	NM_004585	Hs.17466	retinolo acid receptor respond	SS,TM,pkinase	4.7 4.7
	428469 405189	BE549205	Hs.184488	flotillin 2 Target Exon	Band_7,Flotillin,TM SS	4.7
	404256			NM_024018*:Homo sapiens butyro	SS,TM,SPRY,SPRY,lg	4.7
	457955	A1208986	Hs.121647	ESTs	SS,zf-B_box,SPRY,SS,NoI1_	4.7
15	413201	BE275378	Hs.13972	hypothetical protein MGC12972	SS,SH2,RhoGAP,SH3,GILT	4.7
	431115	AB015427	Hs.250493	zinc finger protein 219	zf-C2H2,SS	4.7
	442414 418289	BE408758 AW403103	Hs.8297	ribonuclease 6 precursor Hermansky-Pudlak syndrome	ribonuclease_T2,SS,ribonu SS	4.7 4.6
	436730	AA045767	Hs.83951 Hs.5300	bladder cancer associated prot	SS	4.6
20	444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept	4.6
	433019	Al208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP,SS	4.6
	431522	AI625859	Hs.258609	protein tyrosine phosphalase,	fn3,Y_phosphatase,SS,TM	4.6
	400846	T70045	11- 400040	sorfilin-related receptor, L(D	ldi_recept_a,fn3,ldl_rece SS	4.6
25	422154 420321	T79045 D78761	Hs.168812 Hs.96657	`ESTs _hyothetical protein	SS,tsp_1,SS	4.6 4.6
23	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	SS,LACT,SS,TM,aa_permease	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
	426899	AL043221	·Hs.172825	KIAA1037 protein	WD40,TPR,SS,TM	4.6
20	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN	SS,TM	4.6
30	412974 426510	R18978 AW861225	Hs.75105 Hs.110613	emopamil-binding protein (ster BANP homolog, SMAR1 homolog	SS,TM,SS,TM,TBC,mm,FtsJ TM	4.6 4.6
	414702	L22005	Hs.76932	cell division cycle 34	UQ_con,SS,trypsin,ig	4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4,SS,p450,Ge	4.6
~ ~	445637	W58459	Hs.8949	hypothetical protein MGC4172	SS	4.6
35	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unkn	SS	4.6
	409680	W31092	Hs.55847	mitochondrial ribosomal protei	SS,TM,synaptobrevin	4.6 4.6
	421140 413407	AA298741 Al356293	Hs.102135 Hs.75339	signal sequence receptor, delt Inositol polyphosphate phospha	Herpes_UL3,SS,TM,Sema,pki SH2,SAM,SS,Folate_rec	4.6
	402463	ANOULU	113.73003	NM_014624:Homo sapiens S100 ca	efhand,S_100,SS,efhand,S_	4.5
40	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc	SS,PGAM	4.5
	406939	M34515		gb:Human omega light chain pro	SS,ig,PH	4.5
	417891	W79410	Hs.82887	protein phosphatase 1, regulat	SS,TFIIS SS	4.5 4.5
	426207 423664	BE390657 NM_004714	Hs.30026 Hs.130988	HSPC182 protein dual-specificity tyrosine-(Y)-	pkinase,SS,Fibrillarin,CK	4.5
45	432562	BE531048	Hs.278422	DKFZP586G1122 protein	zf-C2H2,SS,TM,FG-GAP,Inte	4.5
	427391	W60675		hypothetical protein FLJ10350	SS,SS	4.5
	432893	NM_016154	Hs.279771	Homo sapiens clone PP1596 unkn	ras,arf,SS,2OG-Fell_Cxy,2	4.5
	424954	NM_000546	Hs.1846	tumor protein p53 (U-Fraumeni	P53,SS	4.5
50	413815 448963	AL046341 AA459796	Hs.75562 Hs.331247	discoidin domain receptor fami Homo sapiens, clone IMAGE:3610	F5_F8_type_C,pkinase,SS,T SS,TM	4.5 4.5
50	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr,SS	4.5
	421962	D82061	Hs.288354	FabG (beta-ketoacyl-[acyl-carr	SS,adh_short,SS,TM,zf-C3H	4.5
	426726	AA488915	Hs.171955	trophinin associated protein (SS	4.5
55	414427	L19711	Hs.76111	dystroglycan 1 (dystrophin-ass copper chaperone for superoxid	SS,TM sodcu,HMA,SS,TM,spectrin,	4.5 4.5
55	435891 453997	AW249394 AW247615	Hs.5002 Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras,SS	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (callo	aa_permeases,SS,TM,bZIP	4.5
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	. SS,TM	4.5
60	409650	T08490	Hs.288969	HSCARG protein	SS,SS,WD40	4.5
60	412833	AW960547	Hs.298262	ribosomal protein S19	SS,TM,lg,ITAM,Ribosomal_S SS,TM	4.4 4.4
	424133 414787	AA335721 AL049332	Hs.213628 Hs.77311	ESTs BTG family, member 3	SS,Anti_proliferat	4.4
	433046	AA229553	Hs.279945	HSPC023 protein	SS	4.4
15	417068	AA451910	Hs.85852	hypothetical protein MGC3169	SS,TM	4.4
65	414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synt,SS,TM	4.4
	418267 439902	BE389537 AF174499	Hs.83919 Hs.6764	glucosidase I histone deacetylase 6	Glyco_hydro_63,SS,PH Hist_deacetyl,zf-UBP,SS,G	4.4 4.4
	448847	AI587180	Hs.110906	Homo sapiens, Similar to RIKEN	TM,SS	4.4
	452160	BE378541	11011110000	cysteine sulfinic acid decarbo	SS	4.4
70	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase, SS, TM, GDI	4.4
	449717	AB040935	Hs.23954	cerebral cell adhesion molecul	SS,SS	4.4
	425069 413380	AA687465 A1904232	Hs.298184 Hs.75323	potassium voltage-gated channe prohibitin	SS,aldo_ket_red Band_7,SS,Band_7,SH3	4.4 4.4
	452911	AA541537	Hs.112619	metallothionein 1E (functional	SS,SS,TM,Sec1	4.4
75	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24,SS,TM,Pepti	4.4
	429218	AA225065	Hs.198269	Target CAT	SS,Nop	4.4
	447987	BE621544	Hs.157160	hypothetical protein MGC2616	SS,NDK,LRRNT,LRRCT,LRR	4.4 4.3
	407230 448886	AA157857 AL137291	Hs.182265 Hs.22451	keratin 19 hypothetical protein FLJ10357	filament,bZIP,SS,filament SS,PH,RhoGEF,SS,maseA	4.3 4.3
80	421178	BE267994	Hs.102419	zinc finger protein	zf-C2H2,SS,TM	4.3
	454031	R36772	Hs.71941	hypothetical protein MGC15677	TM	4.3
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin	SS,lg,fn3	4.3
	446557	U68566	Hs.15318	HS1 binding protein	SS,TM,MIP,UBA	4.3
	413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.3
		•		240		

	433251	AB040955	Hs.322735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
	420531	AI652069	Hs.98614	ribosome binding protein 1 (do	bzip,ss	4.3
	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM	4.3
_	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
5	426626	Al124572	Hs.323879	inhibitor of kappa light polyp	zf-C2H2,SS	4.3
	432956	AL037895	Hs.279861	CGI-31 protein	thiored,SS,TM	4.3
	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3,SS,TM	4.3
	428953	AA306610	Hs.348183	turnor necrosis factor receptor	TNFR_c6,SS	4.2
	401128			C12000644:gi[5729785]ref[NP_00	SS	4.2
10	446899	NM_005397	Hs.16426	podocalyxin-like	SS,TM,SS,TM	4.2
	407151	H25836	Hs.301527	ESTs, Moderately similar to un	SS,TNF	4.2
	426613	U96132	Hs.171280	hydroxyacyl-Coenzyme A dehydro	edh_short,SS	4.2
	408616	R51604	Hs.300842	KIAA1608 protein	SS,DENN,DENN	4.2
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_H	SS,Zn_carbOpept	4.2
15	414457	AW903820	Hs.85752	copine II	SS S	4.2
13	455857	T70192	113.00732	gb:yc18d03.s1 Stratagene lung	SS.TM.isodh	4.2
	401751	170192				4.2
	400563			RAN binding protein 3	SS,Orexin,SH2,STAT	4.2
		A1070444	Hs.236522	Target Exon DKFZP434P106 protein	SS,Pep_M12B_propep	4.2
20	430237	Al272144	HS.230322		abhydrolase,TM	
20	406101	55004000	11- 000440	C11000273*:gi 12656107 gb AAK0	SS,TM,7tm_1	4.2
	421661	BE281303	Hs.299148	hypothetical protein FLJ21801	SS,VHP	4.2
	444590	AA457456		hypothetical protein FLJ20435	SS .	4.2
	408187	AF034373	Hs.43509	ataxin 2 related protein	SS	4.2
25	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	SS,Hydrolase,SS,Gal-bind_	4.2
25	400278			ENSP00000243264:Dollchyl-dipho	SS,TM	4.2
	407394	AF005081		gb:Homo sapiens skin-specific	SS	4.2
	447407	BE387301	Hs.18528	Sjogren's syndrome nuclear aut	SS,HLH,ras,GSHPx	4.2
	410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1,SS	4.1
	415410	AF037332	Hs.278569	sorting nexin 17	PX,fn3,pkinase,SAM,EPH_lb	4.1
30	457757	AA434109	Hs.12271	f-box and leucine-rich repeal	SS,F-box,SS,TM,HSF_DNA-bi	4.1
	446388	AA292979	Hs.7788	NPD007 protein	SS,TM	4.1
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis	SS	4.1
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length	SS,C1q,Collagen	4.1
	422256	M64673	Hs.1499	heat shock transcription facto	NA,SS,TM,F-box	4.1
35	441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C,SS,RNA_pol_H	4.1
	401727			Target Exon	A_deamin,SS	4.1
	411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T,SS,Ribosomal	4.1
	458176	Al961519	Hs.140309	Homo sapiens, clone IMAGE:3677	SS,pkinase,pkinase_C	4.1
	432178	BE265369	Hs.272814	hypothetical protein DKFZp434E	SS.serine_carbpept	4.1
40	421537	BE383488	Hs.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
. •	421380	D31833	Hs.1372	arginine vasopressin receptor	7tm_1	4.1
	422702	AJ011373	Hs.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
	434142	U47927	Hs.3759	ubiquitin specific protease 5	zf-UBP,UCH-2,UBA,UCH-1,SS	4.1
	423696	Z92546	110.0100	Sushi domain (SCR repeat) cont	SS,TPR,vwd,sushi,Somatome	4.1
45	427407	BE268649	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_re	4.1
	413749	Al929320	Hs.75516	tyrosine kinase 2	pkinase,SS,TM,ig	4.1
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
	433320	D60647	Hs.250879			4.1
	433890	AF103801	Hs.16361	ESTs, Highly similar to CTXN R hypothetical protein	SS,TM,rrm DAO,SS	4.1
50	452603	AW410601	Hs.30026	HSPC182 protein	SS .	4.1
50	444496	BE302472	Hs.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
	422556		Hs.118244			4.1
		NM_006245		protein phosphatase 2, regulat	B56,SS,TM,Atrophin-1,Exo_ TM,SS	4.1
	447347 428284	AA570056 AA535762	Hs.122730 Hs.183435	ESTs, Moderately similar to KI NM_004545:Homo saplens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
55	426551	AA381268	Hs.323947	ESTs	SS.sushi	4.0
	417782	T10149	Hs.4243	hypothetical protein FLJ 12650	SS,TM	4.0
	443639	BE269042	Hs.9661	proteasome (prosome, macropain		4.0
	410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	proteasome,SS,TM,LACT,try	4.0
	452715	Z21093	Hs.30352	ribosomal protein S6 kinase, 5	SS,TM,7tm_3,SS,TM pkinase	4.0
60	442549	AI751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF,SS.	4.0
OU	430603	AA148164	Hs.247280	HBV associated factor	SS,zf-C3HC4,zf-RanBP,pkin	4.0
			113.247200	ubiquifin carrier protein	UQ_con,SS,TM	4.0
	427239	8E270447				4.0
	402665	DE4C440F	11- 70	Target Exon	SS,TM,Ig,DSPc	4.0
65	413818	BE161405	Hs.79	hypothetical protein MGC15429 gb:Homo sapiens DNA-binding pr	SS,KH-domain,WD40,Ribosom	4.0
05	406919	M88359	Un 74275	dishevelled 1 (homologous to D	SS,rm	
	412656	AF006011	Hs.74375		SS,PDZ,DEP,DIX,Dishevelle	4.0
	437546	AW074836	Hs.173984	T-box 1	SS,TM,T-box,GTP_CDC,LRRCT	4.0
	419489	AW411280	Hs.90693	replication initiation region	zf-C2H2,LIM,TM	4.0
70	410043	D30612	Hs.58167	zinc finger protein 282	zf-C2H2,KRAB,SS,zf-C2H2,K	4.0
70	430067	U79458	Hs.231840	WW domain binding protein 2	GRAM,SS	4.0
	408449	NM_004408	Hs.166161	dynamin 1	PH,GED,dynamin,dynamin_2,	4.0
	448099	BE621839	Hs.61976	Homo sapiens cDNA FLJ12947 fis	SS	4.0
	436656	N35568	Hs.5245	hypothetical protein FLJ20643	SS,TM,sugar_tr,PID	4.0
75	424512	X53002	Hs.149846	integrin, beta 5	Integrin_B,EGF,SS,TM	4.0
75	440346	Al923985	Hs.59621	ESTs, Weakly similar to A40815	SS,TM,ig,pkinase	3.9
	420065	AW140093	Hs.129926	ESTs	SS,TM_	3.9
	426636	BE242634	Hs.2055	ubiquitin-activating enzyme E1	ThiF,UBACT,SS,pkinase,UCH	3.9
	421579	NM_002975	Hs.105927	stem cell growth factor; lymph	lectin_c,SS,TM	3.9
00	427498	NM_003926	Hs.178728	methyl-CpG binding domain prot	SS,HLH	3.9
80	457820	AA341497	Hs.31408	RAR (RAS like GTPASE)	SS,TM,Rhomboid	3.9
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
	438662	AA223599	Hs.6351	cleavage and polyadenylation s	zf-CCHC,zf-CCCH,thaumatin	3.9
	414303	NM_004427	Hs.165263	early development regulator 2	SAM,SS	3.9
	435406	F26698	Hs.4884	calcium/calmodulin-dependent p	pkinase,SS,hexokinase,hex	3.9

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	414168 451982 418181	AW793296 F13036 U37012	Hs.103845 Hs.27373 Hs.83727	ESTs, Moderately similar to 15 Homo saplens mRNA; cDNA DKFZp5 cleavage and polyadenylation s	SS . SS . CPSF. A.SS.TM	3.9 3.9 3. 9
_	402793		1.0.001.0.	Target Exon	SS,TM,cyclin,cyclin_C	3.9
5	418681	AA287786	Hs.23449	insulin receptor tyrosine kina	SS,SH3	3.9
	412621	L40397	Hs.74137 Hs.28355	transmembrane trafficking prot	EMP24_GP25L,SS,TM	3.9 3.9
	420631 438483	AW976530 AW966735	Hs.321635	hypothetical protein FLJ22402 ESTs, Weakly similar to A46302	SS,TM SS,TM,IP_trans	3.9
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (fer4_NifH,ParA,APS_kinase	3.9
10	447800	AL080092	Hs.19610	DKFZP564N1362 protein	SS,TM,SS,TM	3.8
	436686	AW450205	Hs.305890	BCL2-like 1	TM,Bcl-2,BH4	3.8
	408815 441196	AW957974 BE397802	Hs.25485 Hs.7744	hypothetical protein FLJ22341 NM_007103*:Homo sapiens NADH d	SS,TM Complex1_51K,SNF2_N,helic	3.8 3.8
	433030	AW068857	Hs.279929	gp25L2 protein	SS,TM,EMP24_GP25L,SS,TM,G	3.8
15	408721	BE515274	Hs.47062	polymerase (RNA) II (DNA direc	RNA_POL_M_15KD,SS,COX7a	3.8
	435049	AL122067	Hs.4746	hypothetical protein FLJ21324	SS,pfk8	3.8
	431347	Al133461	Hs.251664	insulin-like growth factor 2 (SS,Insulin,Insulin	3.8
	450835 414134	BE262773 X60188	Hs.25584 Hs.861	hypothetical protein FLJ10767 mitogen-activated protein kina	ArfGap,SS,vwa,TSPN,fn3,Co pkinase,SS,pkinase,T-box	3.8 3.8
20	418090	U57059	Hs.83429	tumor necrosis factor (ligand)	TNF,SS	3.8
	448832	AW245212	Hs.22199	ECSIT	SS,rrm	3.8
	447256	AW593008	Hs.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	3.8
	448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,pkinase,SS,Pepti	3.8
25	426433 431626	L38969 AL035681	Hs.169875 Hs.265327	thrombospondin 3 -hypothetical protein DKFZp761I	TSPN,tsp_3,SS,TM,SEA,TSPN SS	3.8 3.8
23	430956	Al183529	Hs.2706	glutalhione peroxidase 4 (phos	GSHPx,SS,TM,ABC_tran	3.8
	450998	BE387614	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_tr,histone	3.8
	434899	BE613631	Hs.283565	FOS-like antigen-1	bZIP,SS,bZIP,cofilin_ADF,	3.8
20	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	ERG4_ERG24,SS,TM	3.8
30	411090	BE165650	Hs.339697	VPS28 protein KIAA1716 protein	SS,TM,CPSF_A	3.8
	452135 421339	A1492175 AA070224	Hs.21446 Hs.103561	SRp25 nuclear protein) SS,DIX,PDZ,DEP,Dishevelle SS	3.8 3.7
	406535	AAU10224	ris.103301	Target Exon	SS,TM,Ribosomal_S19e,ig,I	3.7
	447281	AA017018	Hs.18021	hypothetical protein FLJ20446	SS,SS,Tektin,Piwi,PAZ	3.7
35	433126	AB021262	Hs.99816	beta-catenin-Interacting prote	SS,TM	3.7
	425215	AF030291	Hs.155165	zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4_ERG24	3.7
	420536	AL117455	Hs.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_dea	3.7
	417998 430890	AW967420 X54232	Hs.2699	gb:EST379495 MAGE resequences, glypican 1	SS,TM Glypican,SS	3.7 3.7
40	427863	AF189712	Hs.181002	MLL septin-like fusion	SS,GTP_CDC,SS,TM	3.7
• •	448606	BE613362	110.10.101	Homo sapiens ubiquitin conjuga	SS,TM	3.7
	421961	AB032993	Hs.109929	likely homolog of rat GRIP-ass	TM,K_tetra,ion_trans,HLH,	3.7
	410293	AK000047	Hs.61960	hypothetical protein	K_tetra,SS	3.7
45	425233 423683	Z17861 BE388699	Hs.155218 Hs.4188	E1B-55kDa-associated protein 5 hypothetical protein MGC10812	SPRY,SAP,SS,TM,SPRY,SAP,p SS,Peptidase_C15,TGF-beta	3.7 3.7
73	423663 415697	Al365603	Hs.78605	OKFZP566I1024 protein	SS,cpn60_TCP1	3.7
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3	SS	3.7
	418052	AA350659	Hs.83347	angio-associated, migratory ce	WD40,Bacterial_PQQ,TM,UPF	3.7
50	444706	AK000398	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
20	407381 423432	AA420659 BE252996	Hs.183110 Hs.44067	ESTs, Weakly similar to ALUC_H ESTs	SS,TM TM	3.7 3.7
	444982	AK002182	Hs.12211	GDP-fucose transporter 1	SS,TM,DUF6,SS,TM	3.7
	407777	AA161071	Hs.71465	squalene epoxidase	SS,TM,Monooxygenase	3.7
<i></i>	422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20,Glyco_hydr	3.7
55	422609	Z46023	Hs.118721	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HSP70	3.7 3.7
	414732 452579	AW410976 AA131657	Hs.77152 Hs.23830	minichromosome maintenance def ESTs	MCM,RIP,SS,zf-C2H2,KRAB SS,CN_hydrolase	3.7
	419032	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS,pkinase,SH2,Insulin,pk	3.6
	411165	NM_000169	Hs.69089	galaclosidase, alpha	Melibiase, Ribosomal_1.44, z	3.6
60	444000	Al095034	Hs.135528	ESTs	SS,HLH	3.6
	441174	BE312775	Hs.294005	Homo sapiens, clone IMAGE:3050	SS,TM	3.6
	429491 438433	NM_012111 AB018274	Hs.204041 Hs.6214	chromosome 14 open reading fra KIAA0731 protein	SS SS	3.6 3.6
	438433	BE514851	Hs.154886	choline kinase-like	Carn_acyltransf,Choline_k	3.6
65	429671	BE379335	Hs.211594	proteasome (prosome, macropain	AAA,NB-ARC,TM	3.6
-	421018	A1569028	Hs.129888	hypothetical protein FLJ14768	zf-C2H2,SS,mm,ENTH	3.6
	433604	NM_013442	Hs.3439	stomatin-like 2	Band_7,SS,TM,AAA,cdc48_N,	3.6
	451544 444369	AK000429 AV649296	Hs.26570	hypothetical protein FLJ20422 ESTs	SS,TM,COX3,SS,TM,SRF-TF SS	3.6 3.6
70	406660	X65371	Hs.282793 Hs.172550	polypyrimidine tract binding p	rm,beta-lactamase,SS,try	3.6
. •	456503	AW977779	Hs.194613	ESTs	SS,TM,bromodomain,abhydro	3.6
	451711	AK000461	Hs.26890	cat eye syndrome chromosome re	SS,SS,TM,A_deaminase	3.6
	425394	AA356730	Hs.323949	kangai 1 (suppression of tumor	SS,TM,transmembrane4	3.6
75	428011	BE387514	Hs.181418 Hs.62620	KIAA0152 gene product chromosome 6 open reading fram	Acyl-CoA_dh,SS,efhand SS	3.6 3.6
, ,	407627 436437	A1419020 F12200	Hs.5811	chromosome o open reading fram	SS.Syja_N,Exo_endo_phos	3.6
•	419418	X75621	Hs.90303	tuberous scierosis 2	Rap_GAP,Tuberin,Peptidase	3.6
	440300	N39760	Hs.8859	Homo sapians, Similar to RIKEN	SS	3.6
00	448136	AA036680	Hs.20447	protein kinase related to S. c	pkinase,PBD	3.6
80	435977	AL138079	Hs.5012	brain-specific membrane-anchor	SS,TM,SS,TM,ubiquitin,Rib	3.6
	419095 447267	AA234009 AL360143	Hs.188715 Hs.17936	ESTs DKFZP434H132 protein	pkinase,PH,pkinase_C SS	3.6 3.6
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR,Lysyl_oxidase,SS,TM,	3.6
	444354	AA847582	Hs.10927	hypothetical protein R33729_1	SS	3.6

	429098	AF030249	Hs.196176	encyl Coenzyme A hydratase 1,	ECH, Herpes_V23, SS, Gal-bin	3.6
	430622	BE616971	Hs.247478	Homo sapiens, Similar to DNA s	G-patch, SS, TM, ubiquitin, a	3.6
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_H	pkinase	3.6 ·
_	409678	NM_005632	Hs.55836	small optic tobes (Drosophila)	TM,Peptidase_C2	3.6
5	413097	BE383876	Hs.75196	ankyrin repeat-containing prot	ank,SET,SS,TM,pkinase,SH2	3.6
	427579 409154	AA366143 U72882	Hs.179669	hypothetical protein FLJ20637 interferon-induced protein 35	HECT, SS, HECT	3.6 3.5
	409154 448528	BE613248	Hs.50842 Hs.172084	Homo sapiens, clone IMAGE:3627	SS,ras,Ribosomal_L27e,KOW SS,PID,SH2	3.5 3.5
	444426	AL121105	Hs.11170	RNA binding motif protein 14	rm,SS,spectrin,PH,rrm,so	3.5
10	409297	R34662	Hs.53066	hsp70-interacting protein	SS	3.5
	441138	T56785	Hs.10101	hypothetical protein FLJ12875	SS	3.5
	435169	AF148509	Hs.279881	mannosidase, alpha, class 1B,	TM,Glyco_hydro_47	3.5
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	TM,SS,TM,SRCR,Glyco_trans	3.5
15	403325	AD014550	U. C000	C2000428*:gi[7705383[ref]NP_05	SS TM,UL21,Lipoprotein_6,GBP	3.5 3.5
1,5	437895 449030	AB014568 Al365582	Hs.5898 Hs.57100	KIAA0668 protein Homo sapiens mRNA for FLJ00016	SS,Synuclein	3.5
	426542	AF190746	Hs.170310	cat eye syndrome chromosome re	A_deaminase,SS,TM,Hydrola	3.5
	439873	BE159253	Hs.300638	ESTs	SS	3.5
00	428950	BE311879	Hs.194673	phosphoprotein enriched in ast	DED,SS,TM,Calsequestrin	3.5
20	421564	AB007864	Hs.105850	KIAA0404 protein	SS	3.5
	441094	U33819	Hs.7647	MYC-associated zinc finger pro	SS,zf-C2H2,LIM,PHD,TFIIS,	3.5
	450007 422898	BE270693 AL043101	Hs.24301	polymerase (RNA) II (DNA direc DKFZP434A163 protein; selectiv	na,ss ss,tm	3.5 3.5
	422050 444914	AA046947	Hs.127401 Hs.12142	`WD repeat domain 13	WD40,SS,TBC,mm	3.5
25	420178	D50550	Hs.95659	Jethal giant larvae (Drosophil	WD40,SS,TM	3.5
	418984	AA421401		ribosomal protein L18	SS,TM	3.5
	414166	AW888941	Hs.75789	N-myc downstream regulated	Ndr,abhydrolase,SS	3.5
	409944	BE297925	Hs.57687	four and a half LIM domains 3	LIM,SS	3.5
30	421458 423599	NM_003654 AI805664	Hs.104576 Hs.31731	carbohydrate (keratan sulfate peroxiredoxin 5	SS AhpC-TSA,SS,hormone_rec,z	3.5 3.5
50	423333	BE245274	Hs.180428	KIAA1181 protein	TM,SS,TM,KOW	3.5
	405496	555,657	1101100120	Target Exon	SS,tubulin,SS	3.5
	417911	AA333387	Hs.82916	chaperonin containing TCP1, su	cpn60_TCP1,SS,cpn60_TCP1	3.5
26	433620	AA604520	Hs.269468	ESTs, Moderately similar to AL	SS,UCH-2,UCH-1	3.5
35	430053	AF052155	Hs.227949	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,E1-E2_ATPase,C	3.5
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	SS chromo,SS	3.5 3.5
	424679 417360	AL117477 AW651703	Hs.119960 Hs.82023	DKFZP727G051 protein hypothetical protein similar t	SS,TM,GDA1_CD39,GDA1_CD39	3.5
	439641	AJ251317	Hs.33184	ESTs	SS,TM,GYF,actin,PA	3.5
40	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,Armadillo_se	3.5
	427117	BE258946	Hs.173611	Target CAT	complex1_49Kd,SS,TM,ITAM,	3.4
	422051	AW327546	Hs.111024	solute carrier family 25 (mito	SS;mito_carr,SS,mito_carr	3.4
	422759	AA316582 U40998	Hs.224571	ESTs	SS SS.glycolytic_enzy	3.4 3.4
45	417230 450158	AK001999	Hs.81728 Hs.24545	unc119 (C.elegans) homolog hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFilS,SS	3.4
1.5	425421	L11669	Hs.157145	tetracycline transporter-like	SS,TM,SS,TM	3.4
	415515	F11327	Hs.167406	gb:HSC2VD101 normalized infant	SS	3.4
	427868	Al360119.comp	Hs.181013	phosphoglycerate mutase 1 (bra	PGAM,SS,TM,Idh	3.4
50	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homeobox,Hydanto	3.4
50	413014	AW250533	Hs.75139	partner of RAC1 (arfaptin 2)	SS,hemopexin,Filamin,NHL,	3.4 3.4
	457655 419432	AA622968 AK001459	Hs.71574 Hs.90375	hypothetical protein FLJ14926 hypothetical protein FLJ10597	SS,P5CR,EF1BD PEP-utilizers,PEP-utilize	3.4
	421066	AU076725	Hs.101408	branched chain aminotransferas	aminotran_4,TM	3.4
	428038	AW134756	Hs.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
55	430352	AW750535	Hs.50742	Homo sapiens cDNA: FLJ23331 fi	TM	3.4
	432647	Al807481	Hs.278581	fibroblast growth factor recep	lg,pkinase,SS,TM,ig,pkina	3.4
	421310	AW630087	Hs.103315	trinucleotide repeat containin	TM,zf-C2H2,SS,PHD SS	3.4 3.4
	420999 409561	AA338903 U58048	Hs.100915 Hs.183138	peroxisomal biogenesis factor procollagen (type III) N-endop	SS,TM	3.4
60	419727	AW160796	Hs.92700	DKFZP564O243 protein	Herpes_env,SS,TM,Peptidas	3.4
	421267	BE314724	Hs.103081	ribosomal protein S6 kinase, 7	pkinase,pkinase_C,SS	3.4
	411501	AB002368	Hs.70500	KIAA0370 protein	SS,TM,SS,TM	3.4
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	SS CC TAA to make	3.4
65	407103	AA424881 AA449014	Hs.256301 Hs.121025	hypothetical protein MGC13170 chromosome 11 open reading fra	SS,TM,trypsin SS,TM,trypsin,CUB,ubiquit	3.4 3.4
UJ	422808 448173	N95657	Hs.6820	ESTs, Moderately similar to YO	SS SS	3.4
	416535	H61851	1 10.0020	gb:yr80e10.r1 Soares fetal liv	SS,TM,homeobox,LIM	3.4
	406656	M16714	Hs.181392	major histocompatibility compl	MHC_I,ig,SS,TM	3.4
70	435669	Al867781	Hs.31819	HT014	SS,abhydrolase_2	3.4
70	411077	AW977263	Hs.68257	general transcription factor I	SS,TM,TGF-beta	3.4
	427062	AW327785	Hs.173421	KIAA1564 protein	SS,Peptidase_M24	3.4 3.4
	421890 412968	AW959486 AW500508	Hs.21732 Hs.75102	ESTs alanyl-tRNA synthetase	SS,zf-C3HC4,SPRY DHHA1,SS,tRNA-synt_2c,DHH	3.4 3.4
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN	SS	3.4
75	433659	AK001301	Hs.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
-	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314	SS	3.3
	441722	AW960504	Hs.173103	FE65-LIKE 2	SS,TM	3.3
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	DSPc,SS,jmjC,F-box SS,TBC,FHA,zf-C3HC4	3.3 3.3
80	451714 410633	AK000344 BE546789	Hs.26898 Hs.346742	hypothetical protein FLJ20337 hypothetical protein MGC3260	SS,TM	3.3 3.3
00	410633	BE298441	Hs.287361	ADP-ribosylation factor relate	arf,ras,SS,arf,Stathmin	3.3
	414775	AA992036	Hs.172702	ESTs, Weakly similar to (defli	SS,PCI	3.3
	428495	NM_013279	Hs.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_J,5_3_exo	3.3
	429215	NM_005341	Hs.2364	GLI-Kruppel family member HKR3	zf-C2H2,BTB,TP2,K_tetra,S	3.3
				243		
						

	446618	AL110307	Hs.15591	COP9 subunit 6 (MOV34 homolog,	Mov34,SS,zf-C2H2,SCAN	3.3
	444868	BE560471	Hs.12101	hypothetical protein	SS,PCI	3.3
	430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,7tm_1,tubulin	3:3 ·
_	416950	AL049798	Hs.80552	dermatopontin	SS	3.3
5	431203	AW248421	Hs.250758	proteasome (prosome, macropain	AAA,Sigma54_activat,SS,TP	3.3
	432714	Y12059	Hs.278675	bromodomain-containing 4	bromodomain, SS, TM, SNF2_N,	3.3
	415674	BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadhe	3.3
	426152	BE299190	Hs.167246	P450 (cytochrome) oxidoreducta	flavodoxin,FAD_binding,SS	3.3
	418440	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3,	ubiquitin,SS,UQ_con	3.3
10	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	ig,fn3,SS,TM,GalP_UDP_tra	3.3
	409428	M33680	Hs.54457	CD81 antigen (target of antipr	transmembrane4,cyclin,SS,	3.3
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membr	TM,MSP_domain	3.3
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb	3.3
	430137	NM_005456	Hs.234249	mitogen-activated protein kina	SS,SH3,PID,SS,PID	3.3
15	446427	AW295863	Hs.119632	ESTs	SS	3.3
13	400747	A11233003	113.113032			3.3
		AF167572	Hs.12912	Target Exon skb1 (S. pombe) homolog	fn3,ig	3.3
	445580				SS,SS	3.3
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp5	SS,rm,Ephrin,pkinase,ATP	
20	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via d	death,DED,SS,TM	3.3
20	401655			Target Exon	SS	3.3
	429460	D56263	Hs.203238	phosphodiesterase 18, calmodul	PDEase,SS,PDEase	3.3
	416448	L13210	Hs.79339	lectin, galactoside-binding, s	SRCR,SS,TM	3.3
	433038	AF192559	Hs.279939	mitochondrial carrier homolog	TM,mito_carr,TM	3.3
0.5	440251	AW796016	Hs.332012	Homo sapiens, clone IMAGE:3687	SS,TM,SS,TM,IRK	3.3
25	412922	M60721	Hs.74870	.H2.0 (Drosophila)-like homeo b	SS,homeobox,SS ⁻	3.3
	432941	W04803	Hs.279851	hypothetical protein FLJ10241	SS,RNase_PH,RNase_PH_C	3.3
	441244	BE612935	Hs.184052	PP1201 protein	SS,TM,WD40	3.3
	438175	Al376727	Hs.122110	ESTs	SS,TM,trypsin,kringle,fn2	3.3
	423024	AA593731	Hs.325823	ESTs, Moderately similar to AL	SS,TM,CD36,CD36	3.3
30	430120	AW675298	Hs.233694	hypothetical protein FLJ11350	SS	3.3
	419571	AW674962	Hs.91146	protein kinase D2	pkinase,DAG_PE-bind,PH,DC	3.3
	413019	BE281604	Hs.75140	low density lipoprotein-relate	SS	3.3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specif	trypsin,SS,trypsin,trypsi	3.3
	433519	BE263901		ESTs, Weakly similar to S37431	SS,TM	3.2
35	434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic	Peptidase_M16,HCO3_cotran	3.2
	422242	AJ251760	Hs.273385	guanine nucleotide binding pro	G-alpha,arf,SS,G-alpha	3.2
	430480	AL079399	Hs.241543	DKFZP586F1524 protein	SS,TM,hemopexin,Somatomed	3.2
	452438	BE514230	Hs.29595	JM4 protein	SS,TM,KOW,HLH	3.2
	456939	AA431633	Hs.163867	NM_002488*:Homo sapiens NADH d	SS,tRNA-synt_2b,WHEP-TRS,	3.2
40	421009	AL049709	Hs.343357	Human DNA sequence from clone	TM	3.2
-10	411969	X12458	Hs.72980	Protein P3	SBF,SS,TM,G6PD,G6PD_C,hex	3.2
	409197	N54706	Hs.303025	chromosome 11 open reading fra	SS	3.2
	417896	AA379770	Hs.82890	defender against cell death 1	DAD,SS,TM	3.2
	418026	BE379727	Hs.83213	fatty acid binding protein 4,	lipocalin, SS, lipocalin	3.2
45	409057	AA702305	Hs.180060	ESTs	SS,TGFb_propeptide,TGF-be	3.2
73	437869	W91976	Hs.290834	ESTs	SS,TM,SH3,zf-C3HC4	3.2
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	SS,TM	3.2
	425080	AI393498	113.103274	inositol 1,4,5-triphosphate re	SS,CTF_NFI	3.2
	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt_B,HEAT_PBS,SS,TM	3.2
50	421943	BE616520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
50	443337	Y07604	Hs.9235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2
	418885	D17530	Hs.89434	drebrin 1	cofilin_ADF,SS,cofilin_AD	3.2
	411817	BE302900	Hs.72241	mitogen-activated protein kina	pkinase,SS	3.2
	413891	BE271020	113.7 2241	tumor suppressor deleted in or	SS,TM	3.2
55	449455	T60748	Hs.278408	hypothetical protein	TM	3.2
<i>33</i> .	419193	D29643	Hs.34789		SS,TM,DDOST_48kD,VP7,SS,T	3.2
			Hs.62954	dolichyl-diphosphooligosacchar ferritin, heavy polypeptide 1	SS,TM,UDPGT	3.2
	406701	AA780613	Hs.91681	ESTs, Weakly similar to DCHUO	SS,tRNA-synt_1b,tRNA_bind	3.2
•	436467	AW450278		polymerase (RNA) II (DNA direc		3.2
60 .	446334 410270	U52427 AF279142	Hs.14839 Hs.195727	tumor endothelial marker 1 pre	S1,SS SS,TM,EGF,lectin_c,sushi,	3.2
.	445411	AF279142 AL137255	Hs.12646	hypothetical protein FLJ22693	SS, I M, EGF, IECUIT_C, SUSTII, SS, hormone_rec, zf-CCCH	3.2
				ESTs	SS,TM,Oxysterol_BP	
	458018 426530	Al199575 U24578	Hs.37716 Hs.278625	complement component 4A	SS,A2M,NTR,A2M_N,prenyltr	3.2 3.2
65	445604	T08566	Hs.12956	Tax interaction protein 1	PDZ,SS,TM,P2X_receptor,FG	3.2 3.2
05	443402	U77846	II- anno	elastin (supravalvular aortic	SS,PDZ,LIM,pkinase	
	432416	BE410937	Hs.2985	emerin (Emery-Dreifuss muscula	LEM,SS,Ribosomal_L10e,Acy	3.2
	429662	AI929701	Hs.211586	phosphoinositide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GILT,SH	3.2
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolo	SS,TM,Fz,Frizzled,7tm_2,S	3.2
70	427729	AB033100	Hs.300646	KIAA1274 protein (similar to m	SS	3.2
70	418151	AA864238.comp	Hs.83583	actin related protein 2/3 comp	RhoGEF,REV,PH,SS,TM,Ribos	3.2
	448250	NM_016034	Hs.20776	mitochondrial ribosomal protei	Ribosomal_S2,SS,lipocalin	3.2
	431158	AW859138	Hs.136280	Homo saplens cDNA: FLJ22288 ff	SS,Exonuclease	3.2
	414292	BE388407	Hs.75875	ubiquitin-conjugating enzyme E	UQ_con,SS,TM,SAM_PNT	3.2
75	406307			Target Exon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
75	423325	R55565	Hs.347286	hypothetical protein FLJ22427	SS,TM,Surp,ubiquitin,TBC	3.2
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis vir	NA,SS	3.1
	419069	AA233801		ESTs, Weakly similar to CA13_H	SS	3.1
	431717	BE396150	Hs.6945	mitochondrial ribosomal protei	SS,TM	3.1
0.0	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp4	RhoGAP,SS,TM,SET,zf-CXXC,	3.1
80	419394	AB011124	Hs.90232	KIAA0552 gene product	SS,ig	3.1
	436240	BE388673	Hs.5086	hypothetical protein MGC10433	SS,TM,Ets,COX6B,transmemb	3.1
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein	TPR,SS,TM,DnaJ	3.1
	417920	S47833	Hs.82927	adenosine monophosphate deamin	A_deaminase,SS,G-alpha,GS	3.1
	421819	NM_013403	Hs.108665	zinedin	WD40,pkinase,pkinase	3.1
				044		

	426362	BE267158	Hs.169474	DKFZP586J0119 protein	IF-2B,SS,PP2C	3.1
	408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS,bZIP,cofilin_ADF,EGF	3.1
	443099	Al372836	Hs.9003	hypothetical protein FLJ13868	TM	3.1
5	427022	AW245839	Hs.173255	small nuclear ribonucleoprotei	rm,SS,rm,SH3,ras,2OG-Fe	3.1
)	452711	AW967047	Hs.293224	ESTs, Weakly similar to T00375	SS	3.1
	407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTR2,7tm_1	3.1
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2_N,helicase_C	3.1
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fi	SS	3.1
	447629	AF034790	Hs.19105	translocase of inner mitochond	Tim17,SS,TM,pkinase,OTU	3.1
10	401097			C12000858*:gi 7363437 ref[NP_0	SS,TM,7tm_1,SS	3.1
	452736	C01164	Hs.4232	Homo sapiens PAC clone RP1-130	SS,SS,TM,TBC,Surp,ubiquit	3.1
	435507	Al143579	Hs.26510	vacuolar protein sorting 33B (SS,Sec1,Sec1	3.1
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial	PPR,SS,TM,cNMP_binding,RN	3.1
		BE244334				3.1
15	413245		Hs.75249	ADP-ribosylation factor-like 6	SS,TM,kazal,Ribosomal_S8,	
13	409858	NM_006586		trinucleotide repeat containin	SS,SS,TM,B56	3.1
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	AAA,SS,PI-PLC-X,PH,PI-PLC	3.1
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489	SS	3.1
	417947	AA323563	Hs.325309	hypothetical protein FLJ 14596	SS,TM,PTPA	3.1
	409283	NM_004860	Hs.52788	fragile X mental retardation,	KH-domain,SS,TM,HMG_box	3.1
20	412813	AF086947	Hs.74617	dynactin 1 (p150, Glued (Droso	CAP_GLY,SS	3.1
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,p450,actin	3.1
	432482	L19267	Hs.275924	dystrophia myotonica-containin	WD40,SS,pkinase,pkinase	3.1
	437256	AL137404	Hs.97871	Homo sapiens, clone IMAGE:3845	TM.SS	3.1
	440191	AI990417	113.37071	tubulin, beta 5	SS,formiminotr,prenyltran	3.0
25		AA827639	114 40507		SS,TM	3.0
25	407972		Hs.18587	- KIAA1588 protein		
	420890	AA434058	Hs.100071	6-phosphogluconolactonase	Glucosamine_iso,SS	3.0
	440060	AI696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3.0
	452222	AW806287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GDI	3.0
	401772			NM_014520:Homo sapiens MYB bin	SS	3.0
30	453754	AW972580	Hs.172753	ESTs	SS,TM,ras,Ribosomal_S19,T	3.0
	423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3.0
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma	SS.TM	3.0
	441954	Al744935	Hs.8047	Fanconi anemia, complementatio	TPR.SS,TM,AAA,cdc48_N,Ban	3.0
	412787	D87452	Hs.74579	KIAA0263 gene product	zf-CCCH,SS,TM,NTP_transfe	3.0
35	422034	AC006486	Hs.333069	Ets2 repressor factor	Ets,SS,pkinase,PAF-AH_lb	3.0
55	450788	Al738410	(13.00000	ESTs	SS,TM	3.0
	452511	BE408178	Hs.285165	Homo sapiens cDNA FLJ20845 fis	SS,thiored,P5CR	3.0
				ubiquitin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3.0
	414380	BE391815	Hs.75981			
40	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (B	SS,TM,SS,TM	3.0
40	434955	BE276128	Hs.284286	mitochondrial ribosomal protei	SS	3.0
	435632	AF220049	Hs.43549	uncharacterized hematopoletic	SS,UQ_con	3.0
	432465	D56165	Hs.275163	non-metastatic cells 2, protei	NDK,SS,NDK	3.0
	430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7tm_3,homeobox,SS,TM	3.0
	453412	AJ003290		gb:AJ003290 Selected chromosom	pkinase	3.0
45	446456	BE613933	Hs.15106	chromosome 14 open reading fra	UPF0143,SS	3.0
	433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3.0
	. 447322	BE617649	Hs.77690	RAB5B, member RAS oncogene fam	SS,oxidored_molyb,heme_1,	3.0
	422268	N25485	Hs.330310	maternal G10 transcript	G10,SS,WD40	3.0
	419578	AF064853	Hs.91299	guanine nucleotide binding pro	WD40,SS,EPO_TPO	3.0
50	446929	AA076132	Hs.9460	Homo sapiens mRNA; cDNA DKFZp5	SS,TM,WD40	3.0
	TABLE 21 Pkey: Uni	B: que Eos probes	et identifier number	Tallo depole in a di, dolo to to to	33,111,112.10	0.0
55		er. Gene cluste			•	
22	Accession	Genbank acce	ession numbers			
	_					
	Pkey		r Accession			
	408215	10478_1		135629 AA338538 Al193603 AA781096 Al680061 A		
~				446461 A1355345 A1343638 A1343640 A1275091 M	178746 AW262795 AW250002 AA503756 A193	4519 AW272086 N
60			AA626639			
	409938	116091_1	AW974648 AA652153			
	411674	1253746_1	AW861123 AW861125	AW856717 AW861116 AW856706 AW856788 AW	856774 AW856787 AW856780 AW856782 AW	/856789 AW85677
				AW856776 AW856635 AW856767		
	413052	1347214 1		E062771 BE062636 BE062813 BE062699 BE0628	95 BE062747 BE062719 BE293541	

60	Pkey 408215	CAT Number 10478_1	BE614290 AA307674 N35629 AA338538 Al193603 AA781095 Al680061 Al613258 AW276647 BE221263 Al348910 Al985031 Al090078 Al359617 AA666391 Al160210 Al446461 Al355345 Al343638 Al343640 Al275091 M78746 AW262795 AW250002 AA503756 Al934519 AW272086 N26520
00	409938 411674	116091_1 1253746_1	AA626639 AW974648 AA652153 AA649671 AA078582 AW861123 AW861125 AW856717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856789 AW856772
			AW856784 AW856786 AW856776 AW856635 AW856767
	413052	1347214_1	BE249841 BE062657 BE062771 BE062636 BE062813 BE062699 BE062895 BE062747 BE062719 BE293541
65	413837	139363_1	AW163625 AW163255 AW163385 AI929359 BE279279 AA132590 AW157329 AA584408 AW157252 AI692198 AW003514 T24436 AI765658 AW157459 AI810740 AI659582 AI969924 AI929284 AI340993 AI349083 AW299522 AW664650 AW299513 AA132529 AI340991 AI912836 AI341293 AI650609 AA279
70	413891	139759_1	BE271020 A1763358 A1926430 A1806151 AW003726 T15590 AA649945 AW129911 A1570748 T57492 AA828002 AW237602 AW003539 A1139045 A1950958 BE042625 AW776973 A1287859 A1983931 AW515101 AW150029 A1358496 A1621173 AA846016 A1470921 AW169748 A1991000 AW513748 A104058
	414023	1410860_1	BE243628 BE246081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417 BE241457 BE242522 BE241989 BE241464
	416535	1599332_1	H61851 H74099 T67099
	417998	171375_1	AW967420 AA210915 AA236991 AA210916
75	418984	181094_1	AA421401 T49326 AA330666 AA328941 W63573 AA758023 AA976306 H52254 AA877107 BE207784 AW664584 AI924890 AA458586 AI422142 AI891097 AI811174 R69866 T49327 AA233722 AA631138 AA910314 AI379416 AI129321 AA861574 AA635649 AI339443 AW009533 AA677036 AA948287 AA62
	419069	181650_3	AA233801 BE383487 AA913939 Al632681 Al813277 Al373652 AW134802 Al863574 AW305364 Al868557 Al670746 Al015036 Al935384 Al935317 AW138668 AW204971 Al765223 AA884146 AA973341 AA234062
80	419250	183289_2	AW770185 AW296271 H11254 AW403510 Al032786 AA767046 Al376115 Al582209 AA460965 Al868663 Al016900 R05715 Al127382 Al660953 Al023644 H00465 AW959578 AA815039 AW292253 R05714 AA815462 AA235654 AA461274 W24933 AA300091 H00515
	420160	191054_1	A1492840 A1287657 AA255989 A1698206 A1468558
	421572	204022_1	AA531607 Al565370 Al376907 Al811618 AW138145 AW139465 AA421658 AA293069 AW118141 Al214980 AW663502 Al343486 Al553789 AA650416 Al498947

	423696	23112_1	792546 AA3	30586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375
		_	AI206100 A	A912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	425080	246559_1		42314 A1088818 A1696468 A1418641 AA573152 F08817 A1910796 AW338984 R39024 AA729145 BE245956 A1093722 AA541730 12755 AA350447 AA865667 T93903 AW081029 AA493711 AA650030 N35995 N21491 T57002 Z25379 A1906851
5	427239	27647 1		W409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
				E513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879
	427391	27815_1		IE621936 AA290724 001212 AA155752 AA878366 AA090872 AB033013 AW249107 AA031890 AA112820 AW366388 N55156 AA326756 AW952294
	421331	2/013_1		03570 C04358 W60676 AW248674 AA034989 AA044781 AA074274 H26212 AI800572 AI127583 AI951785 AA856557 AI571746
10				39543 Al215670
	428092 429545	286920_1 305902_1		NA421182 A1734104 A1733923 AA430600 676005 AW129612 A1825903 AA773987 A1823645 A1823860 AA456229 A1824295 AA454622 A1264049 A1090237 A1669787 A1804012
	429343	303302_1		070003 AW 123012 A1023303 AA7 73307 A1023043 A1023000 AA430223 A1024233 AA434022 A1204043 A1030237 A1003707 A1004012 96164 A1298273 AW884073 AW883986
	430168	313927_1		AA468507 Al478223 AW513008 Al762122 Al554512 AA862642 AA468976
15	433519 438707	368801_2 46360_1		A596086 A1190276 A1094806 A1831250 A1572668 AW204652 A1660600 A1922941 R49621 118914 AW385394 AW385398 AW385401 A1922683 AA907337 AA160504 AA928142 AA601969 AA010594 BE618528 AA160591
	438707 440191	46360_1 48804_3		10514 AV365394 AV365396 AV365401 A1922663 AA907337 AA 100504 AA928142 AA001969 AA017534 BEG 16328 AA170591 304400 A1193071 A1742483 AW003408 AW131566 A1400201 A1656740 A1309186 AW665173 AW204722 A1215122 A1200785
	110101	10001_0		N147599 Al215120 Al076110 Al803429 Al262491 Al808243 Al281007 AW135212 AW205103 Al754349 Al004801 Al051273 AW768918
20	440400	E004 4	AW103289	
20	443402	5681_1		179373 AA346348 AA348194 M26867 AA728901 AA715367 AA377787 R64236 A1752721 R77311 AA339685 BE074254 AW938712 AA330624 AA347098 AA327507 AW391973 AA495763 AA479278 AW605018 T19644 A1204484 AW834745 AW081309 AW090002
				131556 Al56
	444590	6116_1		A907921 AI567715 AA579472 T64216 AA373128 F35533 AA722113 T64403 AA653738 F28806 AA595689 AA047537 AA022499
25			AVV44U532	F36782 Al554180 Al183767 Al806052 AA160379 AA481678 Al185031 Al148988 Al174482 AA868833 Al674395 AA481440 Al914985
	445625	64558_1	BE246743 A	VA436942 AW024744 AW242177 AA975476 AW385185 R07536 R73462 AV654529 T57442 Al399986 R50073 R48743 Al769689
			AI863005 A R50074 AI7	A317806 Al678000 AW189963 Al986207 AW471273 R73463 Al335104 Al590161 Al469257 Al954604 H21954 T25141 AA856793
	448606	77159_1		00203 A12 VA447862 H72036 AA393664 A1681334 AW139128 AA932579 A1302241 A1936800 AW960528 A1492148 C06192 AA336107 AA808008
30				BE297403 BE298978 AI187207 AA928695 AI620631 AA938128 AI346527 AI040261 AA808401 AW130326 AI440313 AA868693
	448677	775217_1	A1653329 A	33246 · · · · · · · · · · · · · · · · · · ·
	450788	846840_1		W016905 AI971725
25	452160	901991_1	BE378541 A	
35	453412 455857	966264_1 1376021_1	AJ003290 A T70192 BE1	J003288 AW276947
	455928	1383899_1		147030 BE158339 BE158290
	457022	274445_1		BE067468 BE067511 BE067515 BE067467 BE067514 AA397442
40	TABLE 21C			
40	Pkev: Uniqu	re number con	responding to	an Eos probeset .
	Ref: Seque	nce source. T	he 7 digit num	bers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
				ı, et al. (1999) <u>Nature</u> 402:489-495 h exons were predicted
45				ns of predicted exons
	Pkey	Ref	Strand	Nt position
	400460	8389428	Pius	35559-36295
50	400563	9844011	Plus	81941-82434
50	400747	7329330	Minus	71249-71441

	Pkey	Ref	Strand	Nt_position
	400460	8389428	Plus	35559-36295
	400563	9844011	Plus	81941-82434
50	400747	7329330	Minus	71249-71441
	400846	9188605	Plus	39310-39474
	401097	9965518	Minus	60356-61096
-	401128	8699792	Plus	37349-37885
	401655	9099093	Plus	79556-80132
55	401727	8134856	Plus	54342-54482
_	401751	9828651	Plus	139165-139322
	401772	9966243	Plus	183917-184042
	402365	9454515	Minus	70928-71185
	402463	9796896	Minus	8818-8952
60	402665	8077033	Minus	11824-12090,14290-14544
	402793	6136940	Minus	69012-69165
	402916	7406502	Minus	361-474,541-687
	403028	7670577	Minus	114150-114272
	403325	8440025	Minus	109763-109926
65	404256	9367203	Plus	146931-147796
	405189	7229907	Minus	168236-168795
	405325	6094661	Minus	25818-26380
	405356	2155224	Plus	36116-36276
	405496	8468968	Plus	147706-148062
70	406101	9124019	Plus	125325-125831
	406307	8576099	Plus	95473-95585,98900-99180
	406535	7711477	Plus	83135-83362

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult lissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult lissues was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 96th percentile value amongst various ovarian cancer specimens, the "average" normal adult lissue level was set to the 76th percentile value amongst various normalignant tissues, the "average" ovarian cancer value was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modulatable by small molecules (e.g., pkinase, peptidase, phosphatase, or lon_transporter). Predicted protein 75 80 domains are noted.

TABLE 22A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigene Title: Unigene gene title Protein Dom.: Predicted protein domain R1: Ratio of tumor to normal body tissue

		of tumor to norma				
5	1111 12001	or annor as morning	000, 00000			
	Pkey	ExAccn	UniGene ID	Unigene Title	Protein Dom.	R1
	407223	H96850		gb:yw03b12.s1 Soares melanocyt		58.9
	430281	AI878842	Hs.237924	CGI-69 protein	milo_can	46.7
10	410418	D31382	Hs.63325	transmembrane protease, serine	Idl_recept_a,trypsin	41.0
10	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH	37.1 35.3
	438424	AI912498	Hs.25895	hypothetical protein FLJ 14996	SH3	35.2
	418969 453028	W33191 AB006532	Hs.28907 Hs.31442	hypothetical protein FLJ20258 RecQ protein-like 4	DEAD,helicase C	28.2
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB	28.2
15	451721	NM_006946		spectrin, beta, non-erythrocyt	spectrin,PH,CH	27.9
10	416819	U77735	Hs.80205	pim-2 oncogene	pkinase	27.9
	430397	AI924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp	27.7
	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2	26.7
•	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT	25.3
20	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG	25.1
	412674	X04105	Hs.74451	calpain 4, small subunit (30K)	efhand	24.4
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	FKBP	24.3
	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF annexin	24.0 23.1
25	413726 438951	AJ278465 U51336	Hs.75510 Hs.6453	annexin A11 inositol.1,3,4-triphosphate 5/	oxidored_nitro	23.0
23	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase	23.0
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2	22.4
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase	22.4
	413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKc	22.3
30	422639	AI929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	21.5
	429869	Al907018	Hs.15977	Target CAT		21.3
	418891	NM_002419		mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC	21.1
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal	RYDR_ITPR,RyR,SPRY,ion_tr	21.0
35	432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	20.9 20.8
33	452875 426997	BE275760	Hs.30928	DNA segment on chromosome 19 (peptidylprolyl isomerase F (cy	Euk_porin pro_isomerase	20.8
	402916	BE620738	Hs.173125	ENSP00000202587*:Bicarbonate t	HCO3_cotransp	20.8
	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfalase	20.7
	400419	AF084545		Target	EGF,ig,lectin_c,sushi,Xli	20.0
40	419444	NM_002496	Hs.90443	Target CAT	fer4	19.5
	459133	U40343	Hs.29656	cyclin-dependent kinase Inhibi	ank	19.2
	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	19.2
	422708	AB017430	Hs.119324	kinesin-like 4	kinesin,homeobox	19.0
45	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	18.8 18.5
43	429712 425848	AW245825 8E242709	Hs.211914 Hs.159637	ENSP00000233627*:NADH-ubiquino valyl-tRNA synthetase 2	oxidored_q6 GST_C,GST_N,Tropomyosin	18.4
	423648 451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	18.1
	447859	AK002194	Hs.19851	peroxisomal biogenesis factor	raises fraise a fraise	17.5
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	DAG_PE-bind,RhoGAP	17.3
50	421612	AF161254	Hs.106196	8D6 antigen	ldl_recept_a	17.1
	421363	NM_001381	Hs.103854	docking protein 1, 62kD (downs	PH,IRS	16.9
	442739	NM_007274		cytosolic acyl coenzyme A thio	Acyl-CoA_hydro	16.8
	420568	F09247	Hs.247735	protocadherin alpha 10	cadherin	16.8
55	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054	asp skings KA11IBA	16.8 16.7
55	425424 446329	NM_004954 NM_013272		ELKL motif kinase solute carrier family 21 (orga	pkinase,KA1,UBA kazal,OATP_N,OATP_C	16.5
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail,I	16.4
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4	PX,SH3,OPR	16.3
	429183	AB014604	Hs.197955	KIAA0704 protein	PH,Oxysterol_BP	16.2
60	444664	N26362	Hs.11615	map kinase phosphatase-like pr	DSPc,Rhodanese	16.2
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,fate_protein_L2	16.2
	425123	AW205274	Hs.154695	phosphomannomutase 2	PMM	16.0
	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	15.8
65	412942	AL120344	Hs.75074	mitogen-activated protein kina	pkinase	15.8 15.7
05	423366 426391	Z80345 AW161050	Hs.127610 Hs.169611	acyl-Coenzyme A dehydrogenase, second mitochondria-derived ac	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXV	p450	15.5
	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red	15.5
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	7tm_2,EGF,cadherin,lamini	15.4
70	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	Collagen	15.3
	427326	A1287878		gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	7tm_1 1	15.2
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668		15.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	15.0
75	449936	AA938293	Hs.60088	hypothetical protein MGC11314	comploy1 24kD	15.0 14.7
15	409230	AA852431 NM : 015071	Hs.51299 Hs.132942	NM_021074:Homo sapiens NADH de GTPase regulator associated wi	complex1_24kD RhoGAP,SH3,PH	14.0
	423801 419639	AK001502	Hs.132942 Hs.91753	hypothelical protein	reloant follows 11	13.6
	419298	AA853479	Hs.89890	pyruvate carboxylase	CPSase_L_chain,PYC_OADA,H	13.6
	426108	AA622037	Hs.166468	programmed cell death 5	DUF122	13.5
80	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec	13.5
_	418736	T18979	Hs.87908	Snf2-related CBP activator pro	helicase_C,AT_hook	13.5
	436543	NM_002212		integrin bata 4 binding protei	elF6	13.3
	431515		Hs.258583	endothelial differentiation, I	7tm_1	13.3
	429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDC-P	13.2
				24	7	

	124.400	414500000	11- 050044	1		40.0
	431462		Hs.256311	granin-like neuroendocrine pep		13.2
	444855	BE409261	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	13.2
	423464	NM_016240	Hs.128856	CSR1 protein	Collagen	13.1
	450787	AB006190	Hs.25475	aquaporin 7	MIP	13.0
5	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr	13.0
_	436014	AF281134	Hs.283741		RNase_PH,RNase_PH_C	12.9
	416866	AA297356		exosome component Rrp46		12.9
			Hs.80324	serine/threonine protein phosp	Metallophos	
	433867	AK000596	Hs.3618	hippocalcin-like 1	efhand	12.9
• •	411408	U76666	Hs.69949	calcium channel, voltage-depen	ion_trans	12.8
10	432329	NM_002962	Hs.2960	S100 calcium-binding protein A	S_100,ethand	12.7
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related c	10م_20,DED,ICEم_200	12.7
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PBD,WH2	12.7
	428820	AA436187	Hs.172631	integrin, alpha M (complement	FG-GAP	12.7
	446603	NM 014835		oxysterol-binding protein-rela	Oxysterol_BP	12.6
15						
13	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	enolase	12.6
	446839	BE091926	Hs.16244	mitolic spindle colled-coll re	Troponin	12.6
	414757	U46922	Hs.77252	fragile histidine triad gene	HIT	12.5
	428593	AW207440	Hs.185973	degenerative spermatocyte (hom		12.5
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosph	Antifreeze.NeuB	12.5
20	401542			C15001413*:gi 10645199 ref NP_		12.4
	428782	X12830	Hs.193400	interleukin 6 receptor	fn3,ig	12.3
	425999	AW513051	Hs.332981	ESTs, Weakly similar to 138022	FAD_binding_2	12.3
	. 422301	Al752163	Hs.114599	collagen, type VIII, alpha 1	C1q,Collagen	12.2
25	410720	AF035154	Hs.65756	regulator of G-protein signall	RGS,G-gamma,DEP	12.2
25	407143	C14076	Hs.332329	EST .,		12.1
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2	12.1
	425251	Z22521	Hs.155342	protein kinase C, delta	pkinase,DAG_PE-bind,pkina	12.0
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	PWWP,PHD "	12.0
	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH_RNase_PH_C	12.0
30	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-	ig,ITAM,Zn_clus	12.0
50	427336			TNF receptor-associated factor	MATH	12.0
		NM_005658			* :**-	
	409799	D1 1928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	11.9
	436319	H90727	Hs.5123	inorganic pyrophosphatase	Pyrophosphatase	11.9
	400748			NM_022122:Homo sapiens matrix		11.9
35	428948	BE514362		FK506-binding protein 3 (25kD)	FKBP,PIP5K	11.8
	401215			C12000457*:gij7512178[pir][T30	trypsin	11.7
	401281			DKFZP586N2124 protein	•	11.7
	427397	AI929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD	11.7
						11.7
40	453496	AA442103	Hs.33084	solute carrier family 2 (facil	sugar_tr	
40	409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	7tm_2,cadherin,GPS,lamini	11.7
	424415	NM_001975		enolase 2, (gamma, neuronal)	enolase	11.7
	447495	AW401B64	Hs.18720	programmed cell death 8 (apopt	pyr_redox	11.6
	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-ci	adh_short	11.6
	405371			NM_005569*:Homo sapiens LIM do	pkinase,LIM,PDZ	11.5
45	416282	R86664	Hs.167257	brain link protein-1	Xlink	11.4
	452295	BE379936	Hs.28866	programmed cell death 10	,	11.4
	430390	AB023186	Hs.241161	KIAA0969 protein	PH	11.4
					PH	
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	rn	11.2
50	443814	BE281240	Hs.9857	carbonyl reductase		11.2
50	440242	AW295871		glucose transporter protein 10		11.1
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	11.1
	400843			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	11.1
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	11.0
	400232			NM_001895*:Homo sapiens casein	pkinase	10.9
55	426828	NM_000020	Hs.172670	activin A receptor type II-lik	pkinase,Activin_recp	10.9
	431157	Al823969	Hs.132678	ESTs	MAPEG	10.8
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	AIRS,AIRS_C	10.8
	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	AINO,AINO_O	10.8
			115,275574		7fm 1 .	10.8
60	400389	AL135841		olfactory receptor, family 2,	7fm_1	
UU	402207	VAFOOR	11- 4075	Target Exon	A2M_N,A2M	10.8
	435615	Y15065	Hs.4975	potassium voltage-galed channe	ion_trans,KCNQ1_channel	10.8
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	tectin_c	10.7
	402053			C11001722*:gi 11436283[ref]XP_		10.7
~~	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Reprotysin,Pe	10.6
65	431512	BE270734	Hs.2795	lactate dehydrogenase A	ldh,ldh_C	10.6
	403213			NM_019595:Homo sapiens interse	SH3,efhand,C2,PH,RhoGEF	10.6
	412158	BE241740	Hs.785	integrin, alpha 2b (platelet g	FG-GAP,integrin_A	10.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m	Peptidase_M10,hemopexin	10.6
	403949	3200007		C10000813*:gi[5453992[ref[NP_0	. oposootop.omppomi	10.6
70		AESSOCO	Nº 33440		cha	
70	457670	AF119666	Hs.23449	insulin receptor tyrosine kina	SH3	10.5
	418416	U11700	Hs.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hydrolas	10.4
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding	BRCT	10.4
	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIRTK	10.4
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI	10.4
75	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2	10.4
	438800	AB037108	Hs.6418	seven transmembrane domain orp		10.3
	402478	AD001 100	1.5.0710	Target Exon	Carn_acyltransf	10.3
		A1 024505	Un 12795			10.3
	444202	AL031685	Hs.12785	KIAA0939 protein	Na_H_Exchanger,ABC2_membr	
9Λ	425597	U28694	Hs.158324	chemokine (C-C motif) receptor	7tm_1	10.3
80	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E	UQ_con	10.2
	415200	AL040328	Hs.78202	SWI/SNF related, matrix associ	SNF2_N,helicase_C,bromodo	10.2
	414874	D26351	Hs.77515	inositol 1,4,5-triphosphate re	RYDR_ITPR.ion_trans,MIR	10.2
	423524	AF055989	Hs.129738	potassium voltage-gated channe	ion_trans,K_tetra,thaumat	10.2
	457558	AF083955	Hs.279852	G protein-coupled receptor	7tm_1,globin	10.2
				24		

	445500	41045704	11 400000	Should be the same		10.1
	445629	Al245701	Hs.193326	fibroblast growth factor recep		10.1
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf	10.1
	402497	. ========		C1001261*:gij2695979[emb]CAA70		
_	449853	AF006823	Hs.24040	potassium channel, subfamily K	lon_trans	10.0
5	427672	AA356615	Hs.336916	death-associated protein 6		10.0
	412048	AW866863	Hs.73090	nuclear factor of kappa light	RHD,TIG,ank,death	10.0
	410079	U94362	Hs.58589	glycogenin 2	Glyco_transf_8	10.0
	420319	AW406289	Hs.96593	hypothetical protein	ras,arf	10.0
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinas	serpin	9.9
10	405474			NM_001093*:Homo sapiens acetyl	CPSase_L_chain,blotin_lip	9.9
	401507			C15000810°:gi 11131272 sp P793		9.9
	431434	BE267696	Hs.254105	enolase 1, (alpha)	enolase	9.9
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha		9.8
	432343	NM_002960		S100 calcium-binding protein A	S_100	9.8
15	408931	AA251995	Hs.334648	poly(A) polymerase alpha	NTP_transf_2	9.8
	421542	AA411607	Hs.118964	ESTs, Weakly similar to KIAA11		9.8
	430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101	9.8
	412270	AC005262	Hs.73797	guanine nucleotide binding pro	G-alpha,arf	9.7
	424649	BE242035	Hs.151461	embryonic ectoderm development	WD40	9.7
20	400772	DL242000	115.101401	NM_003105*:Homo sapiens sortil	ldi_recept_a,fn3,ldi_rece	9.7
20	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	flavodoxin,FAD_binding,NO	9.7
	401510	141537 10	ns. 1000/3	NM_017434:Homo sapiens dual ox	efhand,Ferric_reduct	9.7
		•			emain, emo_reduct	9.7
	404596	4 4000700	11- 00000	Target Exon	pkinase	9.7
25	451367	AA923729	Hs.26322	cell cycle related kinase		9.6
25	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	
	432855	AF017988	Hs.279565	secreted frizzled-related prot	Fz,NTR	9.6
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hyd	fn3,lg,lRK	9.6
	430398	AF105202	Hs.241376	potassium voltage-gated channe	lon_trans,KCNQ1_channel	9.6
20	424339	BE257148		endoglycan	MCM	9.6
30	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	PGAM	9.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF	9.6
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta		9.6
	409649	AA159216	Hs.55505	hypothetical protein FLJ20442	Y_phosphatase,DSPc	9.6
	404968			C4001170:gi[6863176]gb[AAF3040		9.5
35	400833			C11000890:gij3746443jgbjAAC639	7tm_1	9.5
	410191	Al609645		NM_021075*:Homo sapiens NADH d		9.5
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	lg .	9.4
	427747	AW411425	Hs.180655	serine/threonine kinase 12	pkinase	9.4
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F	9.4
40	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis	CARD	9.4
	422328	X60459	Hs.1513	interferon (alpha, beta and om		9.4
	445143	U29171	Hs.75852	casein kinase 1, delta	pkinase	9.4
	450883	NM_001348		death-associated prolein kinas	pkinase	9.4
	414625	AA335738	Hs.76686	glutathione peroxidase 1	GSHPx	9.3
45	401935	771000730	113.70000	Target Exon	PH	9.3
43	418329	AW247430	Hs.84152	cystathionine-beta-synthase	PALP,CBS	9.3
	425242	D13635	Hs.155287	KIAA0010 gene product	HECT,IQ	9.3
	400404	AF161221	H3.13320/	kallikrein 14	trypsin	9.2
	442332	Al693251	Hs.8248	Target CAT	fer2,molybdopterin,bac_dn	9.2
50					ierz,moryboopterar,bac_urr	9.2
50	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4		9.1
	402823			C1002456*:gi[9930918]emb[CAC05	CD44 CD20	9.1
	404527	414047500	11- 0700	peptide YY, 2 (seminalplasmin)	GDA1_CD39	
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_Jb,Lipase_GDSt_	9.1 9.1
55	412970	AB026436	Hs.177534	dual specificity phosphalase 1	Rhodanese, DSPc	9.1
55	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fami	ABC_tran	9.0
	400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD	
	403268	040004	11- 45034	NM_002210*:Homo sapiens integr	FG-GAP	9.0
	446673	NM_016361		LPAP for lysophosphatidic acid	acid_phosphat	9.0
60	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2	pkinase	9.0
00	421658	X84048	Hs.301760	frequenin (Drosophila) homolog	efhand	9.0
	401885			Target Exon	kinesin	9.0
	402651			NM_000721*:Homo sapiens calciu	ion_trans	9.0
	457432	NM_005136	Hs.268538	potassium voltage-gated channe	ISK_Channel	9.0
	433146	AB033002	Hs.21413	solute carrier family 12, (pot		9.0
65	420090	AA220238	Hs.94986	ribonuclease P (38kD)	Ribosomal_L7Ae	9.0
	425281	AA444390	Hs.155482	hydroxyacyl glutathlone hydrol	lactamase_B	9.0
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	SNF2_N,helicase_C	9.0
	407986	U32659	Hs.41724	interleukin 17 (cytotoxic T-ly		9.0
	431131	N84730	Hs.250616	Isocitrate dehydrogenase 3 (NA	isodh .	9.0
70	422802	NM_004278	Hs.27008	phosphatidylinositol glycan, c	DUF158	9.0
·	447958	AW796524	Hs.68644	Homo sapiens microsomal signal		9.0
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		9.0
	418843	AJ251016	Hs.89230	potassium intermediate/small c	CaMBD,SK_channel	9.0
	419244	Al436567	Hs.89761	ATP synthase, H transporting,	ATP-synt_DE	8.9
75	404676			Target Exon	• =	8.9
. •	428744	BE267033	Hs.192853	ubiquitin-conjugating enzyme E	UQ_con	8.9
	421474	U76362	Hs.104637	solute carrier family 1 (gluta	SDF	8.9
	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-	lg,ITAM	8.9
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy,Glycos_trans	8.9
80	424025 444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2	8.9
00		301120	113.646	ENSP00000211797*:Helicase SKI2	RasGAP,PH	8.9
	404199 428826	AL048842	Hs.194019	attractin	lectin_c,CUB,Kelch,PSI,EG	8.9
				calbindin 1, (28kD)	efhand	8.8
	410681	AW246890	Hs.65425			8.8
	415056	AB004662	Hs.77867 .	adenosine A1 receptor	7tm_1	0.0
				2.44	^	

	100171			Towart From		8.8
	400471 406591			Target Exon NM_003888*:Homo saplens retina	aldedh	8.8
	425427	AI652662	Hs.157205	branched chain aminotransferas	aminotran_4	8.8
_	410839	NM_006849		protein disulfide Isomerase	thiored,Rho_GDI,gntR	8.7
5	430037		Hs.227789	mitogen-activated protein kina	pkinase	8.7
	450848	A1677994	Hs.428	fms-related tyrosine kinase 3	flt3_lig	8.7
	414534	BE257293	Hs.76366	BCL2-antagonist of cell death		8.7
	401454			NM_014226*:Homo sapiens renal	pkinase	8.7
10	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM	8.7
10	433333	Al016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	8.7 8.7
	430432 406128	A8037758	Hs.241419	KIAA1337 protein NM_002920*:Homo sapiens regula	Patched Oest_recep,zf-C4,hormone_	8.7
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI	8.7
	439569		Hs.222399	CEGP1 protein	CUB,EGF	8.6
15	401134	, , , , , , , , , , , , , , , , , , , ,		C12001198:gi[3183183[sp[Q92142	biopterin_H	8.6
	442286	W31847	Hs.50335	cylochrome P450 monooxygenase	, -	8.6
	428376	AF119665	Hs.184011	pyrophosphatase (Inorganic)	Pyrophosphatase	8.6
	433494	AB029396		beta-1,3-glucuronyitransferase	Glyco_tranf_43	8.6
20	427001	NM_006482		dual-specificity tyrosine-(Y)-	pkinase	8.6
20	437278		Hs.290145	ESTs	cNMP_binding	8.6
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin	lipocalin,Kunitz_BPTI	8.6 8.6
	421871 447827		Hs.306122 Hs.19718	glycoprotein, synaptic 2 protein tyrosine phosphatase,	Steroid_dh Y_phosphalase,fn3,ig,MAM	8.6
	403379	UISIZI	rts. 131 10	Target Exon	DNA_pol_A	8.6
25	446872	X97058	Hs.16362	pyrimidinergle receptor P2Y, G	7tm_1	8.6
	432857	NM_016103		GTP-binding protein Sara	arf,ras	8.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B .	8.5
	427221	L15409	Hs.174007	van Hippel-Lindau syndrome	VHL	8.5
20	402209			Target Exon	A2M_N,A2M	8.5
30	400518			C10002057*:gi[3211705lgb AAC21		8.5
	425606	U52112	Hs.158331	renin-binding protein	PagCEE	8.5 8.5
	437965 433392	AA843222 AF038535	Hs.193534 Hs.127588	ESTs, Moderately similar to AL synaptotagmin VII	RasGEF C2	8.5
	402191	AF030333	NS. 127300	NM 021733*:Homo saptens testis	C2	8.5
35	458963	A1701393	Hs.278728	Rad and Gem-related 2 (rat hom	ras	8.5
-	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg	8.5
	457579	AB030816	Hs.36761	HRAS-like suppressor		8.5
	409656	NM_005133	Hs.288626	RCE1, prenyl protein protease	Abl	8.5
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, s		8.4
40	432499	BE276633		RAB6B, member RAS oncogene fam	ras,arf	8.4 8.4
	400565			Target Exon	Branch	8.3
	401960 432545	X52486	Hs.3041	Target Exon uracil-DNA glycosylase 2	cyclin	8.3
	445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	sushi	8.3
45	404528	////D02100	110.12000	peptide YY, 2 (seminalplasmin)	GDA1_CD39	8.3
	428542	D79989		KIAA0167 gene product	ank,PH,ArfGap,ras	8.3
	406868	AA505445	Hs.300697	Immunoglobulin heavy constant		8.3
	405473			NM_001093*:Homo sapiens acetyl	CPSase_t_chain,blotin_lip	8.3
50	408601	U47928	Hs.86122	protein A	7tm_1	8.3
50	415008	NM_002777		proleinase 3 (serine proteinas	trypsin	8.3 8.3
	430258 436483	AU076644 AJ272063	Hs.236963 Hs.283010	protein phosphatase 2A, regula vanilloid receptor subtype 1	ank,ion_trans	8.3
	459302	NM_002314		LIM domain kinase 1	and out a mis	8.3
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	lectin_c	8.3
55	421707	NM_014921		lectomedin-2	Latrophilin,OLF,7tm_2,Gal	8.2
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/m	COesterase	8.2
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	•	8.2
	424053	AF057036	Hs.138520	collagen-like tall subunit (si	Collagen	8.2
60	457398	BE258532	Hs.251871	CTP synthase	GATase	8.2
60	421504 406495	AW402997	Hs.105052	adaptor protein with pleckstri Target Exon	SH2,PH SRCR	8.1 8.1
	453610	AW368882	Hs.33818	RecQ protein-like 5	DEAD,helicase_C	8.1
	424880	NM_000328		retinitis pigmentosa GTPase re	RCC1	8.1
	423847	U16997	Hs.133314	RAR-related orphan receptor C	hormone_rec,zf-C4	8.1
65	409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	8.1
	401180			eukaryotic translation elongat	ion_trans,IQ	8.1
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf	8.1
	426484	AA379658	Hs.272759	KIAA1457 protein	IP_trans	8.1
70	402453	14/000000	11- 000750	C1002496:gi 7363439 ref NP_039	7tm_1	8.1 8.1
70	457310 422069	W28363 AJ010063	Hs.239752 Hs.343603	nuclear receptor subfamily 2, titin-cap (telethonin)	globin,cNMP_binding,pkina	8.1
	400275	A3010003	115,543000	NM_006513*:Homo sapiens seryi-	NA	8.0
	434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases	8.0
	430299	W28673	Hs.106747	serine carboxypeptidase 1 prec	-	8.0
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR	8.0
	402393			ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH	8.0
	429252		Hs.198312	RAS protein activator like 1 (C2,PH,RasGAP,BTK	8.0
	456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9	7.9
80	431493	Al791493	Hs.129873	ESTs, novel cytochrome P450	p450 ABC_tran,SRP54	7.9 7.8
ou	451558 415758	NM_001089 BE270465	Hs.26630 Hs.78793	ATP-binding cassette, sub-fami protein kinase C, zeta	pkinase,DAG_PE-bind,pkina	7.8
	419270	NM_005232		EphA1	EPH_lbd,pkinase,SAM,fn3	7.8
	422837	U25441	Hs.121478	doparnine receptor D3	7tm_1	7.8
	401118			Target Exon	pkinase	7.8
				0.5	0	

	426440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr	7.8
	418635	L11329				7.8
			Hs.1183	dual specificity phosphatase 2	DSPc,Rhodanese,Y_phosphat	
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin	7.8
_	403672			C4001244:gij539933[piri]A61275	tubulin	7.8
5	437806	AJ424921	Hs.122487	ESTs, Weakly similar to A54854	RasGAP	7.7
-						
	456890	U48213	Hs.155402	D site of albumin promoter (al	DAGKc,bZIP	7.7
	424107	AB014606	Hs.139648	kinesin family member 1C	kinesin,FHA	7.7
	452695	AW780199	Hs.30327	mitogen-activated protein kina	•	7.7
					-MAID EXP	
1.0	433262	Al571225	Hs.284171	KIAA1535 protein	cNMP_binding,ion_trans	7.7
10	424198	AB029010	Hs.143026	KIAA1087 protein	Na_Ca_Ex,Calx-beta	7.6
	406496			Target Exon	SRCR	7.6
		MM 005007	LI- 457400			
	425423	NM_005897	ns. 13/160	intracistemal A particle-prom	BTB,Kelch	7.6
	402211			KIAA0430 gene product	ion_trans,K_tetra	7.6
	408710	Y10256	Hs.47007	mitogen-activated protein kina	pkinase,SAM_decarbox	7.5
15		W56321				
13	457615	1750544	Hs.111460	calcium/calmodulin-dependent p	pkinase	7.5
	402760			NM_021797*:Homo sapiens eosino	Glyco_hydro_18,CBM_14	7.5
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	C1q, Collagen	7.4
	423579	NM_004121		gamma-glutamyltransferase-like	G_glu_transpept	7.4
	413104	L42374	Hs.75199	protein phosphatase 2, regulat	B56	7.4
20	419660	BE280337	Hs.194693	solute carrier family 7 (catio	aa_permeases	7.4
	424774	BE244179	Hs.153022		44_5064666	7.4
		DC244173	HS. 153022	TATA box binding protein (TBP)		
	402632			Target Exon	Fz,kringle,ig	7.4
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like	ARID, SNF	7.4
	405714			ENSP00000221137:Olfactory rece	7tm_1	7.3
25		A A DE74 C4	11- 0CC0			
25	442732	AA257161	Hs.8658	hypothetical protein DKFZp434E	EGF,laminin_EGF,Xlink,S_m	7.3
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	7.3
	415995	NM_004573		phospholipase C, beta 2	PI-PLC-X,PI-PLC-Y,C2	7.3
		*****			111 20 741 11 20 1,02	
	405137			Target Exon		7.3
	402460			C1001261*:gi 2695979 emb CAA70		7.3
30	431398	BE616547	Hs.2785	keratin 17	filament	7.3
-0						
	429592	AB029041	Hs.209646	KIAA1118 protein	Troponin	7.3
	429225	BE250337	Hs.198273	Target CAT		7.2
	423015	U18548	Hs.123034	G protein-coupled receptor 12		7.2
	454373				ALI	7.0
25		NM_005133		RCE1, prenyl protein protease	Abi	7.2
35	440188	AK001812	Hs.7036	N-Acetylglucosamine kinase	ROK	7.2
	432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc		7.2
	446143	BE245342			secY	7.0
			Hs.306079	sec61 homolog		7.2
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1	7.2
	440869	NM_014297	Hs.7486	protein expressed in thyroid	lactamase_B	7.1
40	435099	AC004770	Hs.4756	flap structure-specific endonu	XPG_N,XPG_I,5_3_exonuclea	7.1
-10					VLQ_W'VLQ_1'2_2_exoundreg	
	437161	AA054477	Hs.25391	ESTs	•	7.1
	429683	AF148213	Hs.211604	a disintegrin-like and metallo	tsp_1,Reprolysin,Pep_M12B	7.1
	426268	AF083420	Hs.168913	serine/threonine kinase 24 (St	pkinase	7.1
AF	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	7.1
45	416377	AA179930	Hs.293867	caspase recruitment domain pro		7.1
	421748	NM_014718	Hs 107809	KIAA0726 gene product	cadherin	7.1
	426691					
		NM_006201		PCTAIRE protein kinase 1	pkinase	7.0
	428599	AB033078	Hs.186613	sphingosine-1-phosphate lyase	pyridoxal_deC	7.0
	411898	BE409714	Hs.44856	hypothetical protein FLJ12116		7.0
50	427010	AW138332		muscle RAS oncogene homolog	ras	7.0
20			11 000404			
	457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	ras,arf	7.0
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	7.0
	457764	AW028284	Hs.4815	nudix (nucleoside diphosphate	NUDIX	6.9
		AF213457				
55	435575		Hs.44234	triggering receptor expressed	ig	6.9
55	456488	AW015098	Hs.301946	ESTs, Weakly similar to T30867		6.9
	428761	AF236119	Hs.193076	GRB2-related adaptor protein 2	SH2,SH3	6.9
	430396	D49742	Hs.241363	hyaluronan-binding protein 2	trypsin,kringle,EGF	6.9
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	6.9
	445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2	6.9
60	457499	AA953015	Hs.274370	hypothetical protein FLJ20260	PH	6.8
-5		74 000010	· 13,4,1 TO 1 V			
	400845			NM_003105*:Homo saplens sortil	ldl_recept_a,fn3,ldl_rece	6.8
	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen	6.8
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistan	dynamin_2,dynamin,GED	6.8
65	432990	AL036071	Hs.279899	tumor necrosis factor receptor	TNFR_c6	6.8
65	458128	W32474	Hs.301746	RAP2A, member of RAS oncogene	ras,arf,ldh	6.8
	429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,ig	6.8
	401488			Target Exon	Glyco_hydro_1	6.7
	456243	Al345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	6.7
	424321	W74048	Hs.1765	lymphocyte-specific protein ty	SH2,SH3,pkinase	6.7
70		*** *****	.13.1100			
70	405187		44	NM_014272:Homo sapiens a disin	Reprolysin,tsp_1,Pep_M12B	6.7
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	p450	6.7
	448496	BE379077	Hs.130849	ESTs, Weakly similar to 138022	NADHdh_2	6.7
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
	417103	Z33905	Hs.81218	hypothetical protein MGC3597	TPR,zf-C3HC4,PHD	6.7
75	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	FAD_Synth	6.7
. •						
	456469	NM_005109		oxidative-stress responsive 1	zf-C2H2.pkinase	6.7
	449546	W86248	Hs.58819	ESTs	hexokinase	6.6
	428926	NM_001702		brain-specific angiogenesis in	7tm_2,tsp_1,GPS,HRM	6.6
				C1002000*:gi]12735712 ref XP_0		
90	404953	44.40	11			6.6
80	449401	AL135401	Hs.23557	serologically defined colon ca	pro_lsomerase	6.6
	429962	M69113	Hs.226795	glutathione S-transferase pi	GST_C,GST_N	6.6
	421547	AA489908	Hs.1390	proteasome (prosome, macropain	Ctathrin_lg_ch,proteasome	6.6
	430035	NM_003463		protein tyrosine phosphatase t	Y_phosphatase,DSPc	6.6
	406867	AA157857	Hs.182265	keratin 19	filament,bZIP	6.6
				25		

	404946 435213	AA092510	Un Enge	Target Exon	3Beta_HSD	6.5
	411201	T74588	Hs.5985 Hs.8509	non-kinase Cdc42 effector prot ESTs, Weakly similar to C3HU c	A2M_N,A2M	6.5 · 6.5
	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	6.5
5	426194	T50872	Hs.2001	thromboxane A synthase 1 (plat	p450	6.5
	424681	AA054400	Hs.151706	KIAA0134 gene product	helicase_C,PRK	6.5
	417903	NM_002342		lymphotoxin beta receptor (TNF	TNFR_c6	6.5
	408905 438646	AV655783 AI973076	Hs.661 Hs.231958	Target CAT		6.5 6.5
10	431530	X61615	Hs.2798	matrix metalloproteinase 28 leukemia inhibitory factor rec	fn3	6.5
	428883	AA436959	Hs.258802	ATPase, (Na)/K transporting, b	Na_K-ATPase	6.5
	404757			Target Exon	_	6.4
	406370			interleukin 11	trypsin	6.4
15	443611	NM_014397		NIMA (never in mitosis gene a)	pkinase	6.4
13	424008 444912	R02740 AW247380	Hs.137555 Hs.12124	putative chemokine receptor, G putative prostate cancer susce	7tm_1 lactamase_B	6.4 6.4
	454460	X66945	Hs.748	fibroblast growth factor recep	ig,pkinase	6.4
	432269	NM_002447		macrophage stimulating 1 recep	pkinase,Sema,PSI,TIG,A4_E	6.4
20	458718	AI359476	Hs.157699	ESTs		6.4
20	405282			Target Exon	Cache	6.4
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	6.3
	442297 400894	NM_006202	ns.09901	phosphodiesterase 4A, cAMP-spe C11000129:gij9938014 ref NP_06	PDEase 7tm_1	6.3 6.3
	440446	NM_013385	Hs 7189	pleckshin homology, Sec7 and	PH,Sec7	6.3
25	430886	L36149	Hs.248116	chemokine (C motif) XC recepto	7tm_1	6.3
	451394	NM_003595		tyrosylprotein sulfotransferas	Sulfotransfer	6.3
	436523	BE612990	Hs.5212	single-strand selective monofu		6.3
	422714	AB018335	Hs.119387	KIAA0792 gene product	DUF221	6.3
30	408924 414551	AW295606 Al815639	Hs.236131 Hs.76394	homeodomain-interacting protei	ECH,Peptidase_U7	6.3 6.3
50	413254	U40272	Hs.75253	encyl Coenzyme A hydratase, sh isocitrate dehydrogenase 3 (NA	isodh	6.3
	415010	NM_004203		membrane-associated tyrosine-	pkinase	6.3
	449761	AB009698	Hs.23965	solute carrier family 22 (orga	sugar_tr	6.3
25	432221	M21191	Hs.273415	aldolase A, fructose-bisphosph	glycolytic_enzy,Adeno_E3_	6.3
35	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C	6.2
	458516 417985	BE010749 AA187545	Hs.255097 Hs.83114	ESTs crystallin, zeta (quinone redu	adh aine	6.2 6.2
	447507	H59696	Hs.18747	POP7 (processing of precursor,	adh_zinc	6.2
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibi	Y_phosphatase,DSPc	6.2
40	428443	BE618106	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDC,M	6.2
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin	6.2
	408903	BE244377	Hs.48876	famesyl-diphosphate famesylt	SQS_PSY,dsrm,z-alpha	6.2
	426176 421395	AB000462 D90084	Hs.167679	SH3-domain binding protein 2	PH,SH2	6.1 6.1
45	430517	S80071	Hs.1023 Hs.241597	pyruvate dehydrogenase (lipoam solute carrier family 6 (neuro	E1_dehydrog SNF	6.1
	435906	AI686379	Hs.110796	SAR1 protein	arf,ras	6.1
	402758			C1001899*:gi]12722636[ref]XP_0	Glyco_hydro_18	6.1
	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
50	402115	A C0003300	11- 27400	NM_021624:Homo saplens histami	7tm_1	6.1
50	407601 404679	AC002300	Hs.37129	sodium channel, nonvoltage-gat Target Exon	ASC	6.1 6.0
	450739	Al732707		ESTs, Weakly similar to ALU7_H	V1R	6.0
	439888	AB040949	Hs.6733	pancreas-enriched phospholipas	C2,PI-PLC-Y,PI-PLC-X,RasG	6.0
	415742	BE410243	Hs.78769	thimet oligopeptidase 1	Peplidase_M3	6.0
55	453190	AB002354	Hs.32312	KIAA0356 gene product	PH,PHD,RUN	6.0
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleo	Ham1p_like	6.0 6.0
	412800 432805	AW950852 X94630	Hs.74598 Hs.3107	polymerase (DNA directed), del CD97 antigen	homeobox 7tm_2,GPS,EGF	6.0
	418964	T74640	110.0107	gb:yc57c12.r1 Stratagene liver	A2M_N,A2M	6.0
60	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	6.0
	419755	H18444	Hs.134846	BAI1-associated protein 3	C2 C2	6.0
	457276	AF235097	Hs.227583	Homo sapiens chromosome X map	DU 4-70	6.0
	423908 432118	AJ006422 N98718	Hs.135183	centaurin-alpha gb:yy65g02.r1 Soares_multiple_	PH,ArfGap	6.0 5.9
65	427334	R44789	Hs.33191	Homo sapiens, Similar to trans		5.9
	424959	NM_005781		activated p21cdc42Hs kinase	pkinase,SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans	5.9
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB	p450	5.9
70	422287	F16365	Hs.114346	cytochrome c oxidase subunit V	COX7a,Phage_G	5.9
70	401736 434755	AA648502		C16000492*:gi 3127193 gb AAD05 ESTs	AMP-binding	5.9 5.9
	414962	AF273304	Hs.235376	XPMC2 protein	Exonuclease	5.8
	407338	AA773213		gb:ab66f10.s1 Stratagene lung	ig	5.8
7.	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting an	•	5.8
75	409686	AK000002	Hs.55879	Homo saplens mRNA; cDNA DKFZp4	ABC_tran	5.8
	450778	U81375	Hs.25450	solute carrier family 29 (nucl	Nucleoside_tran	5.8
	423612 430845	NM_002067 AF024690	Hs.1686 Hs.248056	guanine nucleotide binding pro G protein-coupled receptor 43	G-aipha,arf 7tm_1	5.8 5.8
	424741	AF051941	Hs.343824	nucleoside diphosphate kinase	NDK	5.8
80	412958	BE391579	Hs.75087	Fas-activated serine/threonine		5.8
-	415701	NM_003878	Hs.78619	gamma-glutarnyi hydrolase (conj	GATase	5.8
	423158	H97991	Hs.193313	Target CAT	MoaA_NifB_PqqE	5.8
	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	5.8
	412915	AW087727	Hs.74823 .	NM_004541:Homo saplens NADH de	_	5.7
				25	7	

	420904	AL035954	Hs.100221	nuclear receptor subfamily 1.	hormone_rec,zf-C4	5.7
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransfera	Sulfotransfer	5.7
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ11214 fis	DEAD,helicase_C,dsrm,Vira	5.7
-	409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha		5.7
5	428270	BE501549	Hs.107040	ESTs		5.7
	435114	AA775483	Hs.288936	mitochondrial ribosomal protei	ODC_AZ	5.7
	425211	M18667 A1878908	Hs.1867	progastricsin (pepsinogen C)	asp	5.7
	453054 420730	NM_002691	Hs.31547 Hs.99890	Target CAT polymerase (DNA directed), del	ICL	5.7 5.7
10	415117	AF120499	Hs.78016	polynucleolide kinase 3'-phosp	Viral_helicase1	5.7
	400985	7.1. (20 100	110.1 0010	Target Exon	Thu_nemast	5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase	5.7
	413858	NM_001610	Hs.75589	acid phosphatase 2, lysosomal	acid_phosphat	5.7
	457308	AI416988	Hs.238272	inositol 1,4,5-triphosphate re	ion_trans,RYDR_ITPR,MIR	5.7
15	400551			C10001991*:gij6624920jembjCAB6	SRCR	5.7
	433472	Al541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	5.7
	409531	BE384319	Hs.54702	xylosylprotein beta1,4-galacto	Galactosyl_T_2	5.7
	449139 450207	BE268315 T87615	Hs.23111 Hs.14716	phenylalanine-IRNA synthetase- ESTs	neur	5.7 5.7
20	400266	10/015	113.14F10	NM_002858*:Homo sapiens ATP-bi	ABC_tran	5.6
	430713	AA351647	Hs.2642	eukaryotic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (TPR	5.6
	405683			Target Exon		5.6
25	449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
25	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-synt_C	5.6
	415193	AL048891	Hs.12185	hypothetical protein MGC14333		5.6
	434883 433135	AW381538 AA443873	Hs.19807 Hs.110477	hypothetical protein MGC12959 dolichyl-phosphate mannosyltra		5.6 5.6
	413049	NM_002151		hepsin (transmembrane protease	trypsin	5.6
30	420899	NM_001629		arachidonate 5-lipoxygenase-ac	MAPEG	5.6
	423397	NM_001838		chemokine (C-C motif) receptor	7tm_1	5.5
	443759	8E390832	Hs.134729	FXYD domain-containing ion tra		5.5
	454112	NM_000885	Hs.40034	integrin, alpha 4 (antigen CD4	integrin_A,FG-GAP	5.5
25	405594		11	NM_021949:Homo saplens ATPase,	E1-E2_ATPase,Hydrolase	5.5
35	416322	BE019494 AW451473	Hs.79217	pyrroline-5-carboxylate reduct	P5CR,Octopine_DH_N	5.5
	446755 411030	BE387193	Hs.16134 Hs.67896	serine/threonine kinase 10 7-60 protein	pkinase,TYA	5.5 5.5
	431498	AK001777	Hs.258551	aspartyl aminopepildase	Peptidase_M18	5.5
	433012	NM_004045		ATX1 (antioxidant protein 1, y	HMA	5.5
40	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	pkinase,POLO_box	5.5
	424572	M19650	Hs.92909	2',3'-cyclic nucleotide 3' pho		5.5
	406617			Target Exon	efhand,Ferric_reduct	5.5
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pomp	trefoil,Glyco_hydro_31	5.4
45	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	lectin_c	5.4 5.4
73	448093 411574	AW977382 BE242842	Hs.15898 Hs.6780	2,4-dienoyl CoA reductase 2, p protein tyrosine kinase 9-like	adh_short cofilin_ADF	5.4
	406432	00242042	115.07 00	CD1E antigen, e polypeptide	Sulfotransfer	5.4
	428921	Z43809	Hs.194638	polymerase (RNA) II (DNA direc	0.000.000	5.4
	430337	M36707	Hs.239600	calmodulin-like 3	efhand	5.4
50	427162	AB011133	Hs.173864	KIAA0561 protein	pkinase,PDZ	5.4
	414216	D86970	Hs.75822	TGFB1-induced anti-apoptotic f	oxidored_q4,myosin_head,b	5.4
	422083	NM_001141		arachidonate 15-lipoxygenase,	Ipoxygenase,PLAT	5.4
	424373 449405	AJ133798 AA001350	Hs.146219	copine VII gb:zh83h05,r1 Soares_fetal_liv	C2 mito_car .	5.4 5.4
55	409983	D50922	Hs.57729	Kelch-like ECH-associated prot	BTB.Kelch	5.4
	455818	AI733747	Hs.71174	interleukin 21 receptor		5.4
	424357	AW961058	Hs.44856	hypothetical protein FLJ12116		5.4
	423606	AB011094	Hs.129892	KIAA0522 protein	PH,bZIP,IQ,Sec7	5.3
60	432311	BE083080	Hs.274323	similar to sialytransferase 7	Glyco_transf_29	5.3
60	450080 423778	AB037831 Y09267	Hs.24372 Hs.132821	ESTs, Weakly similar to dJ207H	DEAD,GSPII_E FMO-like,pyr_redox	5.3 5.3
	100000	103201	H8.132021	flavin containing monooxygenas	. 400	5.3
	402338 412276	BE262621	Hs.73798	narget Exon macrophage migration inhibitor	MIF	5.3
	437967	BE277414	Hs.5947	mel transforming oncogene (der	ras,arf	5.3
65	424766	BE388855	Hs.152978	proteaseome (prosome, macropal	PA28_alpha,PA28_beta	5.3
	447766 ·	NM_016011		CGI-63 protein	adh_zinc	5.3
	453660	X98507	Hs.286226	myosin IC	myosin_head,IQ	5.2
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	HLH,Myc_N_term,Myc-LZ	5.2
70	432336	NM_002759		protein kinase, interferon-ind	dsrm,pkinase C2	5.2 5.2
, 0	445139 429214	AB037848 AB012722	Hs.12365 Hs.198256	synaptolagmin XIII kinesin-like 3	kinesin	5.2 5.2
	432462	AK000013	Hs.274701	thymidine kinase 2, mitochondr	dNK	5.2
	424387	Al739312	Hs.284163	ANKHZN protein		5.2
75	405697			gb:Human homeobox-like mRNA		5.2
75	450321	Y16521	Hs.24812	CDP-diacylglycerol synthase (p	Cytidylyltrans,Adeno_VII	5.1
	412939	AW411491	Hs.75069	eukaryotic translation elongat	SHMT	5.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate di	GDA1_CD39	5.1
	419073	AW372170 NM_001523	Hs.183918 Hs.57697	Homo sapiens cDNA FLJ12797 fis hyaluronan synthase 1	ig,tsp_1,ZU5 Glycos_transf_2	5.1 5.1
80	409958 442599	AF078037	Hs.324051	RelA-associated inhibitor	SH3,ank	5.1
	424305	BE386095	Hs.112272	histone deacetylase 8	Hist_deacetyl	5.1
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD1	wwa,integrin_A,FG-GAP	5.1
	429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
	420849	X52221	Hs.99987 .	excision repair cross-compleme	_	5.1

	453337	R73417	Hs.25391	gb:yj92g12.r1 Soares breast 2N	GSPII_III	5.1
	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH	5.1
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyro	SH2,SH3,pkinase,PH,BTK	5.1
_	405202			NM_021734*:Homo sapiens deoxyn	mito_carr	5.1
5	451452	BE560065	Hs.26433	dolichyl-phosphate (UDP-N-acet	Glycos_transf_4	5.0
	418231	AA326895	Hs.83848	triosephosphate isomerase 1	TIM	5.0
	425165	NM_014434		Target CAT		5.0
	407876	NM_004519		polassium voltage-gated channe	ion_trans,KCNQ1_channel	5.0
10	417831	H16423	Hs.82685	CD47 antigen (Rh-related antig	ig .	5.0
10	404716			NM_007313*:Homo sapiens v-abl	SH2,SH3,pkinase	5.0
	405020			Target Exon	7tm_1	5.0
	426236	NM_004798		kinesin family member 3B	kinesin	5.0
	433178	AB038269	Hs.253706	cysteinyl leukotriene CysLT2 r	7tm_1	5.0
1.5	422340	AW296219	Hs.115325	RAB7, member RAS oncogene fami	arf,ras	5.0
15	439414	NM_001183		ATPase, H transporting, lysoso		5.0
	425846	AA102174	Hs.159629	myosin IXB	myosin_head,DAG_PE-bind,I	5.0
	413599	AJ006239	Hs.75438	quinoid dihydropteridine reduc	adh_short	5.0
	424168	L29277	Hs.321677	signal transducer and activato	SH2,STAT,STAT_bind,STAT_p	5.0
20	436042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
20	410775	AB014460	Hs.66196	nth (E.coli endonuclease III)-	HhH-GPD	5.0
	428734	BE303044	Hs.192023	eukaryotic translation initial	WD40	5.0
	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide	ITAM	4.9
	433075	NM_002959		sortilin 1	BNR	4.9
25	400300	X03363		HER2 receptor tyrosine kinase	pkinase	4.9
25	426811	BE259228	Hs.172609	nucleobindin 1	efhand	4.9
	401577			NM_000761:Homo sapiens cytochr	p450	4.9
	409637	AA323948	Hs.55407	Homo saplens mRNA; cDNA DKFZp4	Collagen	4.9
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase	4.9
20	430904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
30	423552	AF107028	Hs.129783	sodium channel, voltage-gated,	lg_Adeno_E3_CR2	4.9
	421487	AF027406	Hs.104865	serine/threonine kinase 23	pkinase	4.9
	402183			NM_004491*:Homo sapiens glucoc	FF.	4.9
	456748	AW137749	Hs.125902	ubiquitin specific protease 2	UCH-1,UCH-2	4.9
25	424771	BE397151	Hs.153003	serine/threonine kinase 16	pkinase	4.9
35	406441			Target Exon	Aa_trans	4.9
	437053	AU077018	Hs.3235	keratin 4	filament,bZIP,Tropomyosin	4.9
	443044	N28522	Hs.8935	quinolinate phosphoribosyltran	QRPTase,QRPTase_N	4.9
	431204	F28841	Hs.250760	cytochrome c oxidase subunit V	dUTPase,COX6A,ras,ATP-syn	4.9
40	456417	L36531	Hs.91296	integrin, alpha 8	integrin_A,FG-GAP	4.8
40	436735	L48489	0	mannosyl (beta-1,4-)-glycoprot	_	4.8
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip	4.8
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-co		4.8
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation	4.8
45	403771			NM_003061:Homo sapiens slit (D	EGF,laminin_G,LRR,LRRNT,L	4.8
43	403248	1 20555	11- 204000	ESTs, Weakly similar to 178885	SLT	4.8
	410214	L29555	Hs.301698	sialyltransferase 4A (beta-gal	Glyco_transf_29	4.8
	407047	X65965	U- 440400	gb:H.saplens SOD-2 gene for ma	sodfe	4.8 4.8
	422668	AF199364	Hs.119120	E3 ubiquitin ligase SMURF1	C2,WW,HECT	4.8
50	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding	
50	431262	NM_006672		solute carrier family 22 (orga	sugar_tr	4.8 4.8
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta	FA_desaturase	
	428659	U66579 Al762964	Hs.188859	G protein-coupled receptor 20 ESTs		4.8 4.8
	432716	L00727	Hs.205180 Hs.898		pkinase	4.8
55	414460 400287	S39329	Hs.181350	dystrophia myotonica-protein k kallikrein 2. prostatic	trypsin	4.8
55	428946	D42046	Hs.194665	DNA2 (DNA replication helicase	UvrD-helicase,Viral_helic	4.7
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosam	Sulfotransfer	4.7
	402912	ABU 14000	FIS.0700	Target Exon	pkinase	4.7
	443329	BE262943	Hs.9234	hypothetical protein MGC1936	philipse	4.7
60	426120	AA325243	Hs.166887	copine i	C2	4.7
50	430609	AA302921	Hs.247362	dimethylarginine dimethylamino	~ -	4.7
	451320	AW118072	1 13.241 002	diacylglycerol kinase, zeta (1	zf-C2H2,BAR,SH3	4.7
	447131	NM_004585	Hs 17466	retinoic acid receptor respond	an was layor is qui to	4.7
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A	zona_pellucida	4.7
65	406458	20111	113.273730	C14000133*:gi[1082739[pirl]C44	proteasome	4.7
00	427804	AL049654	Hs.180871	protein kinase C, alpha bindin	PDZ	4.7
	450748	AI733093	Hs.247686	ESTs	7tm_1	4.7
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	efhand	4.7
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul	PDEase	4.7
70	428773	BE256238	Hs.193163	bridging integrator 1	SH3,BAR	4.7
. •	456444	AA884517	Hs.31856	ESTs. Weakly similar to KIAA14		4.7
	405574		10.0100	Target Exon	pkinase	4.7
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	ribonuclease_T2	4.7
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome		4.6
75	421601	AI660190	Hs.106070	cyclin-dependent kinase inhibi	CDI	4.6
	422795	AB033109	Hs.120866	KIAA1283 protein	kazal,A2M,A2M_N	4.6
	433019	AI208513	Hs.279915	translocase of inner mitochond	zf-Tim10_DDP	4.6
	431522	A1625859	Hs.258609	protein tyrosine phosphalase,	fn3,Y_phosphatase	4.6
	400846			sortilin-related receptor, L(D	ldi_recept_a,fn3,ldi_rece	4.6
80	456881	AW028302	Hs.155079	protein phosphatase 2, regulat	B56	4.6
	418172	X61157	Hs.83636	adrenergic, beta, receptor kin	pkinase,PH,RGS	4.6
	408433	AW162931	Hs.45002	ras-related C3 botulinum toxin	ras	4.6
	439921	AL110209	Hs.6770	LCAT-like lysophospholipase	LACT	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	pkinase,Furin-like,Recep_	4.6
				O.F.	•	

	427945	AW137156	Hs.181202	hypothetical protein FLJ 10038	Collagen		4.6
	451777	U09210	Hs.459	solute carrier family 18 (vesi	sugar_tr		4.6
	429938	BE296804	Hs.226377	phosphate cytidylyltransferase	Cytidylyltransf,COX6C	4	4.6
_	412974	R18978	Hs.75105	emopamil-binding protein (ster		4	4.6
5	414702	L22005	Hs.76932	cell division cycle 34	UQ_con		4.6
	425795	AJ000479	Hs.159543	endothelial differentiation, G	7tm_1	- 4	4.6
	422454	U49070	Hs.161362	protein (peptidyl-prolyl cis/t	Rotamase,WW		4.6
	408135	AA317248	Hs.42957	methyltransferase-like 1	Methyltransf_4		4.6
				cadherin-like 22	cadherin,Cadherin_C_term		4.6
10	457388	AF035300	Hs.264157				4.6
10	421140	AA298741	Hs.102135	signal sequence receptor, delt	Herpes_UL3		
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-a	Acyltransferase		4.6
	413407	Al356293	Hs.75339	inositol polyphosphate phospha	SH2,SAM		4.6
	402463			NM_014624:Homo sapiens S100 ca	efhand,S_100		4.5
	417891	W79410	Hs.82887	protein phosphatase 1, regulat			4.5
15	421681	AA384922	Hs.195175	CASP8 and FADD-like apoptosis	ICE_p20,DED	4	4.5
	426516	BE262660	Hs.170197	glutamic-oxaloacetic transamin	aminotran_1_2		4.5
	418963	BE304571	Hs.89529	aldo-keto reductase family 1,	aldo_ket_red		4.5
	423664	NM_004714		dual-specificity tyrosine-(Y)-	pkinase		4.5
							4.5
20	427681	AB018263	Hs.180338	tumor necrosis factor receptor	TNFR_c6,death,PH,Xlink,Rh		
20	432893	NM_016154		Homo sapiens clone PP1596 unkn	ras,arf		4.5
	413815	AL046341	Hs.75562	discoldin domain receptor fami	F5_F8_type_C,pkinase		4.5
•	405546			NM_018833*:Homo sapiens transp	ABC_membrane,ABC_tran	4	4.5
	416297	AA157634	Hs.79172	solute carrier family 25 (mito	mito_carr		4.5
	421962	D82061	Hs.288354	FabG (beta-ketoacyl-(acyl-carr	adh_short		4.5
25	415341	R00602	110.200001	gb:ye74c04.r1 Soares fetal liv	pkinase		4.5
23		W81526	Hs.118329	ESTs, Moderately similar to GA	Neur_chan_LBD,Neur_chan_m		4.5
	456668						4.5
	456652	AW327546	Hs.111024	solute carrier family 25 (mito	mito_carr		
	407863	AA317089	Hs.597	glutamic-oxaloacetic transamin	aminotran_1_2		4.5
20	435891	AW249394	Hs.5002	copper chaperone for superoxid	sodcu,HMA		4.5
30	453997	AW247615	Hs.37003	v-Ha-ras Harvey rat sarcoma vi	ras		4.5
	449029	N28989	Hs.22891	solute carrier family 7 (catio	aa_permeases		4.5
	424829	NM_002507		nerve growth factor receptor (death,TNFR_c6		4.5
	429362	T25833	Hs.200478	ublquitin-conjugating enzyme E	UQ_con		4.5
	429133	N31854	Hs.197116	solute carrier family 7 (catio	aa_permeases		4.5
35			Hs. 166168		7lm_1		4:4
55	426079	D31220		peter pan (Drosophila) homolog			4.4
	414814	D14697	Hs.77393	famesyl diphosphate synthase	polyprenyl_synt		
	433261	AB040967	Hs.112034	KIAA1534 protein	PH,Oxysterd_BP		4.4
	402915			ENSP00000202587*:Bicarbonate t	HCO3_cotransp		4.4
40	418267	BE389537	Hs.83919	glucosidase I	Glyco_hydro_63		4.4
40	430716	BE387257	Hs.247831	Homo sapiens, Similar to myosi	efhand		4.4
	420874	X66357	Hs.336478	cyclin-dependent kinase 3	pkinase		4.4
	439902	AF174499	Hs.6764	histone deacetylase 6	Hist_deacetyl,zf-UBP		4.4
	400223			Eos Control	Skp1		4.4
	450611	NM_004405	He #19	distal-less homeo box 2	homeobox		4.4
45	412965	L06419	Hs.75093	procollagen-lysine, 2-oxogluta	20G-Fell_Oxy		4.4
73					2001 011_014		4.4
	435564	AF210652	Hs.16614	5(3)-deoxyribonucleotidase (dN	Acultonafarono		4.4
	416121	X92762	Hs.79021	tafazzin (cardiomyopathy, dila	Acyltransferase		
	423323	Al951628	Hs.127007	potassium channel, subfamily K	lon_trans		4.4
	448191	NM_005881	Hs.20644	branched chain alpha-ketoacid	HATPase_c		4.4
50	456217	BE253181	Hs.81687	non-metastatic cells 3, protei	NDK,Arteri_glycop		4.4
	436415	BE265254	Hs.343258	proliferation-associated 2G4,	Peptidase_M24		4.4
	429218	AA225065	Hs.198269	Target CAT			4.4
	407433	AF209923		gb:Homo sapiens orphan G-prote	7tm_3		4.4
	425955	T96509	Hs.248549	ESTs, Moderately similar to S6			4.4
55	407230	AA157857	Hs.182265	keratin 19	filament,bZIP		4.3
55	410197	NM_005518		3-hydroxy-3-methylglutaryl-Coe	HMG_CoA_synt		4.3
							4.3
	416409	R61573	Hs.79300	ubiquitin-conjugating enzyme E	UQ_con Filomin UECT		4.3
	447957	NM_014821		KIAA0317 gene product	Filamin,HECT		
co	421771	NM_001224		caspase 2, apoptosis-related c	ICE_p20,CARD,ICE_p10		4.3
60	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	PH,RhoGEF		4.3
	414821	M63835	Hs.77424	Fc fragment of IgG, high affin	lg .		4.3
	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clone			4.3
	429892	NM_003803		myomesin 1 (skelemin) (185kD)	ig,fn3		4.3
	450126	BE018138	Hs.24447	sigma receptor (SR31747 bindin			4.3
65	413781	J05272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD		4.3
	406530	*****		NM_005546*:Homo sapiens IL2-in	SH2.SH3.pkinase.PH.BTK		4.3
		AK000284	Hs.183860	hypothetical protein FLJ20277	GNT-I		4.3
	428363			galactose-1-phosphate uridylyl	GalP_UDP_transf,GalP_UDP_		4.3
	413954	AL037111	Hs.75641				4.3
70	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3,pkinase,SAM		
70	456529	AF014643	Hs.100072	connexin46.6	connexin		4.3
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m		4.3
	426626	Al124572	Hs.323879	Inhibitor of kappa light polyp	zf-C2H2		4.3
	432956	AL037895	Hs.279861	CGI-31 protein	thiored		4.3
	428970	BE276891	Hs.194691	retinoic acid induced 3	7tm_3		4.3
75	428953	AA306510	Hs.348183	tumor necrosis factor receptor	TNFR_c6		4.2
	423922	AK001663	Hs.135458	muscle-specific beta 1 Integri	· · · - · ·		4.2
				hydroxyacyl-Coenzyme A dehydro	adh_short		4.2
	426613	U96132	Hs.171280		Tropomodulin,pkinase		4.2
	426566	AF131836	Hs.170453	tropomodulin	(topomousii, pailase		
00	425179	AJ224442	Hs.155020	putative methyltransferase			4.2
80	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)			4.2
	459298	R86701		gb:ym86d09.r1 Soares adult bra			4.2
	404879			NM_030807:Homo sapiens glucose			4.2
	400836			Target Exon	Apolipoprotein		4.2
	430940	Z25470	Hs.248145	melanocortin 5 receptor			4.2
				•			

255

	400563			Target Exon	Pep_M12B_propep	4.2
	430237	Al272144	Hs.236522	DKFZP434P106 protein	abhydrolase	4.2
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	DAG_PE-bind,C2	4.2
5	409067 419982	BE260459	Hs.50267	putative GTP-binding protein s	ras	4.2 4.2
,	428394	AA252544 AU076472	Hs.55610 Hs.184141	solute carrier family 30 (zinc glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh,Acyl-CoA_dh_M	4.2
	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase	4.2
	454034	NM_000691		aldehyde dehydrogenase 3 famil	aldedh	4.2
10	410237	AI750589	Hs.61258	argininosuccinate lyase	lyase_1	4.1
10	451478	NM_012331		methlonine sulfoxide reductase	PMSR	4.1
	415410 406538	AF037332	Hs.278569	sorting nextin 17 Target Exon	PX,fn3,pkinase,SAM,EPH_lb trypsin	4.1 4.1
	424349	AF141289	Hs.145550	solute carrier family 7 (catio	aa_permeases	4,1
	441164	AB023180	Hs.7724	KIAA0963 protein	helicase_C	4.1
15	421318	U63973	Hs.103501	rhodopsin kinase	pkinase,pkinase_C,RGS	4.1
	439340	AB032436	Hs.6535	brain-specific Na-dependent in	sugar_tr,BT1	4.1
	417447	N73703	Hs.293267	ESTs	Glyco_hydro_31 WHEP-TRS,GST_C,HGTP_antic	4.1 4.1
	409693 403655	AA010233	Hs.55921	glutamyl-protyl-tRNA synthetas NM_003071:Homo sapiens SWI/SNF	SNF2_N,helicase_C,zf-C3HC	4.1
20	411142	NM_014256	Hs.69009	transmembrane protein 3	Galactosyl_T	4.1
	437016	AU076916	Hs.5398		GMP_synt_C,GATase	4.1
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor a	SH3,HS1_rep	4.1
	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	Tissue_fac	4.1
25	421380 434142	D31833 U47927	Hs.1372 Hs.3759	arginine vasopressin receptor ubiquitin specific protease 5	7tm_1 zf-UBP,UCH-2,UBA,UCH-1	4.1 4.1
	427407	BE268649 ·	Hs.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,re	4.1
	413749	AI929320	Hs.75516	tyrosine kinase 2	pkinase	4.1
	411927		Hs.772	glycogen synthase 1 (muscle)	Glycos_transf_1	4.1
20	419726	U50330	Hs.1274	bone morphogenetic protein 1	EGF,CUB,Astacin	4.1
30	423814 451355	AF105020 NM_004197	Hs.132989	putative protein O-mannosyltra serine/threonine kinase 19	PMT,MIR	4.1 4.1
	422556	NM_006245		protein phosphatase 2, regulat	B56	4.1
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH de	200	4.1
	431968	AF117222	Hs.272261	UDP-Gal:betaGlcNAc beta 1,3-ga	Galactosyl_T	4.0
35	443639	BE269042	Hs.9661	proteasome (prosome, macropain	proteasome	4.0
	410039	AF207989	Hs.58014	Homo sapiens, Similar to G pro	7tm_3	4.0
	431066 452715	AF026273 Z21093	Hs.249175 Hs.30352	interleukin-1 receptor-associa ribosomal protein S6 kinase, 5	pkinase,death pkinase	4.0 4.0
	403692	221033	NS.30302	NM_007037*:Homo sapiens a disi	Reprolysin,tsp_1,Pep_M128	4.0
40	442549	AI751601	Hs.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF	4.0
	427239	BE270447		ubiquitin carrier protein	UQ_con	4.0
	451125	AA015779	Hs.226923	ESTs	Y_phosphatase	4.0
	425081	X74794	Hs.154443	minichromosome maintenance def	MCM	4.0
45	402171 402665			Target Exon Target Exon	C2	4.0 4.0
	420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH4,SH3,	4.0
	412187	U68487	Hs.73739	5-hydroxytryptamine (serotonin	7tm_1	4.0
	412656	AF006011	Hs.74375	dishevelled 1 (homologous to D	PDZ,DEP,DIX,Dishevelled	4.0
50		U35234	Hs.159534	protein tyrosine phosphatase,	fn3,lg,Y_phosphatase,DSPc	4.0 4.0
30	424288 452230	AW137198 AW135360	Hs.278682 Hs.224170	Phosphatidylglycerophosphate S ESTs	pkinase	4.0
	408449	NM_004408		dynamin 1	PH,GED,dynamin,dynamin_2	4.0
	423883	AF250238	Hs.134514	ATP-binding cassette, sub-fami	ABC_tran,photoRC,SRP54,Ca	4.0
F F	422676	D28481	Hs.1570	histamine receptor H1	7tm_1	. 4.0
55	458639	BE247683	Hs.14611	dual specificity phosphatase 1	DSPc	4.0
	400726 405370			C13000717*:gi 129376 sp P26196 NM_005569*:Homo sapiens LIM do	DEAD,helicase_C pkinase,LIM,PDZ	4.0 4.0
	413654	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA	4.0
	432917	NM_014125		PRO0327 protein		4.0
60	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L	sugar_tr	4.0
	424512	X53002	Hs.149846	Integrin, beta 5	Integrin_B,EGF	4.0
	TABLE 22B:					
		e Eos ombese	t identifier number			
65		Gene cluster				
	Accession: 0	Senbank acces	sion numbers			
				•		
	Pkey	CAT Number		* * * * * * * * * * * * * * * * * * *	10 F04070 HI0F040 AMMOOOC44 MOOTOC	A 404570 A 4070007 A1005005 A1707005
70	410191	11824_1		24 Al000871 AW242322 AW007204 W682		AA431579 AA970887 AI885085 AI767835
70			AA776726 At040970		.03 AA43 1430 A11400373 BE222344 AA	MOSHS4 MISUOUSU 1185513 MISU 1017
	415341	1534442_1	R00602 Z42921 F08			
	415995	1564_1				N933994 AW751282 AW374413 AA578823
75					V950600 AA912021 Al524064 AW18309	8 Al416986 AW769231 Al767111 AA293723
75	445004	4000000 4	AI422290 AA46503	8A •		
	418964 424339	1809680_1 23827_1	T74640 T74649	11 AE210137 NM 015720 RE313658 RE3	82852 RE252205 RE251553 F12128 T6	6208 BE255806 BE254484 AA324163 H07952
	12-1003			2 Al204971 Al282924 AW192547 Al65276		
0.0	427010	27436_1	AW138332 AW2074	150 AW138931 AW136963 NM_012219 A	F043938 AA931386 AI084600 AA97599	9 BE551105 AA450260 Al080368 AA324154
80	40-00-	07047		11 AL118847 W44458 AI765270 AA45312		
	427239	27647_1		21 BE207288 BE207170 D56355 BE2632 76 BE295291 BE297066 AA210923 BE40		
			BE269633 BE62193		1913 1101044 DEUZZ303 M1424020 I MYV	2000 10 1 10021 PM3001 13 PM310013
	427326	277229_1	AI287878 AI804160			
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	428542	29266_1		_014770 U81031 AA352392 AA984512 H38328 AL120358 AL134787 AL134589 Al637763 Al671506 AA526909 Al651627 AW243560						
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	432118 432499	3417021 34857_1		IM_016577 AF166492 BE276152 AF091031 AA908607 U66623 AI570393 AA682567 AW593957 AI148105 AW002431 AI637463						
10	433075	35820_1	NM_002959 AI475049 H	A339439 R13005 R23431 AW961068 AA233819 AA224118 R19618 Al890314 Z46184 X98248 AA233278 AA846376 Al470560 Al470533 BE327147 AW291971 AA017125 Al198417 Al365213 Al168442 Al337018 85459 AA969895 AA888000 AA418326 AA418378 N71981 AL043634 AA426361 AA418275 AA232975 AL036861 BE277220 BE387505						
	433494	3679_1		04934 R21715 R19005 H11563 H14256 R46605 Z40857 BE218899 Al457785 BE550988 Al693847 AA961017 H40944 M78617 0090 BE549719 BE550952 AW005546 Al332686 Al928848 N49234 R44075 Al694943 Al858538 Al290722 BE550759 R43116 H40212						
15	434755 436735	392764_1 425_1	AA648502 / L48489 AL0 AA837368 /	548502 AAB 14365 AW976711 AA746117 1489 AL022312 D13789 Al761974 AW173260 AW271715 AA837437 Al075278 Al367012 Al953032 Al571173 H44868 AA743691 H47026 B37368 AA829826 AA713585 AW502618 AW500856 AW501353 AW499765 AA339125 H19141 H29645 R18883 AW450375 AA326081						
20	440242	489536_1	AW295871	BE263659 N52684 A AI005144 AA909877 T52634 AI239684 AA875959 BE171353 AI767633 AW510907 AI742007						
20	449405 450739	80651_1 844917_1	A1732707 A							
	451320	86576_1	AA224388 /	Al631982 T15734 AA224195 Al701458 W20198 F26326 AA890570 N90552 AW071907 Al671352 Al375892 T03517 R88265 Al124088 Al084316 Al354686 T33652 Al140719 Al720211 T03490 Al372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303						
25	459298	983107_1	T33623 R86701 R8	4600 AL157655.						
	TABLE 22C									
20	Ref: Seque	nce source. T	he 7 digit num	an Eos probeset bers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of						
30				ı, et al. (1999) <u>Nature</u> 402:489-495 h exons were predicted						
	Nt_position:	Indicates nuc	electide positio	ns of predicted exons						
35	Pkey 400471	Ref 9931670	Strand Minus	NL_position 105629-105760						
	400471	9796703	Plus	37240-37774						
	400551 400563	9801071 - 9844011	Minus Plus	40629-40934 81941-82434						
	400565	9863505	Minus	93178-93429						
40	400726	8118950	Plus	51524-51786						
	400748 400772	8119063	Plus	84237-84398 34896-35021,41078-41197						
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55	401281	9800073	Minus	13622-15130						
	401454	9186923	Minus	114659-114832						
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	401885	8140731	Plus	148234-148321,150365-150559						
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	402207	8576119	Plus	41683-41851						
	402209 402211	8576119 7689783	Minus Minus	53315-53472 67414-68229						
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90	402478	9797301	Minus	106204-106535						
80	402497 402632	9797775 9931268	Plus Plus	98984-99452 101166-101419						
	402651	7960391	Plus	174215-174380						
	402665	8077033	Minus	11824-12090,14290-14544						
	402758	9213869	Plus	87638-87924						
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             40324B
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                            7230852
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7382189
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             404946
404953
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                                             Plus
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                             2078469
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                                             Minus
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                                             Plus
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                                             Plus
             405546
                             1054740
                                                             124010-124183
                                             Plus
                                                             33200-33646
161628-161734,162823-163014,164439-164652
             405574
                            3820491
6960456
4508157
                                             Minus
             405594
                                             Plus
40
                                                             21701-21844
             405683
                                             Minus
             405697
                             4309923
                                             Minus
                                                             56765-57010,57696-58016
                            4156179
9159110
                                                            42789-43553
50425-50876
             405714
                                             Minus
             406128
                                            Plus
                                                             125320-125482
             406370
                            9256130
                                             Plus
45
             406432
                             9256504
                                                             3804-3930,4026-4120,4929-5109
             406441
406458
                            9280715
9756020
                                                            26200-26458
145874-146911
                                            Plus
                                            Plus
                                                             174661-174978
             406495
                            7711328
                                             Minus
             406496
                            7711328
                                             Minus
                                                             178947-179264,181779-182087
50
                                                            11703-11850,14711-14829,14920-14984,16232-16448,16916-17087
35196-35367,38229-38476,40080-40216,43522-43840
2117-2257,2436-2540
             406530
406538
                            7711474
                                             Minus
                            7711478
                                            Phrs
             406591
                             8224230
                                            Minus
             406617
                             8439858
                                                             36430-36552
                                             Plus
55
```

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

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Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number 65

Title: UniGene gene title Protein Dom.: Predicted protein domain

R1: Ratio of tumor to normal ovaries

50	Pkey	Ex. Accn	UG ID	Title	Protein Dom.	R1
70	421296	NM_002666	Hs.103253	perilipin	perilipin,SS	37.8
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,zf-DHHC	29.2
	453028	AB006532	Hs.31442	RecQ protein-like 4	DEAD,helicase_C,Fork_head	27.6
	441021	AW578716	Hs.7644	H1 histone family, member 2	· -	27.2
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,ig	26.5
75	454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	25.9
	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	SS,TM	25.8
	435017	AA336522	Hs.12854	angiotensin II, type I recepto		25.0
	409518	BE384836	Hs.3454	KIAA1821 protein	SS	23.3
	410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ldl_recept_a,trypsi	22.8
80	439924	A1985897	Hs.125293	ESTs	SS	22.7
	446374	AA329256	Hs.24756	ESTs, Moderately similar to al		22.6
	431773	BE409442	Hs.268557	pleckstrin homology-like domai	PH,SS,LIM,Troponin	21.4
	420839	AI792682	Hs.282960	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	21.4
	413436	AF238083	Hs.68061	sphingosine kinase 1	DAGKC	21.2

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	424420	BE614743	Hs.146688	prostaglandin E synthase	MAPEG,SS,TM,MAPEG	20.7
	422645	L40027	Hs.118890	glycogen synthase kinase 3 alp	pkinase,SS,Ets	20.7
	436725	BE045223	Hs.136912	hypothetical protein MGC10796	·	20.4
_	422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
5	429556	AW139399	Hs.98988	ESTs	SS,pkinase,PMP22_Claudin	20.1
· .	434068	AA977935	Hs.127274	ESTs	SS	20.0
	423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	19.9
	423652	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABC1,SS,PID,PID	19.8
				dynein, axonemal, intermediate	WD40,SS	19.3
10	422179	AF091619	Hs.112667			
10	441356	BE384361	Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ank	18.5
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	17.2
	432631	H08379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,ArfGap,homeob	17.2
	439108	AW163034	Hs.6467	synaptogyrin 3	Synaptogyrin,SS,TM,PDZ,WD	17.2
	451643	M64437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.2
15	434518	H56995	Hs.37372	Homo sapiens DNA binding pepti	SS	16.9
	413244	AW955951	Hs.159265	kruppel-related zinc finger pr	SS,TM,BTB,Pep_M12B_propep	16.3
		AW451623	Hs.109752	putative c-Myc-responsive	oo, mio toti ob miss propob	16.2
	456642				MT 22 a faces the	16.0
	421612	AF161254	Hs.106196	8D6 antigen	ldi_recept_a,SS,TM	
20	456177	NM_012391		prostate epithelium-specific E	Ets,SAM_PNT	15.7
20	409261	BE315042	Hs.19210	hypothetical protein MGC11308	A	15.6
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 famil	aldedh	15.6
	401278			Target Exon	Band_41	15.4
	444804	AI084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
	406620	M81105	Hs.146550	myosin, heavy polypeptide 9, n	myosin_head, Myosin_tail, I	15.1
25	421495	AI583067	Hs.149152	ESTs, Weakly similar to RHOP M		15.0
23					SS,rm,SS	15.0
	416893	AA455588 C00138	Hs.62406	hypothetical protein FLJ22573		14.9
	442620		Hs.8535	Homo sapiens mRNA for KIAA1668	SS,RNA_pol_K	
	406901	M14624		gb:Human 4-beta-galactosyltran	e4 1.1.1	14.6
00	416006	AA324251	Hs.78950	branched chain keto acid dehyd	E1_dehydrog	14.6
30	455557	AW995839		gb:QV4-BN0044-110200-108-h07 B	Metallophos	14.4
	416819	U77735	Hs.80205	plm-2 ancogene	pkinase, SS, TM, OTU, K_tetra	14.3
	444441	AW613841	Hs.301394	hypothetical protein MGC3101		14.0
	406918	M88357	110.001001	gb:Homo sapiens DNA-binding pr	zf-C2H2,SS	14.0
			Un 6470	hypothelical protein MGC13272	SS,Sema,pkinase,TIG,PSI,e	13.6
25	407605	W03512	Hs.6479			
35	447304	Z98883	Hs.18079	phosphatidylinositol glycan, c	SS,Peptidase_C2	13.6
	402365			Target Exon	SS,SS,TM,ig	13.4
	407767	W15398	Hs.38628	hypothetical protein	SS,zf-CCCH	13.3
	432931	AF174487	Hs.293753	Bcl-2-related ovarian killer p		12.7
	439233	AA831893	Hs.292767	hypothetical protein FLJ23109	zf-C3HC4,TM,Sulfate_trans	12.7
40	423801	NM_015071		GTPase regulator associated wi	RhoGAP,SH3,PH	12.6
	430397	Al924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.6
	411570	BE144584	Hs.314341	ESTs		12.5
		BE144504	113.011-011	Eos Control	SS,SS,Glyco_tranf_43,COLF	12.3
	400206	1100 4505	11. 44507			12.2
15	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF1518	SS,TM,SS,TM	
45	412674	X04106	Hs.74451	calpain 4, small subunit (30K)	efhand,SS,CAP_GLY	12.0
	400460			C11002253*:gij129091 sp P23267	SS,TM,SCAN,zf-C2H2,KRAB	12.0
	417595	AA424317	Hs.6259	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.6
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	SS	11.5
	424707	BE061914	Hs.10844	Homo saplens cDNA FLJ14476 fis	SS,SS,TM,Sema	11.5
50	444359	AJ697160	Hs.143594	ESTs, Weakly similar to HS4L_H		11.5
	435158 -	AW663317	Hs.65588	DAZ associated protein 1	rrm,SS,rrm	11.3
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA		11.3
	450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.2
	427448	BE246449	Hs.2157	Wiskolt-Aldrich syndrome (ecze	WH1,PBD,WH2,SS	11.2
55		DE240443	NS.2137		**************************************	11.2
55	406230	41.040402	11- 402404	Target Exon	CCTM are deb ECED	
	432143	AL040183	Hs.123484	Homo saplens, clone IMAGE:4178	SS,TM,cys_rich_FGFR	11.2
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,EGF,cadherin,	11.1
	413726	AJ278465	Hs.75510	annexin A11	annexin,SS,annexin	11.1
	431974	AW972689	Hs.200934	ESTs	bZIP	11.0
60	428167	AA770021	Hs.16332	ESTs	SS,ig,fn3	11.0
	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	SS ·	10.9
	412738	N34731	Hs.74562	siah binding protein 1; FBP in	homeobox	10.9
	445434	BE391690	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,lipoc	10.9
		BE544855	Hs.236572	ESTs, Weakly similar to SFR4_H	SS,SS,SAC3_GANP	10.7
65	444008					
05	444410	BE387360	Hs.33719	ESTs, Moderately similar to S6	SS	10.6
	444607	AW405635	Hs.293687	ESTs ·	SS,PI-PLC-X,PH,PI-PLC-Y,C	10.6
	404333			C7001735*:gi 7768636 dbj BAA95	vwd	10.5
	401210			C12000519:gi[7710046]ref[NP_05		10.5
=-	434743	Al363410		ribosomal protein S18	SS,TM	10.4
70	434030	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	10.4
	450029	AW073380	Hs.267963	hypothetical protein FLJ10535	SS,Pyridox_oxidase,zf-C2H	10.4
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	SS.TM.transmembrane4	10.3
	438185	Y19188	Hs.320461	ESTs	SS	10.2
		AF039196	Hs.272367	hairless protein (putative sin	jmjC	10.2
75	432031	WL093 130	170.2/230/		pkinase,UM,PDZ	
13	405371	14107000	11- 404400	NM_005569*:Homo sapiens LIM do		10.1
	456741	W37608	Hs.184492	ESTs	SS,pkinase	10.1
	458130	AA115811	Hs.6838	ras homolog gene family, membe	ras,arf	10.0
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	(A	10.0
0.0	420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldo_ket_red,SS,TM,gla	10.0
80	445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.9
	423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh,Acyl-CoA_dh_M	9.8
	458216	AW024282	Hs.104938	hypothetical protein MGC15906		9.8
	451721	NM_006946		spectrin, beta, non-erythrocyt	spectrin,PH,CH,SS,Peptida	9.7
		· AA913059		Homo sapiens, clone IMAGE:4054	asp,SS,TM,ion_trans,K_tet	9.7
	421445	W-1903	Hs.104433	PEOP. SEAVER BRIDE (GROUPE GREEN)	•	3.1
					259	

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	104054	DEGAGGG		500 C 1 C 51 W N C	00 004400 0140	
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransf	SS,PWWP,PHD	9.7
	443780	NM_012068		activating transcription facto	bZIP,NTP_transf_2,SS,TBC	9.7
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
5	444202	AL031685	Hs.12785	KIAA0939 protein	SS,TM,Na_H_Exchanger,ABC2	9.7
J	427640	AF058293	Hs.180015	D-dopachrome tautomerase	MIF,Iate_protein_L2,SS,GS	9.6 9.6
	419167	AI589535	Hs.94875	ESTs, Weakly similar to A35363	SS TM:- MIC II had SS TM A	
	424618	L29472	Hs.1802	major histocompatibility compl	TM,ig,MHC_II_beta,SS,TM,A	9.6 9.6
	427497	AW139476	Hs.31240	ESTs	00	9.6
10	420423	AA827718	Hs.88218	ESTs	SS haveldages 2 haveldages	9.6
10	414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	9.5
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,arf,ras,fn3,ras	
	408294	BE141732	11- 007400	gb:QV0-HT0101-061099-032-e07 H	Ammonium_transp	9.5
	442232	Al357813	Hs.337460	ESTs, Weakly similar to A47582	SS,TM,TGFb_propeptide,TGF	9.4
15	416866	AA297356	Hs.80324	serine/threonine protein phosp	Metallophos, Metallophos	9.4
15	419823	AW271708	Hs.118918	ESTs, Weakly similar to M2OM_H	SS,TM	9.4
	422625	AW504698	Hs.155976	cullin 4B	SS,SS,Cullin,Cullin	9.3
	401264			C18000090*:gi[6678656[ref]NP_0	SS,laminin_Nterm,laminin_	9.3
	407507	U73799		gb:Human dynactin mRNA, partia	SS,TM,HCO3_cotransp,CAP_G	9.2
20	400833			C11000890:gi 3746443[gb AAC639	SS,TM,7tm_1	9.2
20	422064	AW452589	Hs.335742	ESTs	TM	9.2
	452434	D30934	Hs.29549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
	421363	NM_001381	Hs.103854	docking prolein 1, 62kD (downs	PH,IRS,TM,PH,IRS,trypsin,	9.1
	427397	A1929685	Hs.177656	calmodulin 1 (phosphorylase ki	efhand,RrnaAD,SS,efhand	9.1
~ ~	431462	AW583672	Hs.256311	granin-like neuroendocrine pep	SS	9.0
25	434796	AA812046		ESTs -,	SS,myb_DNA-binding,myb_DN	9.0
	422639	Al929377	Hs.173724	creatine kinase, brain	ATP-gua_Ptrans,ATP-gua_Pt	9.0
	447867	AI525268	Hs.164303	ESTs	TM	9.0
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 S	SS,TM,inos-1-P_synth,Occl	8.9
	455588	Al129903	Hs.74669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
30	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
	429527	AA454184	Hs.289014	ESTs		8.9
	432603	AA554920	Hs.105794	UDP-glucose:glycoprotein gluco	SS,TM	8.9
	410338	W03445	Hs.38205	gb:za05g11.r1 Soares melanocyt	pkinase	8.9
	452833	BE559681	Hs.30736	KIAA0124 protein	WD40	8.9
35	407363	AF035032	Hs.181125	gb:Homo sapiens clone MCA1L my	SS,lg,SS,G_glu_transpept	8.8
	414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.8
	421694	BE387430	Hs.106880	bystin-like		8.8
	453683	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
40	418736	T18979	Hs.87908	Snf2-related CBP activator pro	SS,helicase_C,AT_hook,SS,	8.7
	450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
	419725	U66048	Hs.92683	Homo sapiens clone 161455 brea		8.7
	415126	D60945		gb:HUM141D048 Clontech human f	SS,TM	8.7
	406301			Target Exon	TM	8.6
45	418843	AJ251016	Hs.89230	potassium intermediate/small c	TM, CaMBD, SK_channel, TM	8.6
	433396	Al742071	Hs.133205	ESTs	SS,TM	8.6
	434333	AA186733	Hs.292154	stromal cell protein		8.6
	407065	Y10141		gb:H.sapiens DAT1 gene, partia	SNF,SS,TM	8.6
	452851	AW173191	Hs.213117	ESTs	SS,Sema	8.6
50	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	RhoGEF	8.6
-	447859	AK002194	Hs.19851	peroxisomal biogenesis factor	14.002.	8.6
	420836	AW958453	Hs.204959	hypothetical protein FLJ14886	SS.ras	8.6
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2	pkinase,SS,SNF2_N,helicas	8.6
	419639	AK001502	Hs.91753	hypothetical protein	prantasoro oponia a_riginosis as	8.6
55	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquino	oxidored_q6,SS,TM,rrm	8.5
-	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_H	SS,PAS,HLH	8.5
	441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		8.5
	428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
	421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,TM,rrm,PDZ	8.4
60	441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	SS,TM,HSP20,7tm_1	8.4
	443801	AW206942	Hs.253594	intron of: trichorhinophalang	GATA	8.4
	432862	AW004958	Hs.236720	amnionless protein	SS,MATH,zf-TRAF,zf-C3HC4	8.4
	431849	A1670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.3
65	404365			Target Exon	SS	8.3
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	8.3
	423098	AA321980	Hs.204682	ESTs		8.3
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
_	418361	AW505368	Hs.12460	gb:UI-HF-BNO-alu-d-03-0-Ul.r1		8.2
70	· 427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pkinase	8.2
	420138	BE268854	Hs.177729	ESTs	SS	8.2
	426391	AW161050	Hs.169611	second mitochondria-derived ac	SS	8.1
	457613	AA598869	Hs.173770	ESTs	V	8.1
	427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	8.1
75	437215	AL117488		Human clone 23564 mRNA sequenc	SS	8.1
. –	423384	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4		8.1
	447151	AI022813	Hs.92679	Homo sapiens clone CDABP0014 m	SS,TM,LRR,aminotran_1_2	8.0
	431898	AK000020	Hs.272018	hypothetical protein FLJ20013		8.0
	454291	AW384847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,lactamase	8.0
80	430354	AA954810	Hs.239784	human homolog of Drosophila Sc	SS,TM,ig	8.0
	459302		Hs.36566	LIM domain kinase 1		8.0
	422765	AW409701	Hs.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	8.0
	425944	AK000664	Hs.164256	hypothetical protein FLJ20657		7.9
	450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,rrm	7.9
					260	

	454246	AW245185	Hs.6996	ESTs		7.9
	450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.9
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.9
5	425760	D17629	Hs.159479	galactosamine (N-acetyl)-6-sul	Sulfatase,SS,TM	7.9
J	413534	BE146961	11- 04007	gb:QV4-HT0222-011199-019-b12 H	SS,TM	7.8
	446931 421726	Al348856 AK001237	Hs.21627	gb:tb05a05.x2 NCI_CGAP_Lu26 Ho	TM	7.8
	427461	AA531527	Hs.319088 Hs.332040	hypothetical protein FLJ 10375 hypothetical protein MGC13010	TM SS,TM,ACAT,LRR	7.8 7.8
	448993	AI471630	113.332040	KiAA0144 gene product	30,1NIAGAT,ERK	7.8
10	443136	NM_001440	He 9018	exostoses (multiple)-like 3	Exostosin,SS,TM	7.8
	427725	U66839	Hs.180533	mitogen-activated protein kina	pkinase	7.8
	400923			Target Exon	SS,TM,DUF289	7.8
	419757	AA773820	Hs.63970	ESTs	SS,TM	7.8
	458834	AI566883	Hs.196446	ESTs		7.8
15	427899	AA829286	Hs.332053	serum amyloid A1	SS,SAA_proteins,SS,SAA_pr	7.7
	452399	BE513301	Hs.29344	hypothetical protein, clone 24	SS,perilipin	7.7
	436543	NM_002212		Integrin beta 4 binding protei	elF6	7.7
	431811	AB040972	Hs.301696	hypothetical protein FLJ11560	SS,TM,Band_7,AAA,cdc48_N,	7.7
20	414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS,hormone_rec,zf-C4	7.7
20	455885	BE153524	11- 4004FF	gb:PM0-HT0339-241199-002-C03 H	SS,pkinase	7.7
	427721 430432	AI582843 AB037758	Hs.180455	RAD23 (S. cerevisiae) homolog	ubiquitin,UBA,integrin_B,	7.6 7.6
	427273	AW139032	Hs.241419 Hs.107376	KIAA1337 protein hypothetical protein DKFZp434N	TM,Patched,TM SS,SS,TM	7.6
	450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	7.6
25	413564	BE260120	113.24010	gb:601146990F1 NIH_MGC_19 Homo	7 A. 2,00	7.6
	410397	AF217517	Hs.63042	DKFZp564J157 protein	SS,hameobox,UPF0160,DUF23	7.6
	439539	BE348395	Hs.121589	ESTs	SS,Fork_head	7.5
	400286			C16000922:gij7499103[pirj]T209	TM,ABC_tran,ABC_membrane	7.5
•	416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.5
30	418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,ReprolysIn,Pe	7.5
	419492	AA243547	Hs.19447	PDZ-LIM protein mystique	LIM,SS,SH3,Sorb,Metalloph	7.5
	420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.5
	406495	4145555		Target Exon	SRCR,TM,Acetyltransf	7.5
35	448043	Al458653	Hs.201881	ESTs	PHD	7.4
33	401724	M77640	U. 1757	C16001374:gi 6755086 ref NP_03	TMPLAT,SS	7.4
	424263 428092	M77640 AW879141	Hs.1757	L1 cell adhesion molecule (hyd ESTs	fn3,ig,1RK,SS,TM,fn3,ig,R SS,TM	7.4 7.3
	453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BPTI,SS,TM,ion_tra	7.3
	400137	A11020100	115.51405	Eos Control	rumz_br 11,00,1W,lor_ua	7.3
40	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	Corona_7,SS,TM	7.3
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	UPP_synthetase,HMG14_17	7.3
	432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22_Claudin,SS,TM,PMP22	7.3
	448859	BE272446	Hs.265317	hypothetical protein MGC2562	SS,TPR	7.3
AF	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.3
45 .	429299	AI620463	Hs.347408	hypothetical protein MGC13102	SS,TM,gla	7.3
	401674	***********	11. 470400	C16001417*:gi[7500345[pir][T21	FAD-oxidase_C,FAD_binding	7.2
	412289 424198	AW935967 AB029010	Hs.170162	KIAA1357 protein	SS SS TM No. Co. Ev Colv bolo	7.2 7.2
	412173	T71071	Hs.143026	KIAA1087 protein gb:yc50b05.r1 Stratagene liver	SS,TM,Na_Ca_Ex,Calx-beta, CPSase_L_chain	7.2
50	438113	Al467908	Hs.8882	ESTs	SS,TM,7im_1	7.2
-	429869	Al907018	Hs.15977	Target CAT	um	7.2
	439963	AW247529	Hs.6793	platelet-activating factor ace	PAF-AH_lb,Lipase_GOSL,SS,	7.2
	425041	Al377150	Hs.150914	ESTs	SS	7.2
c c	448340	A1492910	Hs.32362	ESTs		7.1
55	406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg	SS,SS	7.1
	431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	WD40	7.1
	421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sm,SS,tRNA-synt_1,GST_C,G	7.1
	409649 430281	AA159216 Al878842	Hs.55505 Hs.237924	hypothetical protein FLJ20442 CGI-69 protein	Y_phosphatase,DSPc,TM mito_carr,SS,TM	7.0 7.0
60	444672	Z95636	Hs.11669	laminin, alpha 5	laminin_EGF,laminin_G,EGF	7.0
	405928		. 10. 1 1000	Target Exon	SS,cystatin,Coprogen_oxid	7.0
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase	aminotran_1_2,SS,TM,LRR	6.9
	439905	AW799755	Hs.110953	retinoic acid induced 1	HLH	6.9
	451937	AF119664	Hs.27299	transcriptional regulator prot	SS,integrin_B,fn3,Calx-be	6.9
65	426675	AW084791	Hs.133122	hypothetical protein FLJ14524	SS,TM,aminotran_1_2	6.9
	438627	AI087335	Hs.123473	ESTs	TM,Reticulon	6.9
	438951	U51336	Hs.6453	inositol 1,3,4-triphosphate 5/	SS,oxidored_nitro,SS	6.8
	421758	BE397336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,pkinase	6.8
70	423228 405346	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS,TM,sushi	6.8 6.8
, 0	405346 432746	AA564512	Hs.24301	Rag C protein polymerase (RNA) II (DNA direc	RCC1 SS,TM,EF1BD	6.8
	452798	AI918771	Hs.257170	ESTs	SS,TM,TNFR_c6	6.7
	426315	AA854219	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,crystall	6.7
	440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
75	438857	A1627912	Hs.130783	Forssman synthetase	SS,RA,RasGEF,RasGEFN	6.7
	452072	BE258857	Hs.27744	RAB3A, member RAS oncogene fam	ras,arf,SS,PDEase	6.7
	433938	AF161536	Hs.284292	ubiquinol-cytochrome c reducta	TM	6.7
	423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.7
80	453101	AW952776	Hs.94943	ESTs	TM .	6.7
οU	420307	AW502869	Hs.66219	ESTs	SS,TM	6.7
	415056 454262	AB004662 AW612232	Hs.77867 Hs.254835	adenosine A1 receptor ESTs	7tm_1,SS,TM SS TM voltage, CLC CBS	6.7 6.7
	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960	SS,TM,voltage_CLC,CBS	6.6
	413908	BE409966	Hs.323813	Homo sapiens, clone MGC:2867,	SS,zf-C2H2	6.6
					261	
					ZO I	

	457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin_lg_c	6.6
	419157	AA234540	Hs.23871	ESTs	pkinase	6.6
	431424	A1222969		ESTs	SS	6.6
5	412464	T78141	Hs.22826	ESTs, Weakly similar to 155214	SS,cadherin,crystall	6.6
5	430168	AW968343		DKFZP434I1735 protein	SS,TM,efhand,efhand	6.6
	455035	AW851734	11-04246	gb:MR2-CT0222-011199-007-e10 C	00 711 05 40 1 - 5 01	6.6
	422682 453367	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.6
	450593	AW732847 AF129085	Hs.70573 Hs.25197	PKCI-1-related HIT protein	SS,TM TDB SS TM Bhombaid losters	6.6
10	420319	AW406289	Hs.96593	STIP1 homology and U-Box conta hypothetical protein	TPR,SS,TM,Rhomboid,lactam ras,arf	6.6 6.6
10	431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh,isodh	6.6
	431297	AA651771	Hs.3076	ESTs	ioonijisoon	6.6
	410082	AAD81594	Hs.158311	Musashi (Drosophila) homolog 1	SS,HECT,phoslip	6.5
	441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.5
15	454682	AW816029		gb:MR3-ST0220-151299-027-b10 S	filament	6.5
	407299	AA460205	Hs.289770	ESTs, Wealdy similar to 138022		6.5
	422837	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	6.5
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	pfkB,SS	6.4
20	417810	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_deam	6.4
20	445333	BE537641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
	402197	11704460	1	Target Exon	SS,TM,ATP1G1_PLM_MAT8,ig,	6.3
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMP22_Claudin,PMP22	6.3
	447754 444664	AW073310 N26362	Hs.163533	intron of HER4	DCDs Chadanas CC TM	6.3 6.3
25	421190	U95031	Hs.11615 Hs.102482	map kinase phosphatase-like pr mucin 5, subtype B, tracheobro	DSPc,Rhodanese,SS,TM	6.3
LJ	432872	A1908984	Hs.279623	selenoprotein X, 1	Cys_knot,vwc DUF25,SS,Ribosomal_L3,PDZ	6.3
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.3
	413343	BE392026	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	6.2
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
30	403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_t	6.2
	413055	AV655701 ·	Hs.75183	cylochrome P450, subfamily IIE	p450	6.2
	427812	AA770424	Hs.98162	ESTs	SS	6.2
	457761	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	6.2
25	453099	H62087	Hs.31659	thyroid hormone receptor-assoc	SS	6.2
35	426048	A1768853	Hs.134478	ESTs	TM	6.2
	407223	H96850	11 044640	gb:yw03b12.s1 Soares melanocyt	SS,TM,SS,TM,DDOST_48kD	6.2
	445634	A1624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	6.2
	441197 421707	BE244638 NM_014921	Hs.166	sterol regulatory element bind lectomedin-2	HLH	6.1
40	435750	AB029012	Hs.4990	KIAA1089 protein	Latrophilin,OLF,7tm_2,Gal SS,TM	6.1 6.1
	432353	NM_016558		SCAN domain-containing 1	SCAN	6.1
	427326	A1287878	*10121 ****	gb:qv23f06.x1 NCI_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	6.1
	447128	Al271898		cyclin K		6.1
4.5	419444	NM_002496	Hs.90443	Target CAT	fer4,SS,TM,V_ATPase_sub_a	6.1
45	457978	AA776638		gb:ae78g04.s1 Stratagene schiz	SS,PH,IQ,RasGEF,RasGEFN,R	6.1
ļ	410445	AA199830		gb:zq75h01.r1 Stratagene hNT n		6.1
	431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD; p	PARP,PARP_reg,SS,TM,Pepti	6.1
	407143	C14076	Hs.332329	EST	SS,TM	6.0
50	408724 436685	A1685842	Hs.294143	ESTs, Weakly similar to T22914	SS,pkinase,tubulin	6.0
50	441583	W28661 Al791499	Hs.5288 Hs.205742	Homo sapiens mRNA; cDNA DKFZp4 ESTs, Weakly similar to ALUA_H	SS,TM,pkinase,Activin_rec	6.0 6.0
	418802	AB028989	Hs.88500	mitogen-activated protein kina	WD40,Pico_P2A,M,SS	6.0
	414927	T83587	Hs.186476	ESTs .	SS,Sulfatase	6.0
	434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,arf,SS	6.0
55	414157	BE297801	Hs.103845	ESTs, Moderately similar to 15	SS	6.0
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	enolase, SS, Atrophin-1, Atr	6.0
	406487			Target Exon	SS,TM	6.0
	447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SH3,PH,RhoGEF	6.0
60	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,	WD40,SS,TM,fn3,EGF,fn3,ig	6.0
UU	442297	NM_006202		phosphodiesterase 4A, cAMP-spe	PDEase	5.9
	426440 418256	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_tr,SS,TM,sugar_tr SS,SS,TM,HSF_DNA-bind	5.9
	431543	AW845318 AW969619	Hs.12271 Hs.259768	f-box and leucine-rich repeat adenylate cyclase 1 (brain)	TM	5.9 5.9
	430344	AA476827	Hs.171012	hypothetical protein FLJ22349	HLH .	5.9
65	428539	AW410063	Hs.184877	solute carrier family 25 (mito	mito_carr,SS,TM,profilin,	5.9
-	403938		10.10.1011	Target Exon	Ephrin	5.9
	456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.9
70	434357	AW732284	Hs.3828	mevalonate (diphospho) decarbo	GHMP_kinases,SS,TM	5.9
70	443553	AL040535	Hs.9573	ATP-binding cassette, sub-famil	ABC_tran,SS	5.9
	433333	AI016521	Hs.71816	v-akt murine thymoma viral onc	homeobox,pkinase,PH,pkina	5.9
	430600	AW950967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.9
	409034 421542	AI684149	Hs.172035	hypothetical protein similar t	\$\$ ee ee	5.9
75	421542 431534	AA411607 AL137531	Hs.118964 Hs.258890	ESTs, Weakly similar to KIAA11 Homo saplens mRNA; cDNA DKFZp4	SS,SS SS,TM,r2s	5.9 5.9
, 5	409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G	SS,TM,7tm_2,cadherin,GPS,	5.9 5.9
	423464	NM_016240		CSR1 protein	Collagen,SS	5.9
	422379	AA932860	Hs.133864	ESTs		5.8
	443887	NM_004729		Ac-like transposable element	zf-BED	5.8
80	450122	BE313765	Hs.343443	ESTs, Weakly similar to 138022	SS,TM,Y_phosphalase,LON,A	5.8
	404807			Target Exon	UPF0027	5.8
	445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	SS,sushi,SS	5.8
	445631	AK001822		Homo saplens cDNA FLJ10960 fis	00.744/00.000	5.8
	412091	R06185		gb:ye94d03.r1 Soares fetal liv	SS,TM,IBR,IBR	5.8
				•	0.40	
					262	

	446536	W74413	Hs.15251	hypothetical protein	SS	5.8
	432866	BE395875	Hs.279609	mitochondrial carrier homolog	mito_carr	5.8
	402393			ENSP00000085284*:CDNA FLJ20404	RhoGEF,PH,SS,zf-CCCH,vwd	5.8
_	413041	BE061580	Hs.61622	gb:MR0-BT0249-091299-201-c07 B	SS	5.8
5	414356	AW505085	Hs.335147	gb:UI-HF-BN0-als-a-10-0-UI.r1	SS,TM	5.8
	402916			ENSP00000202587*:Bicarbonate t	HCO3_cotransp,SS	5.7
	459133	U40343	Hs.29656	cyclin-dependent kinase inhibi	ank,SS,Adap_comp_sub	5.7
	404757			Target Exon	TM.zf-C2H2	5.7
	409879	BE083422	Hs.56851	hypothetical protein MGC2668	SS,TM	5.7
10	411219	AW832917		gb:QV2-TT0003-161199-013-h06 T		5.7
	421871	AK001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.7
	434067	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fis		5.7
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116		5.7
	446562	BE272686	Hs.15356	hypothetical protein FLJ20254	hormone,SS,pfkB	5.7
15	407117	AA146625	113.13330	gb:zo71c07.s1 Stratagene pancr	SS S	5.7
13			D- 12004			5.7
	444855		Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.7
	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	
	407757	BE048414	Hs.165215	hypothetical protein MGC5395	SS,EF1G_domain,GST_C,GST_	5.7
20	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS SO THE Change Amount A	5.7
20	437141	BE304917	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glycos_transf_4	5.7
	408905	AV655783	Hs.661	Target CAT		5.7
	450787	AB006190	Hs.25475	aquaporin 7	MIP,SS,TM	5.7
	432496	D45576	Hs.187959	ESTs		5.7
0.5	429367	AB007867	Hs.278311	plexin B1 ~	Sema,PSI,TIG,SS,TM,TIG,Se	5.7
25	422708	AB017430	Hs.119324	kinesin-like 4.,	kinesin,homeobox,SS,TM,zf	5.7
	417442	AA199940	Hs.124039	ESTs		5.7
	432751	AF152099	Hs.278911	Interleukin 17C	SS	5.7
	432004	BE018302	Hs.2894	placental growth factor, vascu	PDGF,SS	5.7
	454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.7
30	456145	BE299427	Hs.21446	KIAA1716 protein	SS,DIX,PDZ,DEP,Dishevelle	5.6
	417677	NM_016055	Hs.82389	CGI-118 protein		5.6
	451558	NM_001089		ATP-binding cassette, sub-famil	ABC_tran,SRP54,SS,TM,ECH	5.6
	408795	AW749126	Hs.170345	hypothetical protein FLJ13710	hormone_rec.zf-C4	5.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_H	SS, histone, histone	5.6
35	452849	AF044924	Hs.30792	hook2 protein	bZIP,SS,AhpC-TSA	5.6
55	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	DEST TOOK TIPE TOO	5.6
	459271	AL045934	113.114011	gb:DKFZp434M116_r1 434 (synony	SS,PI3_PI4_kinase,PI3Ka	5.6
	401609	ALU40304		C16001614:gil7801278jemblCAB91	30,F10_F14_KIII838,F10/KB	5.6
		1172727	Un 10710		V shorshatasa fa2 ia MAM	5.6
40	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,ig,MAM,	
40	409125	R17268	Hs.343567	axonal transport of synaptic v	SS,kinesin,PH,FHA,kinesin	5.6
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.6
	415514	F11301	Hs.138329	ESTs	SS,TM	5.6
	437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.6
4.5	406663	U24683		Immunoglobulin heavy constant	SS	5.6
45	421678	AA419008	Hs.106730	chromosome 22 open reading fra	SS,TM,UBA,Rhomboid,SS,TM	5.6
	422472	R59096	Hs.279939	mitochondrial carrier homolog	mito_carr	5.6
	414918	Al219207	Hs.72222	hypothetical protein FLJ13459	SS,TM,efhand	5.6
	434906	BE410573	Hs.283636	Homo sapiens, clone IMAGE:4053	SS,TM,Exo_endo_phos,BNR,A	5.6
	414757	U46922	Hs.77252	fragile histidine triad gene	HIT	5.6
50	436014	AF281134	Hs.283741	exosome component Rrp46	RNase_PH,RNase_PH_C,SS,TG	5.6
	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA		5.6
	408015	AW136771	Hs.244349	epidermal differentiation comp		5.6
	445871	AI702901	Hs.145582	ESTs, Wealty similar to FOR4 M	SS,TM,efhand,efhand	5.5
	411813	NM_014931	Hs.72172	KIAA1115 protein	SS,TM,Y_phosphatase	5.5
55 .	425098	AW295349	Hs.8038	ESTs	SS,TM	5.5
	429720	M79091		gb:EST01239 Subtracted Hippoca		5.5
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	SS,TM,lipoxygenase,PLAT,s	5.5
	449225	R39108	Hs.6777	ESTs	SS,TM,Na_sulph_symp	5.5
	423233	BE048021	Hs.11067	ESTs, Highly similar to T46395	=	5.5
60	432538	BE258332	Hs.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
	408215	BE614290		syntaxin 10	SS,SS,TM,HLH,TRM,zf-CCCH	5.5
	406244			Target Exon		5.5
	436041	AI803516	Hs.272891	hippocalcin-like protein 4	SS,efhand,TGF-beta,TGFb_p	5.5
	422013	N92696	Hs.293354	ESTs	SS,TM	5.5
65	442451	A1498080	Hs.129616	ESTs	SS	5.5
05	427859	AA416856	Hs.98170	ESTs	SS,TM,DUF60,trypsin,CUB,u	5.5
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS,TM	5.5
				serine/threonine kinase 12	pkinase,SS,TM,synaptobrev	5.4
	427747 441456	AW411425 Al458911	Hs.180655 Hs.127765	ESTs	handoloo! I molitabanio	5.4
70					integrin A EC CAR Phobd a	5.4
70	431630		Hs.265829	integrin, alpha 3 (antigen CD4	integrin_A,FG-GAP,Rhabd_g	5.4 5.4
	415976	R43144	Hs.21919	ESTs	TM	
	447374	AF263462	Hs.18376	KIAA1319 protein	SS,Myosin_tail,M	5.4
	431275	T56571	Hs.10041	ESTS	SS,HLH	5.4
76	404343			C7002191*:gi[5053028 gb]AAD388	SS,ABC_tran	5.4
75	431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.4
	421779	Al879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.4
	418678	NM_001327		cancer/testis antigen (NY-ESO-	SS,TM,zf-C2H2	5.4
	457310	W28363	Hs.239752	nuclear receptor subfamily 2,	22\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	5.3
00	417193	Al922189	Hs.288390	hypothetical protein FLJ22795	SS	5.3
80	432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin,SS,cyclin	5.3
	456573	A1279811		Homo sapiens, clone IMAGE:3953		5.3
	409164	AA706639		gb:ag90e09.r1 Stratagene hNT n	SS,TM,Hint,HH_signal,tubu	5.3
	442296	NM_007275		lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.3
	438670	A1275803	Hs.123428	ESTs		5.3
					0.60	

	400257			ENGROSSISSISSISSISSISSISSISSISSISSISSISSISSI	PC harmon	
	400257	A14/070440	U- 22612	ENSP00000000452:BAD protein (B	SS,hormone_rec,zf-C4	5.3
	449514	AW970440	Hs.23642	protein predicted by clone 236	SS,PX,arf,lipocalin,PHD,z	5.3
	427336	NM_005658		TNF receptor-associated factor	MATH,SS,MATH,A2M_N,A2M,NT	5.3
5	414551	AI815639	Hs.76394	encyl Coenzyme A hydratase, sh	ECH,Peptidase_U7,SS,TM	5.3
5	447960	AW954377	Hs.26412	ring finger protein 26	SS,TM,Cbl_N,Cbl_N2,Cbl_N3	5.3
	430605 456849	AJ245433	Hs.247323	G4 protein	SS,TM,G-patch,ubiquitin,a	5.3
	430513	AA622394	Hs.153177	ribosomal protein S28	SS,TM	5.2 5.2
	424437	AJ012008	Hs.241586	G6C protein	SS,TM,GST_C,abhydrolase	5.2 5.2
10	427815	BE244700 BE072019	Hs.147049 Hs.12851	cut (Drosophila)-like 1 (CCAAT	CUT,homeobox,beta-lactama SS,TM,7tm_1	5.2
10	417903			phosphatidylserine synthase 2		5.2
	420476	NM_002342		lymphotoxin beta receptor (TNF	TNFR_c6,SS	5.2
	409960	AW575863 BE261944	Hs.136232	ESTs hexokinase 1	SS,HLH	5.2
	436325		Un 7202		SS,TM	5.2
15	444439	AL390088	Hs.7393 Hs.143545	hypothetical protein from EURO hypothetical protein MGC11303	SS,Synapsin_C,SS SS,TM,PAF-AH_p_II	5.2
IJ		A1458883			33,1M,FAF-AH_P_II	
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de	CU2 akinana ausidawal daC	5.2
	418891	NM_002419		mitogen-activated protein kina	SH3,pkinase,pyridoxal_deC	5.2 5.2
	430323	U40714	Hs.239307	tyrosyl-tRNA synthetase	DUF101,SS,IRNA-synt_1b,IR	
20	432396 457843	AW295956	Hs.11900	hypothetical protein FLJ14972	SS	5.2 5.2
20	429252	AW138211 NM_004658	Hs.128746	ESTS	CO DU DOCAD DTV CC CO DU	5.1
	429232		Hs.198273	RAS protein activator like 1 (C2,PH,RasGAP,BTK,SS,C2,PH WD40	5.1 5.1
	412104	BE250337 AW205197	Hs.240951	Target CAT	SS,TM	5.1
	449750	H28586	Hs.32325	Homo saplens, Similar to RIKEN		5.1
25	442725			ESTS	SS,ras	5.1
23	430390	Al935786 AB023186	Hs.131035	ESTs, Weakly, similar to CA24_H	SS,SS,TM,PX,PH,PLDc,arres	5.1 5.1
	421658	X84048	Hs.241161 Hs.301760	KIAA0969 protein	PH,SS,TM	5.1
	426928		Hs.172914	frequenin (Drosophila) homolog	efhand	5.1
		AF037062 AI016405		retinol dehydrogenase 5 (11-ci	adh_short,SS,adh_short,TG	
30	428924		Hs.98959	ESTs, Weakly similar to JC5314	SS,TM,lectin_c	5.1
50	458876	A1650896	Hs.195347	ESTs	Calidada la	5.1
	402632	A14444470	LLo DAO	Target Exon	Fz,kringle,ig	5.1 5.1
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	FKBP,TPR,SS	
	419451	Al907117 R85182	Hs.90535	syntaxin binding protein 2	Sec1,SS,TM	5.1 5.1
35	456155		Hs.7175	ESTs, Weakly similar to AF1568	SS -	
55	422396	W21872	Hs.7907	ESTs, Weakly similar to T19486		5.1
	413983 447598	BE348384 A1799968	Hs.279194 Hs.199630	ESTS	CC TM	5.0 5.0
	447598 425858	AA364923	us. 199090	ESTs	SS,TM	5.0
	440511	AF132959	Hs.7236	gb:EST75602 Pineal gland II Ho eNOS interacting protein	SS,TM,Peptidase_M10,fn2,h	5.0
40	452661	AW449413	Hs.257152	ESTs	SS,TM,MAGE,Ribosomal_S17,	5.0
70	412800	AW950852	Hs.74598	polymerase (DNA directed), del	homeobox,SS,efhand,hexoki	5.0
	446603	NM_014835		oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	402884	1414/1014022	16.10010	ENSP00000164597:PR00566.	faminin_Nterm,laminin_Nte	5.0
	448680	AW245890	Hs.21753	JM5 protein	WD40,SS,TM,KOW,HLH	5.0
45	431515	NM_012152		endothelial differentiation, I	7tm_1	5.0
73	427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
	425169	AW292500	Hs.128514	ESTS	SS	5.0
	412940	8E295701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	440839	Al142078	Hs.135562	EST8	SS ;	5.0
50	443814	BE281240	Hs.9857	carbonyl reductase	00	5.0
-	434243	AA628062	Hs.200358	ESTs, Moderately similar to AL	SS,TM	5.0
	435605	AF151815	Hs.4973	hypothetical protein	SS,TM,SS,TM,ABC_tran,ABC_	5.0
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287	SS,TM,filament,IF_tail	5.0
	403055	2-0510	12.7007	C2002219*:gij12737280 ref[XP_0	act militariands Tem	5.0
55	420856	BE513294	Hs.205736	HLA class II region expressed	kazal,SS,TM,lg,pkinase	4.9
-	405594	02010254	18.250100	NM_021949:Homo sapiens ATPase,	E1-E2_ATPase, Hydrolase, SS	4.9
	405334			Target Exon	SS,TM,MIP	4.9
	419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI,SS,CDK5_activator	4.9
	413764	BE162704	(15.50144	gb:PM1-HT0454-301299-001-d08 H	SS .	4.9
60	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light		4.9
	446933	AL137659	Hs.297214	HSPC141 protein	SS,TM,ank,EGF,notch,MATH,	4.9
	409139	AI681917	Hs.3321	ESTs, Highly similar to IRX1_H	SS,homeobox	4.9
	456672	AK002016	Hs.114727	Homo saplens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	4.9
	420842	AI083668	Hs.50601	hypothetical protein MGC10986	SS	4.9
65	421909	NM_013375		TATA-binding protein-binding p		4.9
	419667	AU077005	Hs.92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	4.9
	443496	AJ006973	Hs.9482	target of myb1 (chicken) homol	VHS.GAT.TM.Heme_oxygenase	4.9
	400933			NM_004347:Homo sapiens caspase	ICE_p20,ICE_p10,CARD,SS,I	4.9
	456143	H11097	Hs.61960	hypothetical protein	SS,pkinase	4.9
70	427527	AI809057	Hs.153261	immunoglobulin heavy constant	SS,TM,lg	4.9
	414265	BE410411	Hs.75864	endoplasmic reticulum glycopro		4.9
	433933	Al754389	500 .	Homo saplens clone TCCCIA00164	SS,TM,SS,TM,SH2,Y_phospha	4.9
	452302	AF173867	Hs.28906	glucocorticoid modulatory elem	SAND,SS	4.9
	409938	AW974648		gb:EST386752 MAGE resequences,	SS,Adap_comp_sub,GYF	4.8
75	400845			NM_003105*:Homo sapiens sortil	ldl_recept_a,fn3,ldl_rece	4.8
	425976	C75094	Hs.334514	NG22 protein	SS,TM,pkinase,SH2,SH3,BNR	4.8
	452969	W92792	Hs.77575	hypothetical protein MGC3136		4.8
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	fn3,ig,Y_phosphatase,SS,T	4.8
	434962	AK001574	Hs.4291	golgi perepheral membrane prot	- · · · · · · · · · · · · · · · · · · ·	4.8
80	418572	AI751740	Hs.86172	paired related homeobox protei	homeobox	4.8
	440869	NM_014297		protein expressed in thyroid	lactamase_B,SS,XRCC1_N,BR	4.8
	453446	BE299996		gb:600944574F1 NIH_MGC_17 Homo	•	4.8
	412159	AF286598	Hs.9271	KIAA1071 protein	bZIP	4.8
	438999	AW276811		gb:xp66c02.x1 NCI_CGAP_Ov39 Ho		4.8

	420233	AA256714	Hs.194864	hypothetical protein FLJ22578	SS	4.8
	414576	AK000405	Hs.76480	ubiquitin-like 4	ubiquitin, SS, TM, G6PD, G6PD	4.8
	433669	AL047879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RasGAP,C2	4.8
_	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	SS	4.8
5	426912	AL043054	Hs.256657	ESTs, Weakly similar to A46302	SS	4.8
_	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT,SS	4.8
	440333	A1378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	4.8
	425615	AF023614	Hs.158341			
				transmembrane activator and CA	TM	4.8
10	458040	BE280562	Hs.287711	hypothetical protein FLJ22692	00 101141 01	4.8
10	458367	AA088470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,tRNA-synt_2d	4.8
	433294	AA582082	Hs.199410	ESTs		4.8
	437671	AA536047	Hs.9850	hypothetical protein MGC1842		4.8
	425338	H16716	Hs.182648	Homo sapiens cDNA FLJ14444 fis		4.8
1.5	447946	Al566164	Hs.165827	ESTs	SS,PTN_MK,7tm_1,DAGKc,DAG	4.7
15	447205	BE617015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRCT,Sema	4.7
	416880	H99640	Hs.53687	EST		4.7
	440150	AW975738	Hs.7001	Homo saplens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
	426268	AF083420	Hs.168913	senne/threonine kinase 24 (St	pkinase, pkinase	4.7
	429253	Y11739	Hs.198313	winged-helix nude	Fork_head,SS,TM,glycolyti	4.7
20	450261	AA788727	Hs.34068	ESTs, Weakly similar to A43932	SS	4.7
	439246	Al498072	***************************************	membrane-associated tyrosine-	SS,SS,TM	4.7
	419120	BE271922		ESTs, Weakly similar to zinc f	SS,TM,DENN,Cytidylyltrans	4.7
	416487	AW190458	Hs.79347	KIAA0211 gene product	SS,zf-C2H2	4.7
	413837	AW163525	115.15071	titin-cap (telethonin)	SS,Methyltransf_3	4.7
25	419887	AW292562	Hs.187628			
23				ESTs Woolk of House Table N	TM	4.7
	410277	R88621	Hs.26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	4.7
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Filam	4.7
	410892	AW809762	Hs.222056	Homo saplens cDNA FLJ11572 fis		4.7
20	407754	AA527348	Hs.288967	Homo sapiens cDNA FLJ14105 fis	SS,TM,SS,TM,TSPN,tsp_3,SE	4.7
30	409877	AW502498	Hs.15220	zinc finger protein 106		4.7
	431629	AU077025	Hs.265827	interferon, alpha-inducible pr	pkinase,SH2,SH3	4.7
	438800	AB037108	Hs.6418	seven transmembrane domain orp	SS,TM	4.7
	420823	R96881	Hs.63609	Hpall tiny fragments locus 9C	TM	4.7
~ -	418900	8E207357	Hs.3454	KIAA1821 protein	SS	4.7
35	402400			Target Exon	SS,TM,RNase_HII,bZIP,DUF2	4.7
	419625	U91616	Hs.91640	nuclear factor of kappa light	ank,SS,TM	4.7
	433319	AA583232		ESTs	SS	4.7
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	pkinase,SH3	4.7
	432750	NM_014440		interleukin 1, epsilon	IL1	. 4.7
40	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	4.7
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	4.7
	427101	R87591	Hs.172884	ESTs	SS,TM	4.6
	447544	AA401573	Hs.288284			
		M401313	HS.200204	hypothetical protein FLJ22378	SS,TM	4.6
45	400266	41754457	11- 404005	NM_002858*:Homo sapiens ATP-bi	ABC_tran	4.6
43	412841	A)751157	Hs.101395	hypothetical protein MGC11352	SS,TM	4.6
	422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Semia	4.6
	414874	D26351	Hs.77515	Inositol 1,4,5-triphosphate re	TM,RYDR_ITPR,ion_trans,MI	4.6
	418373	AW750770	Hs.84344	CGI-135 protein	SS,TM,PMP22_Claudin,2OG-F	4.6
50	424487	T08754	Hs.6259	KIAA1698 protein	SS,SS,TM,Gfyco_hydro_31,G	4.6
30	426571	AA381642		gb:EST94816 Activated T-cells		4.6
	433941	AA620612		ESTs	SS,TM,TNFR_c6	4.6
	421717	AF230924	Hs.107187	divalent cation tolerant prote		4.6
	450883	NM_001348	Hs.25619	death-associated protein kinas	pkinase,GTP_EFTU,EFG_C,GT	4.6
~ ~	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2,LRR	4.6
55	420421	AF281133	Hs.343589	exosome component Rrp41	RNase_PH,RNase_PH_C	4.6
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RGS,pkinase_C,SS,	4.6
	431498	AK001777	Hs.258551	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,Y_	4.6
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypoth	SS,TM,adh_short	4.6
	404661			C9000306*:gi[12737280[ref]XP_0		4.6
60	412790	NM_014767	Hs.74583	KIAA0275 gene product	kazal,thyroglobulin_1,zf-	4.6
	456243	AI345001	Hs.82380	menage a trois 1 (CAK assembly	zf-C3HC4	4.6
	426222	BE391706	Hs.168073	DKFZP727M231 protein	GSH_synthase	4.6
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	CLP_protease	4.6
	409114	AA070021		gb:zm67h03.r1 Stratagene neuro		4.6
65	429049	AW452125	Hs.119273	KIAA0296 gene product	SS,TM,trypsin	4:6
00	424271	Al991887	Hs.305882	5-oxoprolinase (ATP-hydrolysin	OO, THI, U J POINT	4.6
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044	CC TM akings Activia soc	
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endot	SS,TM,pkinase,Activin_rec flavodoxin,FAD_binding,NO	4.6 4.6
70	433074 444893	AL045019	Hs.323462 Hs.12109	Homo sapiens cDNA FLJ11214 fis WD40 protein Clao1	DEAD,helicase_C,dsrm,Vira	4.6
70		AW249312			WD40	4.6
	420508	AJ270993	Hs.98428	homeo box 86	homeobox,SS,homeobox,home	4.6
	409591	AA532963	Hs.9100	Homo sapiens cDNA FLJ13100 fis	SS,TM,LIM,homeobox	4.6
	456181	L36463	Hs.1030	ras inhibitor	RA,SH2,VPS9,SS,TM,Nudeos	4.6
75	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,TM,HCO3_cotransp	4.6
75	440104	AA132838	Hs.239894	hypothetical protein MGC2803	SS,DS	4.5
	423279	AW959861	Hs.290943	ESTs	SS	4.5
	445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	S1,SH2,Ribosomal_L23,pkin	4.5
	404036			Target Exon	SS,TM,cadherin,cadherin	4.5
00	431832	AW276866	Hs.192715	ESTs	Ets,SAM_PNT	4.5
80	433886	AA613596	Hs.28412	ESTs	SS	4.5
	426735	T78716	Hs.120446	ESTs	Oxysterol_BP,PH	4.5
	417825	AW838994	Hs.6363	heparan sulfate 6-O-sulfotrans	SS,TM	4.5
	455600	BE061053		gb:QV0-BT0041-271099-037-d09 B	C4	4.5
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	4.5
						1.0

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	101000					
	421680 408157	AL031186 AA047685	Hs.289106	Human DNA sequence from clone	SS,SS,rrm,zf-RanBP,rrm,GA	4.5
	434303	AW204058	Hs.62946	ESTs transforming growth factor bet	pkinase SS,TM,SSF,FG-GAP,vwa,inte	4.5 4.5
	440745	AW303627	Hs.143301	ESTs	35, 111,001, 1 GGAP, 4Wa, like	4.5
5	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank,DAGKa,DAGKc,DAG_PE-bi	4.5
	447208	BE315291	Hs.237971	hypothetical protein MGC5627		4.5
	436163	R84938		gb:yt65f04.r1 Soares refina N2		4.5
	456856	AK001528	Hs.347285	Homo sapiens, Similar to DiGeo		4.5
10	410817	AI262789	Hs.93659	protein disulfide isomerase re	SS,thiored	4.5
10	434558	AW264102	Hs.39168	ESTs	SS,TM,LRRCT,LRR	4.5
	440548 450200	AL117408	Hs.7274	DKFZP434P1750 protein	-4 1100 -4 C2UC4	4.5
	432434	AW975625 AL161977	Hs.173088 Hs.2994	ESTs PCTAIRE protein kinase 3	zf-UBP,zf-C3HC4	4.5 4.5
	440042	AL101377	Hs.133898	ESTs	SS,pkinase SS	4.5
15	454328	AW372097	Hs.278429	hepatocellular carcinoma-assoc	00	4.5
	458196	AIB0240B	1.5,2,0,120	ubiquitin A-52 residue ribosom	SS,TM,fn3,FKBP,TPR	4.5
	433472	AI541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,2-Hacid_DH_C,M	4.5
	408928	AW295827	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
20	448093	AW977382	Hs.15898	2,4-dienoyl CoA reductase 2, p	adh_short,NDK	4.5
20	426272	AW450671	Hs.189284	ESTs		4.5
	453610 441327	AW368882	Hs.33818	RecQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
	424681	AK001706 AA054400	Hs.7778 Hs.151706	hypothetical protein FLJ10751 KIAA0134 gene product	SS,TM,7tm_1 helicase_C,PRK,SS,TM,7tm_	4.5 4.5
	443443	Al344042	Hs.9347	regulator of G-protein signall	TM,Na_Pi_cotrans	4.5
25	426677	AW949856	Hs.97165	ESTs	SS	4.5
	412482	A1499930	Hs.334885	mitochondrial GTP binding prot	SS	4.4
	425236	AW067800	Hs.155223	stanniocalcin 2	Stanniocalcin,SS	4.4
	423229	AC003965	Hs.125532	protease, serine, 26	trypsin,SS	4.4
20	412338	AA151527	Hs.69485	hypothetical protein FLJ12436	SS,TM,TIG,Sema,PSI	4.4
30	419395	BE268326	Hs.90280	5-aminolmidazole-4-carboxamide	AICARFT_IMPCHas,MGS,AICAR	4.4
	442462 439975	AF031405	U- C047	gb:AF031405 Soares fetal liver	114- W CC	4.4
	423876	AW328081 BE502835	Hs.6817 Hs.15463	inosine triphosphatase (nucleo Homo sapiens, clone IMAGE:2959	Ham1p_like,SS SS,elhand	4.4 4.4
	423220	BE394920	Hs.125262	aladin	WD40,TM,Activin_recp,pkin	4.4
35	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cofilin_ADF,SS,TM	4.4
	448947	BE615408	Hs.337228	ESTs, Weakly similar to AXHU a	SS,TM,ig,pkinase	4.4
	407755	AJ151353	Hs.29742	Homo sapiens serine palmitoyl	SS,TM,aminotran_1_2	4.4
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,pkinase	4.4
40	458171	AI420016	Hs.192090	ESTs	SS,TM	4.4
40	424443	A1751281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
	427002	AA524093	Hs.23158	ESTs	SS,zf-C2H2	4.4
	404344	0000004	U- 20222	C7002191*:gi[5053028 gb]AAD388	SS,ABC_tran	4.4
	427458 419764	BE208364 BE262524	Hs.29283 Hs.93183	ESTs, Weakly similar to LKHU p vasodilator-stimulated phospho	SS,F5_F8_type_C,EGF,TGT	4.4
45	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	WH1 7tm_1,SS,TM	4.4 4.4
1.5	435615	Y15065	Hs.4975	potassium voltage-gated channe	ion_trans,KCNQ1_channel	4.4
	403945			Target Exon	tar Casarati va va i Canarata	4.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	Herpes_HEPA,SS	4.3
50	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	4.3
50	425245	Al751768	Hs.155314	KIAA0095 gene product	SS,TM	4.3
	423348	AA324687	11 0570	gb:EST27558 Cerebellum II Homo	SS,TM	4.3
	452105	AA022838	Hs.6570	ESTs, Weakly similar to S10889	SS,TM,TBC,rm	4.3
	431934 429499	AB031481 AA453809	Hs.272214 Hs.99350	STG protein ESTs	SS	4.3 4.3
55	453485	BE620712	Hs.33026	hypothetical protein PP2447	SS,TM	4.3 4.3
-	459393	BE409283	Hs.193264	hypothetical protein MGC3234	00,111	4.3
	405364			ENSP00000239138*:Guanine nucle		4.3
	428345	A1242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
C O	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycopro	SS,HLH,Myc_N_term,Myc-LZ,	4.3
60	413053	AW963263	Hs.65377	ESTs, Moderately similar to KI	TM,SS,TM,EF_TS,UBA,transm	4.3
	409983 409936	D50922 AK001691	Hs.57729	Kelch-like ECH-associated prot	BTB,Kelch,SS,TM	4.3
	421592	AF009801	Hs.57655 Hs.105941	hypothetical protein FLJ10829 bagpipe homeobox (Drosophila)	SS,TM homeobox,SS	4.3 4.3
	424251	AA677466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brom	4.3
65	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	pkinase	4.3
•	432805	X94630	Hs.3107	CD97 antigen	SS,TM,7tm_2,GPS,EGF,SS,TM	4.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	SS,TM	4.3
	456863	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	4.3
70	417823	R88869	Hs.102447	TSC-22-like	PWWP	4.3
70	406621	X57809	Hs.181125	immunoglobulin lambda locus	SS	4.3
	431493	Al791493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	4.3
	412958	BE391579	Hs.75087	Fas-activated serine/threonine	SS,pkinase	4.3
	431658 419579	BE409917 W49529	Hs.266935 Hs.296200	tRNA selenocysteine associated hypothetical protein AF053356_	rm,SS,RCC1 MSP_domain,SS,TM,CUB,NTR,	4.3 4.3
75	410076	T05387	Hs.7991	ESTs	MSF_dottialii,SS,TM,COB,NTR, SS	4.3 4.2
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	HSP20,SS	4.2
	424709	AL137589	Hs.152149	hypothetical protein DKFZp434K		4.2
	418419	X55039	Hs.85004	centromere protein B (80kD)	CENP-B,HTH_5	4.2
00	447377	X77343	Hs.334334	transcription factor AP-2 alph	TF_AP-2,TF_AP-2	4.2
80	416931	D45371	Hs.80485	adipose most abundant gene tra	C1q,Collagen,SS	4.2
	411674	AW861123	11 400040	gb:RC3-CT0297-120200-014-a05 C	SS	4.2
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis keratin 19	SS,ig,tsp_1,ZU5,SS,TM,Nuc	4.2
	406867 432183	AA157857 AW151952	Hs.182265 Hs.46679	hypothetical protein FLJ20739	filament,bZiP,SS,filament SS	4.2 4.2
	.02.00			-At amount branes, same as		7.0.
					266	

	418910	Z25821	Hs.89466	Homo sapiens, Similar to dodec	ECH,SS,TM,aminotran_3,ABC	4.2
	437300	AL040504	Hs.25063	PRO0461 protein	SS,TM,pkinase,cyclin,F-bo	4.2
	426615 421453	AA400678 AA234652	Hs.6473	gb:zu70a11.r1 Soares_testis_NH	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2 4.2
5	409616	AA076248	Hs.104555	neuropeptide FF-amide peptide gb:zm18c10.r1 Stratagene pancr	33,0211,2102112,0211,21-0	4.2
•	444744	BE394732	Hs.147562	ESTs	SS	4.2
	412575	AA113177		gb:zm29e05.s1 Stratagene pancr	TM,ER_lumen_recept	4.2
	429542	AF038660	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- g	Galactosyl_T_2,ig,SS,TM,A	4.2
10	435995	BE260415	Hs.348198	hypothetical protein FLJ20262		4.2
10	451585	AK001171	Hs.326422	hypothetical protein MGC4549	SS,Metallophos	4.2
	456153	AW972270	Hs.144054	ESTs	SS,TM	4.2 4.2
	455340 457268	AW901435 AW272279		gb:RCO-NN1012-270300-031-a10 N ESTs, Moderately similar to AL		4.2
	432311	BE083080	Hs.274323	similar to sialyltransferase 7	Glyco_transf_29	4.2
15	409656	NM_005133		RCE1, prenyl protein protease	Abl,SS,CPSase_L_chain,HMG	4.2
	424919	BE314461	Hs.153768	U3 snoRNP-associated 55-kDa pr	WD40,SS,KH-domain	4.2
	416528	H65052	Hs.337621	ESTs		4.2
	415137	A1634834	Hs.72451	Homo sapiens PAC clone RP5-108		4.2
20	417334	AA337572	Hs.157240	hypothetical protein MGC4737	SS,TM,ion_trans	4.2
20	451920	AA224483	Hs.27239	DKFZP586K0524 protein	SS,TM,SS,TM trypsin,SS,TM,ATP1G1_PLM_	4.2 4.2
	413049 458988	NM_002151 AW410431	Hs.283670	hepsin (transmembrane protease CGI-119 protein	nybani,aa,rw,xrerat_edv_	4.2
	406964	M21305	115.205070	FGENES predicted novel secrete		4.2
	451595	AW965569	Hs.20996	ESTs	SS,WD40	4.2
25	449728	AI820751	Hs.107635	ESTs -	SS -	4.1
	453245	T99801	Hs.339751	ESTs .	TM,ABC_tran	4.1
	432238	AL133057	Hs.274135	Homo saplens mRNA; cDNA DKFZp4	WD40,LRR	4.1
	430037	BE409649	Hs.227789	mitogen-activated protein kina	pkinase	4.1
30	442196	A1902646	Hs.31844	hypothetical protein FLJ12586	SS,SCAN pkinase,DAG_PE-bind,pkina	4.1 4.1
30	425251 415014	Z22521 AW954064	Hs.155342 Hs.24951	protein kinase C, delta ESTs	pkinase,DAG_PE-oino,pkina	4.1
	440088	BE559877	Hs.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	4,1
	418837	U48263	Hs.89040	prepronociceptin	Opiods_neuropep,SS	4.1
	410239	AI56B350	Hs.61273	hypothetical protein MGC2650	SS,ART,TM	4.1
35 ·	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1	ThiF,UBACT	4.1
	453968	AA847843	Hs.62711	High mobility group (nonhiston	SS,HMG_box	4.1
	448241	AW811064		gb:MR2-ST0131-211099-008-c06 S	SS STANDARD STANDARD	4.1
	441455	AJ271671	Hs.7854	zinc/iron regulated transporte	Zip,SS,TM,Cytidylyltransf	4.1 4.1
40	450848 429218	AI677994 AA225065	Hs.428 Hs.198269	fms-related tyrosine kinase 3 Target CAT	flt3_lig,SS,Ribosomal_L13 SS,Nop	4.1
70	425437	AK000482	Hs.181780	hypothetical protein FLJ20241	00,100	4.1
	406613	711000102	113.101100	Targel Exon	SS,pkinase,LRR,LRRCT,Ribo	4.1
	431239	AL039971	Hs.251216	hypothetical protein DKFZp434A	ank,WH2	4.1
4.5	436057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.1
45	415193	AL048891	Hs.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LRR	4.1
	424619	BE387282	Hs.207443	hypothetical protein MGC10848	CC THE BCC DIV	4.1
	432968	BE614192 BE269388	Hs.279869	melanoma-associated antigen re mitochondrial ribosomal protei	SS,TM,RGS,DIX SS	4.1 4.1
	428156 414084	AW168771	Hs.182698 Hs.71574	hypothetical protein FLJ 14926	SS,P5CR,EF1BD	4.1
50	424964	AW161271	Hs.153961	ARP1 (actin-related protein 1,	actin,SS	4.1
	431410	AW299534	Hs.105739	ESTs		4.1
	435968	AW161481	Hs.111577	integral membrane protein 3	TM .	4.1
	432351	AI270313	Hs.127762	hypothetical protein MGC12982		4.1
55	426120	AA325243	Hs.166887	copine I	C2,SS,aminotran_5	4.1
55	416877	BE386266	Hs.85658	hypothetical protein FLJ23436	SS,P5CR,Epimerase,zf-C2H2	4.1 4.1
	425970 434848	AK001500 BE256304	Hs.165186 Hs.32148	hypothetical protein FLJ13852 AD-015 protein	SS,TM,SS,TM,LRR,P,Peptida	4.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	IBR,zf-C3HC4,SS,TM,IRF,CK	4.1
	435851	AA700946		ESTs		4.1
60	425538	BE270918	Hs.164026	Homo sapiens, clone IMAGE:3534	SS,SNF2_N,helicase_C,brom	4.1
	444416	AW288085	Hs.11156	hypothetical protein	zf-C3HC4,SpcA,PHD,TM,syna	4.0
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
	444596	BE560662	Hs.11417	Rab acceptor 1 (prenylated)	SS,TM,lig_chan,ANF_recept SS,PWWP,TSC22	4.0 4.0
65	439685 447402	AW956781 H54520	Hs.293937 Hs.18490	ESTs, Weakly similar to FXD2_H hypothetical protein FLJ20452	SS,TWWF,13C22 SS,TM	4.0
05	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447	SS	4.0
	426068	AF029778	Hs.166154	jagged 2	DSL,EGF,vwc,granulin,SS,T	4.0
	459255	A1493244	Hs.239500	hypothetical protein MGC13114	SS	4.0
70	403182			Target Exon	SS	4.0
70	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS,TM	4.0
	459167	BE504370	11- 64460	ESTs, Weakly similar to CA13_H	SS SC TALIG UT U	4.0
	452747 444633	BE153855 AF111713	Hs.61460 Hs.286218	lg superfamily receptor LNIR junctional adhesion molecule 1	SS,TM,ig,HLH Ig,SS,TM,HLH	4.0 4.0
	444633 434171	BE247688	Hs.347349	KIAA0948 protein		4.0
75	422155	AW249152	11010	sirtuin (silent mating type in	SIR2,HLH,Myc_N_term,Myc-L	4.0
. –	433262	AI571225	Hs.284171	KIAA1535 protein	SS,TM,cNMP_binding,ion_tr	4.0
	442599	AF078037	Hs.324051	RelA-associated Inhibitor	SH3,ank,SS,TM,HHH,ig	4.0
	452500	AW373011	Hs.54558	hypothetical protein FLJ22222		4.0
0Λ	437563	A1217204	Hs.144968	ESTs	cc	4.0
80	432234	AA531128	Hs.115803	ESTs	SS	4.0 4.0
	433135 447495	AA443873 AW401864	Hs.110477 Hs.18720	dolichyl-phosphate mannosyltra programmed cell death 8 (apopt	pyr_redox,SS,Ets	4.0
	452857	BE072814	Hs.258519	ESTs, Moderately similar to S6	SS	4.0
	427834	AA506101	Hs.285813	hypothetical protein FLJ11807	SS,TM	4.0
					267	
					201	

5	418963 437340 455928 400607 424825 438143	BE304571 AL353935 BE170313 AF207069 BE500981	Hs.89529 Hs.135917 Hs.153357 Hs.269652	aldo-keto reductase family 1, hypothetical protein DKFZp761D gb:QV4-HT0536-040500-193-g02 H Target Exon procollagen-lysine, 2-oxogluta ESTs	aldo_ket_red TBC,bZIP,WD40,WD40 SS SS,homeobox 2OG-Fell_Oxy,Glycos_trans	4.0 4.0 4.0 4.0 4.0 4.0
	433173 412550	Z35093 R52452	Hs.3196 Hs.26370	surfeit 1 gb:yg80g07.r1 Soares Infant br	SURF1,SS,TM,SURF1,SURF4	4.0 4.0
10	CAT number	e Eos probes : Gene cluste Genbank acce	r number			
15	Pkey 408215	CAT Numbe 10478_1	BE614290 A AA666391 A AA626639	N160210 Al446461 Al355345 Al343638 Al	343640 Al275091 M78746 AW262795 AW	E221263 Al348910 Al985031 Al090078 Al359617 250002 AA503756 Al934519 AW272086 N26520
20	408294 409114 409164 409616 409938	1050553_1 110088_1 110421_1 114348_1 116091_1	AA070021 A AA706639 A AA076248 A		BE141343 BE141298 BE141702 BE14128) AA082183 AA115915 AA085147 AA1259	
25	409960	116270_1	AA205977 C Al567682 A	202043 AA135057 AA078870 AA377395 A A932839 A1056920		BE314003 AA908246 AW960808 AA385346 AW370250 AW370244 T85930 AA759250
30	410445 411219 411674	120374_2 1236055_1 1253746_1	AW832917 AW861123	U143895 AW961629 AA322482 AW832913 AW832906 AW832788 AW832 AW861125 AW856717 AW861116 AW856 AW856786 AW856776 AW856635 AW856	706 AW856788 AW856774 AW856787 AV	/856780 AW856782 AW856789 AW856772
	412091 412173 412575	1276564_1 1280870_1 130769_1	R06185 AW T71071 AW AA113177 A	891805 AW901892 AW901895 902279 AW897608 \W894515 AA113847		
35	413534 413564	1375357_1 1376722_1	BE146961 E BE260120 E	BE146780 BE146788 BE146967 BE146774 BE148538	4 BE146963 BE146907	
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	413037	133303_1	AW157459			AW299513 AA132529 Al340991 Al912836
40	414413.	1443696_1	BE294877 B	BE294759		
	415126 419120	1523506_1 182026_1		1346 D81568 D80539 J54771 AA234233 AA471354 BE171081 A	A253482 AA470113 AA824327 H24470 A	W504757 N51688 Al400700 AA578548 AA714130
	413120	102020_1	AA609917 A	W780349 AW664465 AW467553 AW5716		26817 AA593859 AW952245 AW341739 AA805093
45	422155	21235_1	W39153 AA	AW249153 BE298958 AW192872 AF0957		237 BE258447 BE253088 AA297721 H68948 197 AA297787 Z42780 AA297072 T81280 T83544
	423348	227276_1	AA324687 A	A325155 AW962038		
50	425858 426571	257265_1 269283_1		\W963483 BE182774 C21461 \A381664 AW963560 AW949848 AA38172	28 AA381608	
	427326	277229_1	A1287878 A	804160 AA400787		
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55	430168	313927_1	AW968343	AA468507 AI478223 AW513008 AI762122	Al554512 AA862642 AA468976	
23	431424 433319	333110_1 363095_1	A1222969 A AA583232 A	A806560 AA504839 AA805261 AA601715		
	433933	377703_1			1863355 AW131720 A1674922 A1949042 A	1990060 A1623178 AW469497 AA620354
	433941 434303	377883_1 383224_1		VA994983 AA994990 AI424379 AI669663 AA629077 AW613033		
60	434743	3925_1	Al363410 Al AW505595 A AA278866 A	1356019 H00141 T78748 AL049365 AL079 AF086096 N90340 N63271 AA131836 AW VA044784 AA700	9911 Al750972 Z42602 AW452523 Al2238	26 AA215407 AI633829 AA292122 N42783 1951 AW966080 M78807 N31947 AA521151
	434796 435851	393400_1 411522_1		NW974514 AA764999 AA649302 NA702712 AA947620		
65	·436163	41515_6		047151 AA310309 AW063200 AI569528 AI	I307823 N49975	
	437215	43473_1 467686_1	AL117488 A			
	438999 439246	407000_1 47021_3		AA829050 AA829190 W251083 AA985226 AA852987 Al392809	AA206609 AW190187 AA555262 AF0860	57 F35814 AW516382 AA377885 N50847 F27148
70			AA731186 A	AA417728 AI003145	•	
70	440317 442462	49187_1 543232_1	AF031405 H	3E560615 BE562102 473415		
	442472	543371_1		AW806852 AF049582		
75	445625	64558_1	A1863005 A	A317806 A1678000 AW189963 A1986207 A		T57442 Al399986 R50073 R48743 Al769689 469257 Al954604 H21954 T25141 AA856793
13	445631	6457_1	AI655000 A	AW860325 AA335296 AW965531 AW1309 W418837 AI380485 AA410698 AI520726 I		62527 Al343924 Al380749 AA938153 T66966 AW593995 Al336927 Al336928 Al357036 R60592
80	447128	70934_1				259 AW973696 F25787 F35749 Al568815
	448241 448993	756181_1 79225_1	AW811064	AW811160 AI478413		14 AW956702 Al656234 Al636283 Al567265
	***0333	19669_1	AW340858		AA454908 AA293504 Al659741 Al927478 .	AA399460 AI760441 AA346416 BE047245
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BE299996 BE297115 BE270415 BE295214 BE296526

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1335877_1
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AW995839 AW995907
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           TABLE 23C:
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20
           Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of
                   human chromosome 22° Dunham, et al. (1999) Nature 402:489-495
           Strand: Indicates DNA strand from which exons were predicted Nt_position: Indicates nucleotide positions of predicted exons
25
           Pkey
400460
                                        Strand
                                                       Nt_position
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            400607
                                        Plus
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                          9887666
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                          8705148
                                        Minus
            400845
                          9188605
7637836
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9454515
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                                        Minus
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Plus
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                          7406502
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                                        Plus
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                          4760409
7417725
                                         Plus
65
                                                       39422-39595
            406244
                                         Plus
            406301
                                                        57291-57494
                          8575868
                                         Plus
            406487
                           7711306
                                         Plus
                                                       82039-82902
                                                        174661-174978
            406495
                           7711328
                                         Minus
                                                        5029-5147
                           2957168
            406613
                                         Plus
70
```

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

75

453446

967533 1

Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number 80 Title: UniGene gene title Protein Dom.: Predicted protein domain

R1: Ratio of normal ovaries to tumor

	Pkey	Ex. Accn	UG ID	Title	Protein Dom.	R1 16.9
	428232	BE272452	Hs.183109	monoamine oxidase A	Amino_oxidase,pyr_redox,F SS	10.8
	433563 444931	AI732637 AV652066	Hs.277901	ESTs	SS,Gtypican	8.7
5	451573	AW130351		general transcription factor I ESTs	SS SS	8.3
•	429570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM	7.9
	453510	Al699482	Hs.42151	ESTs	SS	7.5
	410295	AA741357		nidogen (enactin)	SS,EGF,ldl_recept_b,thyro	6.9
10	438549	BE386801	Hs.21858	trinucleotide repeat containin	SS,serpin,SS,WD40,FYVE	6.5
10	407969	AA046217	Hs.105370	ESTs	SS,Pep_M12B_propep,Reprol	6.2
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 famil	aldedh	6.0 5.7
	448438 441422	BE613081 R43777	Hs.24654 Hs.21364	Homo sapiens cDNA FLJ11640 fis ESTs	SS,TM	5.1
	413391	Al223328	Hs.75335	glycine amidinotransferase (L- '	Amidinotransf	3.9
15	428022	Z39686	Hs.27865	ESTs	SS	3.6
	423044	AA320829	Hs.97266	protocadherin 18		3.6
	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	452854	AA437061	Hs.14060	prokineticin 1 precursor	SS	3.4
20	436772	AW975688		metallothionein 1E (functional	SS,TM,7tm_2,HRM	3.2 3.2
20	415162	AF035718	Hs.78061	transcription factor 21	HLH SS	3.1
	427794 433072	AA709186 Al928037	Hs.99070 Hs.158832	ESTs ESTs	SS	3.1
	418318	U47732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.9
	410059	NM_007038		a disintegrin-like and metallo	Reprolysin,tsp_1,Pep_M12B	2.9
25	431933	Al187057	Hs.132554	ESTs	TM,SS,TM	2.9
	420303	AA258282	Hs.278436	KIAA1474 protein		2.8
	438780	M64936		gb:Homo saplens retinolc acid-		2.8
	427661	AA410292	Hs.104761	ESTs	SS,wnt	2.8
30	437342	AW903297	Hs.236438	hypothetical protein DKFZp761K	Sec7,PH SS,Pep_M12B_propep,Reprol	2.8 2.7
30	453828 418444	AW970960 Al902899	Hs.293821 Hs.85155	ESTs butyrate response factor 1 (EG	zf-CCCH,SS	2.7
	453767	AB011792		extracellular matrix protein 2	vwc,LRR,SS,LRR	2.7
	413624	8E177019	Hs.75445	SPARC-like 1 (mast9, hevin)	kazal,SS,kazal	2.7
	413305	NM_000426		Homo sapiens cDNA: FLJ23176 fi	laminin_B,laminin_EGF,lam	2.7
35	414504	AW069181		sterile-alpha motif and leucin	SS,pkinase,SAM	2.7
	439897	NM_015310		KIAA0942 protein	Sec7,PH	2.7
	421639		Hs.106309	Friend of GATA2	SS HATBook & HATBook &	2.7 2.6
	442498 410494	U54817 M36564	Hs.8364 Hs.64016	Homo sapiens pyruvale dehydrog protein S (alpha)	HATPase_c,HATPase_c EGF,laminin_G,gla	2.6
40	452958	AA883929	Hs.40527	ESTs	\$S	2.6
	449648	AW205607	Hs.253499	ESTs	SS	2.5
	435519	Al218950	Hs.125461	hypothetical protein FLJ11539	SS	2.5
	433690	AI373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
45	424319		Hs.96752	ESTs, Weakly similar to ALU8_H		2.5
45	420174	AI824144	Hs.199749	ESTs	CID Verse III 6	2.5 2.4
	421709 417622	AA159394 AW298163	Hs.107056 Hs.82318	CED-6 protein WAS protein family, member 3	PID,Herpes_UL6 WH2	2.4
	453655	AW960427	Hs.342874	transforming growth factor, be	SS,TM,zona_pellucida	2.4
	408468	AI909712	113.072077	phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
50	400829			C11000244:gi]11056030 ref NP_0	SS,TM,SS,TFIID_30kD	2.3
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	ras	2.3
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp5	HLH	2.3
	425462	A(491852	Hs.46783	Homo sapiens cDNA: FLJ22382 fi	Amil CoA dh	2.3 2.3
55	417094 403247	NM_006895	HS.81162	histamine N-methyltransferase Target Exon	Acyl-CoA_dh	2.3
55	441916	AA993571		ESTs		2.3
	422746		Hs.119651	glypican 3	Glypican,SS ·	2.3
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	SS,GTP_CDC,SS	2.3
<i>(</i> 0	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fi	SS,TM	2.3
60	418956	AA234831		KIAA0788 protein	SS .	2.3
	410073	AW408163		catenin (cadherin-associated p	Vinculin,Stathmin harmone_rec,zf-C4,hormone	2.3 2.3
	419461 429319	AI452601 AL023754	Hs.288869 Hs.199068	nuclear receptor subfamily 2, similar to calcium/calmodulin	SS,pkinase	2.2
	452123	AI267615	Hs.38022	ESTs	SS	2.2
65	453305	R39224	Hs.267997	EHM2 gene		2.2
•	416157		Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
	406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p	2.2
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA	p450	2.2
70	408915		Hs.48950	heptacellular carcinoma novel	SS	2.2 2.2
70	420929	A1694143	Hs.326248	programmed cell death 4 ribosomal protein L38	MA3,LRR SS,TM	2.2
	456972 409549	Al054347 AB029015	Hs.2017 Hs.54886	phospholipase C, epsilon 2	C2,PH,PI-PLC-Y,PI-PLC-X	2.2
	410209	A1583661	Hs.60548	hypothetical protein PRO1635	SS,TM,Fork_head	2.2
~ ~	449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
75	447806	W03616	Hs.10432	ESTs, Weakly similar to I38022	•	2.1
	441712	AW391927	Hs.7946	KIAA1288 protein	SC DAG HIDESSSA	2.1
	445025	A1768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,UPF0001 SS	2.1 2.1
	444161	N52543	Hs.142940	ESTs KIAA0603 gene product	SS,TM,TBC	2.1
80	427156 436995	BE621719 A1160015	Hs.173802 Hs.125489	ESTs	SS,TM,RasGEF,actin,RasGEF	2.1
50	436993	N33937	Hs.10336	ESTs	SS .	2.1
	448274	Al268097	Hs.67317	Homo sapiens cDNA FLJ11775 fis		2.1
	426354	NM_004010) Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	2.1
	443906	AA348031	Hs.7913	ESTs		2.1

	444815	AA151539	Hs.1227	aminolevulinate, delta-, dehyd	SS.ALAD	2.1
	420728	AA767718	Hs.93581	hypothetical protein FLJ10512	SS.TM,Sema,PSI.ig	2.1
	404245	741107710	113.35001	NM_007116*:	fibrinogen_C,fn3,SS	21
	436420	AA443966	Hs.31595	ESTs	SS,TM,PMP22_Claudin,SS,TM	2.1
5	410066	AL117664	Hs.58419	DKFZP586L2024 protein	CO, MILT III ZZ_CILIGUI, CO, MI	2.0
-	414476	AA301867	Hs.76224	EGF-containing fibulin-like ex	EGF,TIL,SS	2.0
	424137	AA335769	Hs.16262	ESTs		2.0
	447659	AA017472	Hs.107260	hypothetical protein DKFZp586H	SS	2.0
	444862	Al209158	Hs.143929	ESTs	SS.TM	2.0
10	426086	T94907	Hs.188572	ESTs	PH,CH,spectrin	2.0
10	436080	A1684710	Hs.201645	ESTs	SS,ATP-synt_C	2.0
	424651	A1493206	113.201040	ESTs	SS	2.0
	432939	AL038924	Hs.279849	KIAA0438 gene product	zf-C3HC4.myosin_head.DIL	2.0
	449088	A1654048	Hs.196556	ESTs	SS.MACPF.sushi.ldl_recept	2.0
15	428642	NM_014899		KIAA0878 protein	BTB.ras	2.0
13	419577	L36531	Hs.91296	integrin, alpha 8	TM,integrin_A,FG-GAP	2.0
	450435	AI695975	Hs.201805	ESTs	laminin_B.laminin_EGF.lam	2.0
	450696	Al654223	Hs.16026	hypothetical protein FLJ23191	SS S	2.0
	421255	BE326214	Hs.93813	ESTs	TM	2.0
20	432467	T03667	Hs.239388	Human DNA sequence from clone	SS	2.0
	408654	BE018882	Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
	412611	AA732036	Hs.164478	hypothetical protein FLJ21939		20
	453355	AW295374	Hs.31412	myopodin		2.0
	424665	AW368576	Hs.139851	caveolin 2	SS,TM,Caveolin,Caveolin	2.0
25	458147	AW752597	110.10000	gb:lL3-CT0214-161299-045-806 C	SS,TM,PMM	2.0
	447566	N50432	Hs.102648	ESTs	23,,	2.0
	414496	W73853	1101102010	ESTs	SS,TM,pkinase,F5_F8_type_	2.0
	425618	AW119112	Hs.9052	Homo saplens cDNA: FLJ22042 fi	SS.TM	2.0
	415166	NM_003652		carboxypeptidase Z	Zn_carbOpept,Fz,Dioxygena	2.0
30	422157	AW957295	Hs.112318	6.2 kd protein	SS	2.0
	450253	AL133047	Hs.24715	Homo saplens mRNA; cDNA DKFZp4	SH3	2.0
	418919	AA232635		ESTs	SS,DUF25	2.0
	444846	A1871055	Hs.148477	ESTs	SS,TM	2.0
	418781	T41160	Hs.8404	ESTs	•	2.0
35						

TABLE 24B:

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

7	10	Accession: Genbank accession numbers							
7	•0	Pkey 408468		Accession Al909712 AL039752 BE000369 AA376876 N75269 AA345398 AA349053 AW960062 R76169 R70638 AA054770 Al378587 Al338002 Al762398 N47873 Al066549 Al474112 AW450680 AA668668 R76114 AW242828 N58855 AW080313 Al378491 Al807102 AA417043 Al565444 AW263286 AW297099					
4	15	410295	11922_2	AA741357 AIB70000 W75997 H50726 AV658709 AI498817 AL037804 W67847 BE018553 AI033256 N76810 N31548 AI032084 N36278 AW075272 AI032081 R35753 W93372 AA700790 AI903697 N52985 R82468 AW580252 AL036760 AI052219 R36621 W07047 AA088621 AI249109 W68776 W69374 AA15					
4	50	414496	_	W73853 AA928112 W77887 AW889237 AA148524 AI749182 AI754442 AI338392 AI253102 AI079403 AI370541 AI697341 H97538 AW188021 AI927669 W72716 AI051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144448 W73819 AA604358 N28900 W95221 AI868132 H98					
_		418919		AA232635 Al373703 AA233330					
		418956		AA234831 A1700302 AA906216 AA776957 R49415 A1420777 AA666394 A1830619 AA779469 A1972390 N40980 A1094453 AA826397 AA535994 A1868257 A1804295 AA897791 AA232893 A1348680 A1356232 AA235138 F31396 AW079977 H16405					
4	55	424651	241981_1	Al493206 AA732315 AA344619 AA904035 AW952967 AA488889 AA635644 BE245127 AA669979 AA761874 H28767 AA910081 AA837086 AA766495 W76175 AI521825 AA746092 AA743152 AI478562 H88863					
		436772	426854_1	AW975688 AA731063 NG7084					
		438780	46501_1	M64936 AI025512 AI382987 BE061777 AA089966 BE169930 T41176 AW594624 BE502415 AA121893 AI269283 T40311 AI684569 AA257011 AI079277 AI241318 BE327710 AW975215 AW896268 AA884990 BE327514					
		441916	528799_1	AA993571 AA971518 Al937262					
•	50	444931	62567_1	AV652066 AA459880 T58512 T58561 Al651255 N49838 H87921 AW264447 AA428067 AA364094 AW955685 D62894 AW341452 AA243652 Al98461B Al816803 Al871252 Al376942 Al740496 AA452836 Al277917 Al149141 AA456147 Al784566 Al003975 Al245674 Al433703 Al200208 Al268985 Al38					
		451573	875588_1	AW130351 AW338699 Al803973					
6	55	458147	488021_1	AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700					

TABLE 24C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand: Indicates DNA strand from which exons were predicted
Nt_position: Indicates nucleotide positions of predicted exons

70

	rkey	1461	ORGINO	reciposition
	400829	8570385	Plus	152176-152616
75	403247	7656833	Minus	76626-77140
	404245	7406725	Plus	36019-36282,37073-37813,38946-39314,40355-40651,42738-43028,43391-43696,45698-46030,51110-51415,52779-53072,54648-
				54935,55201-55509,55926-56240,56355-56672,57078-57401,59966-60262,62600-62926,63363-63686,66693-67025,68180-
				68497.68909-69232.71372-71695.720

Table 25A provides UnigeneID, UnigeneTitle, Pkey, and Exemplar Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

80

Table 25A: Pkey: Unique Eos probeset identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number UG ID: UniGene number.
Title: UniGene title
SEQ ID NO: Sequence Identification number for sequences in Table 26

5	SEQ ID NO): Sequence Identil	ication number for s	equences in Table 26	
5	Pkey	Ex. Acon	UGID	Title	SEQ ID NO
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	SEQ ID NO: 1-2
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	SEQ 1D NO: 3-4
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	SEQ ID NO: 5-6
10	458627	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	SEQ ID NO: 9-10
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyl	SEQ ID NO: 11-12
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	SEQ ID NO: 13-22
1.5	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	SEQ ID NO: 23-24
15	451110	A1955040	Hs.265398	PAR-6 beta (partitioning defective 6 h	SEQ ID NO: 25-26
	428187	A1687303	Hs.285529	G protein-coupled receptor 49	SEQ ID NO: 27-28 SEQ ID NO: 29-30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 31-32
	433159	AB035898	Hs.150587 Hs.169840	kinesin-like protein 2 TTK protein kinase	SEQ ID NO: 33-34
20	426427 425371	M86699 D49441	Hs.155981	mesoihelin	SEQ ID NO: 35-38
20	418506	AA084248	Hs.85339	G protein-coupled receptor 39	SEQ ID NO: 39-40
	456546	AI690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	SEQ ID NO: 41-42
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	SEQ ID NO: 45-46
25	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	SEQ ID NO: 47-48
	412078	X69699	Hs.73149	paired box gene 8	SEQ ID NO: 49-52
	409178	BE393948	Hs.50915	kallikrein 5	SEQ ID NO: 53-54
	448243	AW369771	N. 47040E	integrin, beta 8	SEQ ID NO: 55-56
30	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	SEQ ID NO: 57-58 SEQ ID NO: 59-60
30	419452 431130	U33635 NM_006103	Hs.90572 Hs.2719	PTK7 protein tyrosine kinase 7 HE4; epididymis-specific, whey-acidic pr	SEQ ID NO: 61-62
	415539	AI733881	Hs.72472	BMP-R1B	SEQ ID NO: 63-64
	423961	D13666	Hs.136348	periostin (OSF-2os)	SEQ ID NO: 65-66
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	SEQ ID NO: 67-68
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	SEQ ID NO: 69-70
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	SEQ ID NO: 71-72
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	SEQ ID NO: 73-74
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	SEQ ID NO: 75-76
40	450375	AA009647	11. 455000	a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
40	426215	AW963419	Hs.155223	stanniocalcin 2	SEQ ID NO: 79-80 SEQ ID NO: 81
	430044 447033	AA464510 AI357412	Hs.152812 Hs.157601	ESTs ESTs	SEQ ID NO: 82-87
	410418	D31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
	411274	NM_002776	Hs.69423	kallikrein 10	SEQ ID NO: 90-91
45	422260	AA315993	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	SEQ ID NO: 94-95
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	SEQ ID NO: 96-97
	404977			Insulin-like growth factor 2 (somatomedi	SEQ ID NO: 98-99
50	427747	AW411425	Hs.180655	serine/threonine kinase 12	SEQ ID NO: 100-101
50	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	SEQ ID NO: 102-103
	431846	BE019924	Hs.271580 Hs.1904	uroplakin 1B	SEQ ID NO: 104-105 SEQ ID NO: 106-107
	425465 432938	L18964 T27013	Hs. 1904 Hs. 3132	protein kinase C, lota steroidogenic acute regulatory protein	SEQ ID NO: 108-109
	432330	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
55	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	SEQ ID NO: 120-121
	424078	AB006625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	SEQ ID NO: 124-125
60	428450	NM_014791	Hs.184339	KIAA0175 gene product	SEQ ID NO: 126-127
60	438167	R28363	Hs.24286	chemokine binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	SEQ ID NO: 130-131 SEQ ID NO: 132-133
	430691 408081	C14187 AW451597	Hs.157208 Hs.167409	aristaless-related homeobox protein ARX intron of basic-helix-toop-helix-PAS pro	SEQ ID NO: 134
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	SEQ ID NO: 135-138
65	407792	Al077715	Hs.39384	putative secreted ligand homologous to f	SEQ ID NO: 139-140
-	428093	AW594506	Hs.104830	ESTs	SEQ ID NO: 141 -144
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-148
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	SEQ ID NO: 149-150
~~	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
70	431369	BE184455	Hs.251754	secretory laukocyte protesse Inhibitor (SEQ ID NO: 153-154
	436972	AA284679	Hs.25640	claudin 3	SEQ ID NO: 155-156 SEQ ID NO: 157-158
	429504	X99133 AB041036	Hs.204238 Hs.57771	lipocalin 2 (oncogene 24p3) (NGAL) kallikrein 11	SEQ ID NO: 157-158 SEQ ID NO: 159-160
	410001	WD04 1030	ns.9///	POUNCH 11	OF 4 IP MO. 192-100
75	TABLE 25	5B:			

75 TABLE 25B:

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

80 Pkey CAT Number 448243 75629_1 AW369771 AW748174 AA290801 AA419198 AA044331 AA127909 AW995442 Al480343 AA044582 AW956159 AA373451 AA127965 AL134913 AW994956 BE622314 BE006298 BE006312 BE006305 BE006307 BE006303 AA043906 AA234175 AA479726 AA099647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 Al161014 AA099554 R69067

TABLE 25C:

```
Pkey: Unique number corresponding to an Eos probeset
         Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. *Dunham I. et al.* refers to the publication entitled *The DNA sequence of human chromosome 22* Dunham, et al. (1999) Nature 402:489-495
 5
         Strand: Indicates DNA strand from which exons were predicted
         Nt position: Indicates nucleotide positions of predicted exons
                               Strand
                                           Nt position
                    Ref
10
                    3738341
         404977
                                           43081-43229
                               Minus
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				ATTAGTAAGA	ACTTTGTAAA	TAAATACCTA	4080
	AAACCCAAAA	AAAAAAAA.	AAAAA				
	Con ID NO	10 Brokes	80016700				
80		10 Protein cession #:					
	1	11	21	31	41	51	
		1	1	1	1	1	
						TRVILVQEAG	60
85						YKADCRVIGP MGGVIRKDFN	120 180
U.J	E A ATMICSÓKO	EFUPTOURPL	* C = OUNINTAL	CL TGL WWEE		*. IGG A TECHNEN	100

GSPGAGGGRG FQMQPQHQHQ HQHQHHPPGP GQPSPPPEAL PCRDGTDPSQ PAELLGEVDR 360

	SKVTHLVANC						240
	QDCIFSFLGF	SDEEKTNMEE	MTEMOGGKYL	PLGDERCTHL	VVEENIVKDL	PFEPSKKLYV	300
	VKQEWFWGSI						360
	RDTDVSPFPP						420
5	KUTUVSPPPP	RKRPSAEHSL	SIGSPIDISM	TPESSINIGD	IPRSCIRSSR	2215452102	
2	ARWQVAKELY						480
	HTKIKDDLED						540
	HAFLKINQAK	PECGROSLVE	LLIRPVORLP	SVALLLNDLK	KHTADENPDK	STLEKAIGSL	600
	KENWINTED	KAKLEVOKUL	EDVIVVENDCC	DANT.T.CCHRS	LVQRVETISL	GEMPCORGEO	660
	KEAMILITIED	LONGRAINA	COLLOCATION		TARKERTER	T D T D D R D D CO	720
10					LMPLSQIKKV		
10	NAFALLVRPP						780
	FEVNTKDMDS	TLSRASRAIK	KTSKKVTRAF	SFSKTPKRAL	RRALMTSHGS	VEGRSPSSND	840
			LVSLPSFFER				
		002.0					
	C TD NO.	11 DNA sequ					
15 .							
13.			L#: XM_0441	.66			
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	1	11	21	31	41	51	
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	Thirties that the	GCCATGCCTA	GTCTAGTGGT	ATCTGGAATA	ATGGAAAGAA	ATGGGGGCTT	60
20					GGGCTGCTGG		120
20	TGGAGAACTA	GGATGTTTCG	GGGGMAGCGC	TAAGGACCGA	GGGCTGCTGG	ANGACGAGCG	
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					TGCATGGAGT		1500
15					ATCACAGCCA		1560
45	CCGAATATTC	TCCTAAGCCC	CGTGCCCCAT	GCCTCCGGGG	CCCACTCCAC	TGGGCCCACC	1620
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60					CTGACCTGAA		2520
	Value of the same	COTTON	THEFT	GAATCCTCCA	TGCAAATCAT	GGAGTCTGTG	2580
	MICCITALIA	GCTIGHATCC	CACAACCIT	CONTRACTOR AND A STATE OF THE S	FOCUMENT	CTCCCCCCN	2640
	TCCCACCTGA	IGTGGTTGAG	GAGAAGCCAG	GTCTTCAAAG	AGGGGTCAGC	CIGOGGCAAA	
					AATCACATAT		2700
					CTGCCACCAG		2760
65						GGAGATCCTT	2820
	GTAAATAGTG	CCCTCCCACT	GTTCTGAGTG	ATCACCCGAG	CACTTAAAGC	TCCAGAGTCC	2880
	OTHER PROPERTY OF	CCAMCCACCA	CCTCCACCTC	CACACCCCAT	AMICOMOCALCAL	CCTTCCTCCT	2940
	CATTCTTCCT	GGATGGAGCA	GGIGGAGGIG	CAGAGGGGAI	TICCICCICI	CCITCCICCI	
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70						CCGCCTATGT	3060
70						TCGGTTGCCG	3120
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						CAAATTCAAT	3240
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76						CACAGAGGAG	3360
75	AGAAAACAAA	AATAGCAAAA	алалалала	AAAGCAGTTC	TTTATAATTT	AATATTCTAT	3420
					ACCTGGGCTA		
	O	10 December 200					
		12 Protein					
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80	1	11	21	31	41	51	
	1	}	1	1	1		
	FCFAMPSLVV	SGIMERNGGF	GELGCFGGSA	KDRGLLEDER	ALQLALDOLC	LLGLGEPPAP	60
						PKGASDAKLC	120
						KTPVRGEEPV	180
85	ALI KEABLKL	MADELLECA	AUTOCHVAE	TAGUÃGCUIV	SDAIDGOIME		
0)	FMVTGRREDV	ATARREIISA	ALHESMIRAS	KNKSGAAFGV	APALPGQVTI	RVRVPYRVVG	240
					0.0		

5	LVVGPKGATI EYNNENDFLA GEQGGDFGYG KARAGPPGAH VTAALVPCGH	GSPDAAIDSR GYLFPGYGVG RSPATSAGPE	YSDAWRVHQP KQDVYYGVAE LAGLPRRPPG	GCKPLSTFRQ TSPPLWAGQE EPLQGFSKLG	NSLGCIGECG NATPTSVLFS GGGLRSPGGG	VDSGFEAPRL SASSSSSSSA	300 360 420 480
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		TCCTTGTCAT					120
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15		AAAAAACTAA ATATCTGCAA					240 300
		TTCAATATGA					360
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	CTGCAAACCC	TAAGTGAGAC	TTACTTTATA	ATGTGTGCTA	CAGCAGAGGC	CCAAAGCACA	480
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		GAGTAAAGAT					600
		CCCCAGAAGA					660
		ACCATCCACG					720
25		CTGTGCTTTC TGACCCACAA					780 840
23	CACCCTTCAC	CTCCCATAGC	TTCCACCCCT	GECATTGACA	TECCCCCACA	GTCTGAAACG	900
		CTATGCCCCA					960
		CCACCGTGTC					1020
		TCGTCAACAC					1080
30		TGTCCTTGGG					1140
						AAGATTGCTG	1200
		ATGACATTGG					1260
		TGGCTCTGGC					1320
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		ACCTCTCTCT					1560
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	ADACTATTTA	ATACTTACAT	CCGAAAATAC	ATCCTTAAAT	TCTGCATTGT	CGGTTGGGGG	2160
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60						TCTCAGAAGG	2940
	ACTTCAAAGC	GGGGAAGCTT	ACACTTTATT	GAGCAAATGT	GA		
		14 Protein					
65		cession #:					
05	1	11	21 	31 .	41	51 	
	MARCABOOCH	VCPTEFULLT	FKTELVIICI.	I HVVLVTSLEE	DTDNSSLSPP	PDVTLSLLPS	60
						TVPQNQHITN	120
	GTLTGVLSLS	ELKRSELNKT	LOTLSETYFI	MCATAEAQST	LNCTFTIKLN	NTMNACAVIA	180
70	ALERVKIRPM	EHCCCSVRIP	CPSSPEELEK	LQCDLQDPIV	CLADHPRGPP	FSSSQSIPVV	240
						AIDMPPQSET	300
	ISSPMPQTHV	SGTPPPVKAS	FSSPTVSAPA	NVNTTSAPPV	QTDIVNTSSI	SDLENQVLQM	360
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						LNLVFLLDSW	660
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	AIFNTLQGFF	IFIFYCVAKE	NVRKQWRRYL	CCGKLRLAEN	SDWSKTATNO	LKKQTVNQGV	900
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	HMFNEKEDSC	NGKGRMALRR	TSKRGSLHFI	EQM			
05						•	
85	Seq ID NO:	15 DNA seq	lneucė		2	7.0	

Nucleic Acid Accession #: Eos sequence Coding sequence: 12904							
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5	1	OTTOTION COOK			CTGAAGAAGT	ment creates	60
,					TGGTAACATC		120
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15					TGCCTCGGGC ATTATTCACC		660 720
					CCCAGCCTTC		780
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35					CAGTGACTCT TCCTCATCCA		1800 1860
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40	ACCATCATCC	TGACTATATC	CCCAGATAAC	TATGGGCTTG	GATCCTATGG	GAAATTCCCC	2160
					CAGTATTCTA TGTTCATTGT		2220 2280
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43	CAAGGATTTT	GACCAGTTAA	CTTTTACTGT	GTGGCCAAAG	TTGCCATCTT AAAATGTCAG	GAAGCAATGG	2460 2520
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50					ATGGGGTCTC		2760
					AGCACATGTT		2820
		GCAATGGGAA TTGAGCAAAT		GCTCTCAGAA	GGACTTCAAA	GCGGGGAAGC	2880
	IIACACIIIA	110.100.011	0.0				
55		16 Protein		_			
	1	cession #: 11	Eos sequence 21	31	41	51	
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60					DTDNSSLSPP EIMFQYDKES		60 120
00	GTLTGVLSLS	ELNTLNCTFT	IKLNNTMNAC	AVIAALERVK	IRPMEHCCCS	VRIPCPSSPE	180
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	VKORRLNETI	CTCSHLTSFG	VLLDLSRTSV	LPAQMMALTF	ITYICCGLSS	IFLSVTLVTY	600
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					LOSSSNSTNS EDSCNGKGRM	TTLLVNNDCS	900 960
75	LHFIEQM	TERNGVSESV	Qu@D4CTHDF	IGAQIIIIIA	203CNG/GRA	ADMINISTRACO	300
-	_						
		17 DNA seq	uence n #: Eos se	guence			
00		uence: 12		-			
80	1	11	21	31	41	51 I	
	I ATGGTTTTCT	i CTGTCAGGCA	GTGTGGCCAT	GTTGGCAGAA	I CTGAAGAAGT	TTTACTGACG	60
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0,5	GILACILIAN						

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45	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1	sequence Eos sequence	e			
	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11	sequence Eos sequence 21	31 	41	51 	60
	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT	sequence Eos sequence 21 FKIFLVIICL	31 HVVLVTSLEE	41 DTDNSSLSPP	51 PEVETTSLND	60 120
45 50	CTCAGAAGGA Seq ID NO: Protein Acc 1 mvfsvrqcgh vtlsLlpsne	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA	31 HVVLVTSLEE FFRGEIMFQY	41 DTDNSSLSPP DKESTVPQNQ	51 PEVETTSLND HITNGTLTGV	120
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	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE LNKTLQTLSE EPPDYSPVTH	sequence 20 sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP	120 180 240 300
50	CTCAGAAGGA Seq ID NO: Protein Acc NVFSVRQCGH VTISLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPPDYSPVTH VKASFSSPTV	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS	31 	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL	120 180 240 300 360
	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTL5LLPSNE LSLSELKRSE LREMEHCCCS SQUPKATSFA QTHVSGTPPP GSLEPNLAGE	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLE	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQFSAPI APPVQTDIVN QRLLKVVDDI	41 DTDNSSLSPP DKESTVPQNQ IKLMNTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPME VLQMEKALSL ISLTSPSLAL	120 180 240 300 360 420
50	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE ENPDYSPVTH VKASFSSPTV MINQVSRLHE MITTFVAQDP	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SAPANVNTTS SPPDMLAPLA ANLQVSLETQ	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT	41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV	120 180 240 300 360 420 480
50	CTCAGAAGGA Seq ID NO: Protein Acc WYESVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRUNASSF QFNFFETPAL	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLE MITTFVAQDP FQDPSLENLS	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR	41 DTDNSSLSPP DKESTVPQNQ IKLANTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLP NVTVTLKHIN	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPELAL AHDMELASRV PSQDELTVRC	120 180 240 300 360 420 480 540
50	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTISLLPSNE LSLESLKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTI ANLTVRNITR CTCSHLTSFG	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF	120 180 240 300 360 420 480 540
50 55	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTISLLPSNE LSLESLKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTI ANLTVRNITR CTCSHLTSFG	41 DTDNSSLSPP DKESTVPQNQ IKLANTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLP NVTVTLKHIN	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF	120 180 240 300 360 420 480 540
50	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SAPANVNTTS SAPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRDY	31 HVVI.VTSLEE FFRGEIMFQY AQSTINCTFT DFIVCLADHP PLSPQFSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM	120 180 240 300 360 420 480 540
50 55	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LSLSELKRSE LSPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRUNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT	sequence Eos sequence 21 KIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVESPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LISYFKIRRDY WMGLEAFHMY	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY	41 DTDNSSLSPP DKESTVPQNQ IKLINITMAS RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VILDLSRTSV ALLLINLVFL	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV	120 180 240 300 360 420 480 540 600
50 55	CTCAGAAGGA Seq ID NO: Protein Acc 1 MVFSVRQCGH VTISLLPSNE LSLSELKRSB IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY MGSPDDFCWI	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GQQLNFSNTT LPSSLMNNLP LPSSLMNNLP VVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL HIDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VCWGVPAVVV NVSMFIVVLV	120 180 240 300 360 420 480 540 600 660 720
50 55	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MTTTFVAQDP FQDPSLENLE RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY MGSPDDFCWI DLRSIAGLTF	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTYRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILITISPDN QLCRIKKKKQ QGFFIFFYC	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFSIQ VAKENVRKQW	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GQQLNFSNTT LPSSLMNNLP LPSSLMNNLP VVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILITISPDN QLCRIKKKKQ QGFFIFFYC	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFSIQ VAKENVRKQW	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY MGSPDDFCWI DLRSIAGLTF	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTL5LLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFMDLGRNGG ITYIGCGLSS QGLCISVAVE TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV WINQVSRLLE WITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA	sequence 21 PKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQVSRLUM HITTFVAQDP FQDPSLENLS RGGWSDNGCS RFLSVTLVTY LHYFLLVSFT YGLGSYGKFIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPLYCTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession	sequence Eos sequence 21	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPLYCTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQVSRLUM HITTFVAQDP FQDPSLENLS RGGWSDNGCS RFLSVTLVTY LHYFLLVSFT YGLGSYGKFIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq	sequence Eos sequence 21	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVENLTE CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLILNLVFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession	sequence Eos sequence 21	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPLYCTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP LPSSLMNLVFL LPSVILKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VIQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYSMFIVVLV MYLFAIFNTL	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Acc Coding sequence	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid accession	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLE LRRTSKRGSL uence n #: Eos second	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVENLTE CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLILNLVFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLE MITTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession lence: 136 11	sequence Eos sequence 21 KIFILVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVESPIGEIQ SAPANVNTTS SPPDMLAPLI LISYVISSSV VKORRINETI LISYVISSSV WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos seco45 21	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM Quence	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSSG ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NVTVTLKHIN VLLDLSRTSV ALLLILLVLVT LRKYLLKFCI VGYFCVIFLL FAMGPVNVTF ERNGVSFSVQ	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTFL LDSWIALIYM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequal ATGGTTTTCT	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession id Accession cence: 13 11 CTGTCAGGCA	sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKIQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLE LERTSKRGSL LERTSKRGSL LERTSKRGSL LECOLO #: EOS Secolo 21 GTGTGGCCAT	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDIT ANLTVRNLTR CTCSHLTSFG PSKILIQLC LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM Quence 31 CTTGGCAGAA	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNLP NVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRRYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG	120 180 240 360 420 540 600 720 780 840 900
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession Lence: 13 11 CTGTCAGGCA TCCTTGTCAT	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI LIAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE #: EOS Sec	31 HVVI.VTSLEE PFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPLYCTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC	41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NYTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLI FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA	120 180 300 360 420 480 540 660 720 780 900
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE LRPMEHCCCS SQVPKATSFA QTHYSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILITISPDN QLCRIKKKQ QGFFIFFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil I ATGGTTTTCT TTCAAGATAT GATACTGATA	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WANGVSRLLH MTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 13 11 CTGTCAGGCA ATCCCAGTTT	sequence Eos sequence 21 KIFILVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA LISYVISSSV VKDRRLNETI LISYVISSSV WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos sec 045 21 GTGTGGCCAT GTGACCACCA	31 HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM Quence 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFIL FAWGPUNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTR LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC	120 180 240 300 360 480 540 600 720 780 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil ATGGTTTTCT TTCAAGATAT GATACTGATAT GATACTGATAT CCCTCCTCCA	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCAGGTTGA	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos seconds 21 GTGTGGCCAT CATTTGTCTT GTCACCACA AACAACAAGC	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM QUENCE 31 CTTGGCAGAA CCTGCTAAATGATG	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPFSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG	51 PEVETTSLND HITNGTLTGV AVIALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPELAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV NYSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA ACAGTTTGCC CTTACTCCCT	120 180 240 300 360 420 540 600 720 780 840 900
50 55 60 65	CTCAGAAGGA Seq ID NO: Protein Acc	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MTTTFVAQDP FQDPSLENLS IFLSVTLVTY LHYFLLVSFT LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCAGGTTA ATTCAGGTTA ATGAGGTTGA CAGAAAAAAAC	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1 #: EOS Secol45 21 GTGTGGCCAT GATATCACCACCA AACACAAGC	31 HVVI.VTSLEE PFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGATAATA ATAGTTAAAAA	41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NVTVTLKHIN VALLDLSRTSV ALLLINLVFL IRRYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTAGT TTACTTTAGG CCTTCAATGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI LSLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYM VGWGVPAVVV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTCAGGCGTC	120 180 300 360 420 480 540 660 720 780 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFMFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDI GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil I TTCAGAGATAT GATACTGATA CCCTCCTCCA TCAAACGAAA AAACCCCAGA	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV WINGVSRLLH NTTTFVAQDP FQDPSLENLS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFD VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGATAAA CGAAATAATCTG	sequence Eos sequence 21 KIFILVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRTDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL uence n #: Eos se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAGC TAAAATCACT CAATTTGTCA	31 HVVIVTSLEE FFRGEIMFQY AQSTINCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI AMITVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATAA ATCTAATGTAAAA TCTATTTGCA	41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFLL FANGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL AHDMELASRV PSQDELTVRC LPAQMMALTS LDSWIALYKM VGWGVPAVVV NVSMFIVVLV NYSMFIVVLV 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA	120 180 240 300 360 420 480 540 600 720 780 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil ATGGTTTTCT TTCAAGATAT GATACTGATAT GATACTGATAA CCCTCCTCCA TCAAACGAAA AAACCCCAGA GGTGAGATCA	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession id Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTGAGTTGA CAGAAAAAAC GAGAAAAAACG GAGAAAATATCG	sequence Eos sequence 21 FKIFLVIICL RUSSICNDSA TYFIMCATAE ELEKLQCDLQ NVESPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSV VKDRRLNETI IAFEKIRRDY MGGEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL UENCE 1 #: Eos se 045 21 GTGTGGCCAT CATTTGTCA AACAACAAGC TAAAAATCACT CAATTTGTCA TGATAAAGAA	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA ATCTATTTGA	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGC CCCCAGAATCA	51 PEVETTSLND HITNGTLTGV AVIALERVK IPVVPRATVL QSETISSEMF VLQMEKALSL ISLTSPELAL AHDMELASRV PSQDELTVRC LPAQMMALTF LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC TTCAGGCGTC ATTTTTTAGA ACATATAACG	120 180 240 300 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTL5LLPSNE LSLSELKRSE LSLSELKRSE LSLSELKRSE QTHVSGTPPP GSLEPNLAGE AVTRVNASSF QYPKATSFA QTHVSGTPPP GSLEPNLAGE ITYIGCGLSS QGLCISVAVF TIILITISPDN QLCRIKKKQ QGFFIFFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Nucleic Ac: TTCAAGATAT GATACTGATA CCCTCTCCA TCAAACGAAA AAACCCCAGAA GGTGAGATCA AATGGCACCT	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accessic cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG TGTTTCAATA TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TTTCAATA TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TTTCAATA	sequence Eos sequence 21 FKIFILVIICL NLSSICNDSA TYFIMCATAE ELEEKLÇCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1 #: EOS Se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACCACC TAAAATCACT CAATTTGTCAT TGATAAAGAA TGATAAAGAA TGATAAAGAA CCTGTCTCTA	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA TCTATTTGCA AGCACTGTTC AGTGAATTAA	41 DTDNSSLSPP DKESTVPQNQ IKLINITMAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRRYILKFCI FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAGG CCTCAATGC ATGACTCAGC ACGCATCAGA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA	120 180 300 360 480 540 660 720 780 900
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTL5LLPSNE LSLSELKRSE LSLSELKRSE LSLSELKRSE QTHVSGTPPP GSLEPNLAGE AVTRVNASSF QYPKATSFA QTHVSGTPPP GSLEPNLAGE ITYIGCGLSS QGLCISVAVF TIILITISPDN QLCRIKKKQ QGFFIFFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Nucleic Ac: TTCAAGATAT GATACTGATA CCCTCTCCA TCAAACGAAA AAACCCCAGAA GGTGAGATCA AATGGCACCT	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLH MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accessic cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG TGTTTCAATA TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TTTCAATA TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TATACTGGAGT TTTCAATA	sequence Eos sequence 21 FKIFILVIICL NLSSICNDSA TYFIMCATAE ELEEKLÇCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1 #: EOS Se 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACCACC TAAAATCACT CAATTTGTCAT TGATAAAGAA TGATAAAGAA TGATAAAGAA CCTGTCTCTA	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HPIEQM 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA TCTATTTGCA AGCACTGTTC AGTGAATTAA	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTI LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLLLNLVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGC CCCCAGAATCA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA	120 180 240 300 360 420 540 600 720 780 840 900
50 55 60 65 70	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequ I ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCTCA AATGGCACCT AATGGCACCT AATGCCACAA	CTTCAAAGCG 18 Protein ression #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPIV WINGVSRLLH NTTTFVAQDP FQDPSLENLS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA seq id Accession Lence: 13 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA TATTCCAGTTT ATGAGGTTGA TGAGTTCAATTA TATACTGGAGT CCCTTAGTGAG CAGAAAAAAC GAAATATCTG TGTTTCAATTA TAACTGGAGT CCCTTAGTGAG CCCTTAGTGAG TATACTGGAGTGA	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE ##: EOS 6e- 045 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAGC TAAAATCACT CAATTTGTCA TGATAAAGAA CCTGTCTCTA GCCTTTCTTT GTCATTTGTCAT GACTTACTTT	HVVI.VTSLEE FFRGEIMFQY AQSTINCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTYRLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTTGTTC CCTGCTAAAT CTCAATGATGA ATGATTAAAAA TCTATTTGCA AGCACTGTTC AGTGATTAAA ATAATGTGTG	41 DTDNSSLSPP DKESTVPQNQ IKLINITMAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRRYILKFCI FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAGG CCTCAATGC ATGACTCAGC ACGCATCAGA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELAGRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAAGC	120 180 300 360 480 540 660 720 780 900
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLESLKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILITISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: NUCLeic Ac: Coding sequ ATGGTTTCT TTCAAGATAT GCATCAT GATACTGATA CCCTCCCA TCAAACGAAA AAACCCAGA GGTGAGATCA AATGGCACT ACCTGCAAA AATGGCACT ACCTGCAAA AACATTAAATT	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH WINQVSRLLH NTTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATGAGGTTGA CGGAAAAAAC GGAAAAAACG TGTTTCAATA TAAACTGGAGT TCCTAGGGGGG GTACATTCAC	sequence Eos sequence 21	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATTAATGAA AGCACTGTTC AGTGAATTAAA AGCACTGTTC AGTGAATTAAA ATAATGACAA	41 DTDNSSLSPP DKESTVPQNQ IKLNNTMNAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINIVFL IRKYILKFCI VGYFCVIFLL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTCAAGC AACGCTCAGA CCCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTE LDSWIALYEM VGWGVPAVVV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CCAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAAA AGGCCCAAAGC TGCTGCAATA	120 180 240 300 360 480 540 600 720 780 840 900 60 120 180 240 300 420 480 540
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc WYFSVRQCGH VTL5LLPSNE LSLSELKRSE LSLSELKRSE LSLSELKRSE QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QYPKATSFA QYPKATSFA QYPKATSFA CHANGE AVIRVNASSF QYPKETPAL TILLISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Nucleic Ac: TCAAACGAAA ATACGCTTCCA TCAAACGAAA AAACCCCAGA AATGGCACCT ACCCTGCAAA ACATTAAATT GCCGCTTTGG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLE MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG TGTTCAATA TAACTGGAGT ATACTGGAGT TAACTGGAGT ATACTGGAGT ATACTGGAGT ATACTGGAGT ATACTGGAGT ATACTGGAGT ATACTGGAGT AAAGATAAAA AAAGATAAAA	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLÇCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV WKGREAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACCAGC TAAAATCACT CAATTTGTCTT CATTAGTCTT GATAAAGAA CCTGTCTCTA GACTTACTTT AATAAAACCG GATTCGACCAC GATTCGACCACCA CAATTTGTCA TGAAAAACCG TAAAAACCG GATTCGACCCACCA CCACTACACCA TGATAAAACCG TAAAAACCG CAATTGTCACCACCA CCACTACCTTA CATTAGTCACCACCA CCACTACCACCA TGATAAAACCG TAAAAACCG CAATTCGACCCA CGATTCGACCCACCA CCACTACTTT AATAAAACCG GATTCGACCCA	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN APPENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA ATGGTAATTAGA ATAGTATGATG AGTGAATTAA ATAATACAA ATGGAACACT	41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GQQLNFSNTT LPSSLMINLP NVTVTLKHIN VVLDLSRTSV ALLLINLVFL IRRYILKFCI FRWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGA CCCCAGAATCA AACGCTCAGA TGAATCCATG GCTGCTGTTC GCTGCTGTTC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA GCTCAACAAA GGCCCAAAGC GCTCAACAAT TGTCAGGATA	120 180 300 300 480 540 660 720 780 900 60 120 180 240 360 420 480 540 660
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc I WYFSVRQCGH VTLSLLPSNE LSLSELKRSE IRMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TILLTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequ I ATGGTTTCT TTCAAGATAT GATACTGATA CCCTCCTCCT TCAAGATAT GATACTGATA AAACGCACA AATGGACACT ACCCTGCAAA ACATTAAATT GCCGCTTTGG CCCTGCCCTT	CTTCAAAGCG 18 Protein ression #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH VKASFSSPTV VKASF	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI LRSTGGLFF RRYLCCGKLR LRRTSKRGSL UENCE ##: EOS Secoles 45 21 GTGTGGCCAT CATTTGTCTT GTCACCACCA AACAACAGG TAAAATCACT CAATTTGTCA TGATAAAGAAA CCTGTCTCTA GACTTACTTT AATAAAACTG GATTCGACCA AGAGTTGGGACA AGAGTTGGGACA AGAGTTGGGACA AGAGTTGGGACA AGAGTTGGGACA AGAGTTGGGACA	HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTTGTTC CCTGCTAAAT CTCAATGATG ATAGTAAAAA TCTATTTGCA AGCACTGTTC AGTGAATTAA ATGAATCAGT AATGATTCG AATAATACAAA ATGAACACT AAGCTTCAGT	41 DTDNSSLSPP DKESTVPQNQ IKLINITMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMINLP NTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYLLKFCI VGYFCVIFL FANGPUNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAGC CCTCAATGC ATGACTCAGA CCTCAGATCA ACCGTCAGA CCTACAGCAGA CTACAGCAGA CTACAGCAGA CGAGATCAG GCTGCTGTGC GTGACCTGCA	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSL ISLTSPSLAL AHDMELAGRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV NVSMFIVVLV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA GGCCCAAAGC TGCTGCAATA GGCTCACATT GGATC	120 180 240 300 360 480 540 660 720 780 840 900 180 240 360 420 480 540 660 720
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTISLLPSNE LSLESLKRSE IRPMEHCCCS SQVPKATSFA QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: NUCLeic Ac: Coding sequ ATGGTTTCT TTCAAGATAT GCTCCTCCA TCAAACGAAA AAACCCAGA GGTGAGATCA AATGGCACT ACCTGCAAA AATGGCACT ACCTGCCAAA ACATTAAATT GCCCTCTTGC CCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGCCCTT GCCTGTCTTTG GCCTGTCTTTG GCTGTCTTTG GCTGTCTTTG GCTGTCTTTG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE VRIPCPSSPE EPPDYSPVTH WTTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA sequid Accession cence: 13 11 CTGTCAGGCA TCCTTGTCAT ATGAGGTTGA CAGAAAAAAC CAGAAAAAAC GGAACATCAC AAAGAGTAAA ACCTCCCCAGA CTGACCATCC	sequence Eos sequence 21 KIFILVIICL NLSSICNDSA TYFIMCATAE ELEKLQCDLQ NVESPIGEIQ SAPANVNTTS SPPDMLAPLI LISYVISSSV VKDRRINETI LISYVISSSV VKDRRINETI LAFEKIRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL LRRTSKRGSL UENCE 1	HVVLVTSLEE FFRGEIMFQY AQSTLNCTFT DPIVCLADHP FLSPQPSAPI APPVQTDIVN QRLLKVVDDI APENSIGTIT ANLTVRNLTR CTCSHLTSFG FSKILIQLCA LALVKVFNTY NNNAVFYITV LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGCTAAATA CTCAATGATG ATGATAAAA ATCATTATGCA AGGCACTGTC AGTGAATTAA ATGATGAAAA ATGATGATG AATGATGAAA ATGATGTGAATTAAA ATGATGTGAATTAAA ATGATGTGAATAAA ATGATGTGAATAAA ATGATGTGAATAAA ATGATGTGAATAAA ATGATGTGAATAAA ATGATGTGAATAAA CTTTTTCTT CCAATTTTCTT CCATTTTCTT	41 DTDNSSLSPP DKESTVPQNQ IKINTMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFIL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TTGGTTAATGT TTACTTTAGT TTACTTTAGT TTACTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG GTGACTGCG GTGACTGCG CCAGCCAATCC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSEMP VLQMEKALSL ISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTI LDSWIALYIM VGWGVPAVVV MYLFAIFNTL NGDVCLHDFT 51 TTTACTGACG CCTGGAAGAA CAGTTTTGCC CTTACTCCCT TTCAGGCGTC ATTTTTTAGA ACATATAACG GCTCAACAAA AGGCCCAAAGC TGCTGCAATA TGTCAGGATA TGTCAGGATA CGGATCCCATT CATCCCATG	120 180 240 360 480 540 600 720 780 900 60 120 180 240 360 420 480 540 660 720 780
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTL5LLPSNE LSLSELKRSE LSLSELKRSE LSLSELKRSE QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCCAC TCAAACGAAA AAACCCCAGA AAACCCCAGA AATGGCACCT ACCCTGCAAA ACATTAAATT GCCGCTTTGG CCCTGCCCTT GTCGTCTTGG GTGCCTCGGG GTGCCTCGGGG GTGCCTCGGGG GTGCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGTGCCCTCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGCCCTTGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGCCCTCGGGGGTCCTCGGGGGCCCTCGGGGGG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLE MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA Sequid Accession 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG GAATATCTG TGTTCAATA TAACTGGAGT ATACTGGAGT ATACTGGAGT AAAGAGTAAA CCTCCCCAGA AAAGAGTAAA CCTCCCCCAGA CCCACTGTGCT CCCACTGTCCT CCCACTGTCCT CCCACTGTCCT CCACTGTCCC CCACTGTGCT	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLÇCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN APPENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGATAAAT CTCAATGATG ATAGTAAAAA ATGGACACT AGGTACATT AGTGAACACT AATGATCACC AATGATCACC AATGATCACC AATGATCACC AATGATCACC AATGACACT AAGGACACT CCAATTTTCTT CCCCAAAGCTA	41 DTDNSSLSPP DKESTVPQNQ IKLINITMNAG RGPPPSSQS ASSPAIDMPP TSSISDLENQ GQQLNFSNTT LPSSLMINLP NVTVTLKHIN VVLDLSRTSV ALLLINLVFL IRRYILKFCI FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TGGTAACATC TATCTGTTGT TTACTTTAAG CCTTCAATGC ATGACTCAGA CCAGCAATCA AACGCTCAGA TGATCAGGAG TGACTCAGA CCAGCCAATCA CCACTTTTGC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI LISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TITTACTGACG CCTGGAAGAA CCAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTTAGA GCTCAACAAA GGCCCAAAGC GCTCAACAAA TGTCAGGATA TGTCAGGATA TGTCAGGATA TGTCAGGATA TGTCAGGTC TAGGCCTCCA	120 180 300 300 480 540 660 720 780 840 900 60 120 180 300 360 420 480 540 660 720 780 840
50 55 60 65 70 75	CTCAGAAGGA Seq ID NO: Protein Acc MVFSVRQCGH VTL5LLPSNE LSLSELKRSE LSLSELKRSE LSLSELKRSE QTHVSGTPPP GSLEPNLAGE AVIRVNASSF QFNFFETPAL VFWDLGRNGG ITYIGCGLSS QGLCISVAVF TIILTISPDN QLCRIKKKQ QGFFIFIFYC GKQHMFNEKE Seq ID NO: Nucleic Ac: Coding sequil ATGGTTTTCT TTCAAGATAT GATACTGATA CCCTCCCAC TCAAACGAAA AAACCCCAGA AAACCCCAGA AATGGCACCT ACCCTGCAAA ACATTAAATT GCCGCTTTGG CCCTGCCCTT GTCGTCTTGG GTGCCTCGGG GTGCCTCGGGG GTGCCTCGGGG GTGCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGTGCCCTCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGCCCTTGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGTCCTCGGGGGCCCTCGGGGGTCCTCGGGGGCCCTCGGGGGG	CTTCAAAGCG 18 Protein cession #: 1 11 VGRTEEVLLT TGVKPQRNIC LNKTLQTLSE EPPDYSPVTH VKASFSSPTV MINQVSRLLE MITTFVAQDP FQDPSLENLS RGGWSDNGCS IFLSVTLVTY LHYFLLVSFT YGLGSYGKFP LGAQRKTSIQ VAKENVRKQW DSCNGKGRMA 19 DNA Sequid Accession 11 CTGTCAGGCA TCCTTGTCAT ATTCCAGTTT ATGAGGTTGA CAGAAAAAAC GAAATATCTG GAATATCTG TGTTCAATA TAACTGGAGT ATACTGGAGT ATACTGGAGT AAAGAGTAAA CCTCCCCAGA AAAGAGTAAA CCTCCCCCAGA CCCACTGTGCT CCCACTGTCCT CCCACTGTCCT CCCACTGTCCT CCACTGTCCC CCACTGTGCT	sequence Eos sequence 21 FKIFLVIICL NLSSICNDSA TYFIMCATAE ELEKLÇCDLQ NVPSPIGEIQ SAPANVNTTS SPPDMLAPLA ANLQVSLETQ LISYVISSSV VKDRRLNETI IAFEKIRRDY WMGLEAFHMY NGSPDDFCWI DLRSIAGLTF RRYLCCGKLR LRRTSKRGSL UENCE 1	31 HVVI.VTSLEE FFRGEIMFQY AQSTLNCTFT DFIVCLADHP PLSPQPSAPI APPVQTDIVN APPENSIGTIT ANLTVRNLTR CTCSHLTSFG PSKILIQLCA LALVKVFNTY LLGITWGFAF LAENSGNAST HFIEQM QUENCE 31 GTTGGCAGAA CATGTCGTTC CCTGATAAAT CTCAATGATG ATAGTAAAAA ATGGACACT AGGTACATT AGTGAACACT AATGATCACC AATGATCACC AATGATCACC AATGATCACC AATGATCACC AATGACACT AAGGACACT CCAATTTTCTT CCCCAAAGCTA	41 DTDNSSLSPP DKESTVPQNQ IKINTMIAC RGPPPSSQS ASSPAIDMPP TSSISDLENQ GLQLNFSNTT LPSSLMNNLP NVTVTLKHIN VLLDLSRTSV ALLLINLVFL IRKYILKFCI VGYFCVIFIL FAWGPVNVTF ERNGVSFSVQ 41 CTGAAGAAGT TTGGTTAATGT TTACTTTAGT TTACTTTAGT TTACTTCAATGC ATGACTCAGC CCCAGAATCA AACGCTCAGA CTACAGCAGA TGAATGCATG GTGACTGCG GTGACTGCG CCAGCCAATCC	51 PEVETTSLND HITNGTLTGV AVIAALERVK IPVVPRATVL QSETISSPMP VLQMEKALSI LISLTSPSLAL AHDMELASRV PSQDELTVRC LPAQMMALTP LDSWIALYKM VGWGVPAVVV MYLFAIFNTL NGDVCLHDPT 51 TITTACTGACG CCTGGAAGAA CCAGTTTTGCC CTTTACTCCCT TTCAGGCGTC ATTTTTTAGA GCTCAACAAA GGCCCAAAGC GCTCAACAAA TGTCAGGATA TGTCAGGATA TGTCAGGATA TGTCAGGATA TGTCAGGTC TAGGCCTCCA	120 180 240 360 480 540 600 720 780 900 60 120 180 240 360 420 480 540 660 720 780

			AGCTTCCAGC				960
	ACGATCTCTT	CCCCTATGCC	CCAAACCCAT	GTCTCCGGCA	CCCCACCTCC	TGTGAAAGCC	1020
	TCATTTTCCT						1080
_	GTCCAGACAG						1140
5	ATGGAGAAGG	CTCTGTCCTT	GGGCAGCCTG	GAGCCTAACC	TCGCAGGAGA	AATGATCAAC	1200
	CAACTCACCA	CACTCCTTCA	TTCCCCGCCT	CACATICCTICG	CCCCTCTGGC	TCAAAGATTG	1260
							1320
			TGGCCTACAG				
	ACCTCCCCTT	CTTTGGCTCT	GGCTGTGATC	AGAGTGAATG	CCAGTAGTTT	CAACACAACT	1380
	ACCTTTGTGG	CCCAAGACCC	TGCAAATCTT	CAGGTTTCTC	TGGAAACCCA	AGCTCCTGAG	1440
10			TCTTCCTTCA				1500
10							
			TCAGTTCAAT				1560
	CCTTCCCTGG	AGAACCTCTC	TCTGATCAGC	TACGTCATAT	CATCGAGTGT	TGCAAACCTG	1620
	A CCCTTCA CCA	A CTTOOL CARC	AAACGTGACA	CTCACATTAA	AGCACATCAA	CCCGAGCCAG	1680
	ACCGTCAGGA	ACTIGACAAG	MAACGIGACA	GICACATIAA	AGCACATCAA	CCCGAGCGAG	
	GATGAGTTAA	CAGTGAGATG	TGTATTTTGG	GACTTGGGCA	GAAATGGTGG	CAGAGGAGGC	1740
15	TGGTCAGACA	ATGGCTGCTC	TGTCAAAGAC	AGGAGATTGA	ATGAAACCAT	CTGTACCTGT	1800
	***********	ON NOOPPOOR	CGTTCTGCTG	CACCORATIONA	CCACATOTCT	CCTCCCTCCT	1860
			CATTACATAT				1920
	TCAGTGACTC	TTGTAACCTA	CATAGCTTTT	GAAAAGATCC	GGAGGGATTA	CCCTTCCAAA	1980
		- comomomo	TGCTCTGCTT	ORGOROANGO	TO CONCOUNT CON	COTOCACTOC	2040
20	ATCCTCATCC	AGCIGIGIGC	IGCICIGCII	CIGCIGAACC	IGGICITCCI	CCICONCICO	
20	TGGATTGCTC	TGTATAAGAT	GCAAGGCCTC	TGCATCTCAG	TGGCTGTATT	TCTTCATTAT	2100
	THTCTCTTCC	TCTCATTCAC	ATGGATGGGC	CTAGAAGCAT	TCCATATGTA	CCTGGCCCTT	2160
							2220
			CATCCGAAAA				
	GGGGTACCAG	CTGTGGTTGT	GACCATCATC	CTGACTATAT	CCCCAGATAA	CTATGGGCTT	2280
	CCATCCTATC	CCAAATTCCC	CAATGGTTCA	CCGGATGACT	TCTGCTGGAT	CAACAACAAT	2340
25	CONTCUINTO		COMOCOL MAN	mmomomomo s	Th moment (VII)	CARCCTCACC	2400
23			GGTGGGATAT				
	ATGTTCATTG	TGGTCCTGGT	TCAGCTCTGT	CGAATTAAAA	AGAAGAAGCA	ACTGGGAGCC	2460
	CAGCGAAAAA	CCAGTATTCA	AGACCTCAGG	AGTATCGCTG	GCCTTACATT	TTTACTGGGA	2520
	A MA A COMMOCOC	COMMITTEC	CTTTGCCTGG	CCACCACTTA	A COMO A COMM	CATCTATCTC	2580
	ATAACTTGGG	GCIIIGCCII	CITIGCCIGG	GGMCCAGIIA	ACGIGACCII	CAIGIAICIG	
•	TTTGCCATCT	TTAATACCTT	ACAAGGATTT	TTCATATTCA	TCTTTTACTG	TGTGGCCAAA	2640
30	CABBATCTCB	CCAACCAATC	GAGGCGGTAT	CTTTGTGTGTG	GAAAGTTACG	GCTGGCTGAA	2700
-							2760
			TGCTACTAAT				
	GTGTCCAGCT	CTTCAAATTC	CTTACAGTCA	AGCAGTAACT	CCACTAACTC	CACCACACTG	2820
	CTACTCAATA	ATCATTCCTC	AGTACACGCA	ACCCCCAATC	GAAATGCTTC	TACAGAGAGG	2880
	CIAGIGAAIA	AIGALIGUIC	AGIACACGCA	AGCGGGAAIG	GAMMIGCIIC	CA CONCOLUNION	
~ =						CACTGGAAAA	2940
35	CAGCACATGT	TTAACGAGAA	GGAAGATTCC	TGCAATGGGA	AAGGCCGTAT	GGCTCTCAGA	3000
			CTTACACTTT				
	AGGACTICAA	AGCGGGAAG	CIIACACIII	ATTGAGCAM	10101		
	Seq ID NO:	20 Protein	sequence:				
	Protein Acc	ession #: 1	Sos sequence	2			
40			21	31	41	51	
70	1	11	41	3.1	7.1	7.	
						1	
				L			
	MVPSVROCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PAKLSVVSFA	60
	MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PAKLSVVSFA	
	PSSNEVETTS	LNDVTLSLLP	SNETEKTKIT	IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	120
.0	PSSNEVETTS	LNDVTLSLLP	SNETEKTKIT	IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	
45	PSSNEVETTS GEIMFQYDKE	LNDVTLSLLP STVPQNQHIT	SNETEKTKIT NGTLTGVLSL	IVKTFNASGV SELKRSELNK	KPQRNICNLS TLQTLSETYF	SICNDSAFFR IMCATAEAQS	120 180
45	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL	LNDVTLSLLP STVPQNQHIT NNTMNACAAI	SNETEKTKIT NGTLTGVLSL AALERVKIRP	IVKTFNASGV SELKRSELNK MEHCCCSVRI	KPQRNICNLS TLQTLSETYF PCPSSPEELG	SICNDSAFFR IMCATAEAQS KLQCDLQDPI	120 180 240
45	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS	120 180 240 300
45	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS	120 180 240
45	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP	120 180 240 300 360
45	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL	120 180 240 300 360 420
	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE	120 180 240 300 360 420 480
	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE	120 180 240 300 360 420
45 50	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP FQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL	120 180 240 300 360 420 480 540
	PSSNEVETTS GEIMPOYDKE TLNCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC	120 180 240 300 360 420 480 540
	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP FQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA	SNETEKTKIT NGTLITGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFM DELTVRCVFW QMMALTFITY	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL	KPQRNICNLS TIQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK	120 180 240 300 360 420 480 540
	PSSNEVETTS GEIMFQYDKE TLNCTFTIKL VCLADHPRGP FQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA	SNETEKTKIT NGTLITGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFM DELTVRCVFW QMMALTFITY	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL	KPQRNICNLS TIQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK	120 180 240 300 360 420 480 540 600 660
	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VOTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL LILQLCAALL	LMDVTLSLLP STVPQNQHIT INTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLD LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSSP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL	120 180 240 300 360 420 480 540 600 660 720
50	PSSNEVETTS GEIMPQYDKE TLNCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL LTISPONYGL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS	SICNDSAFFR IMCATAEAQS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN	120 180 240 300 360 420 480 540 600 660 720
	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY	LMDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW PCVIFILNVS	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLLHSPP TFVAQDPANL PSLENISLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR	SICNDSAFFR IMCATAEAGY KKQCDLQDPI SPIGEIQPLS ANVNITISAPE QVSLETQAPE YVISSSVANL RRLNETICIC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG	120 180 240 300 360 420 480 540 600 660 720
50	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY	LMDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW PCVIFILNVS	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLLHSPP TFVAQDPANL PSLENISLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR	SICNDSAFFR IMCATAEAGY KKQCDLQDPI SPIGEIQPLS ANVNITISAPE QVSLETQAPE YVISSSVANL RRLNETICIC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG	120 180 240 300 360 420 480 540 600 660 720
50	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVILL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW	LMDVTLSLLP STVPQNQHIT INTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW PCVIPLLNVS GPVNVIFMYL	SNETEKTKIT NGTLTGVLSI NGTLTGVLSQV VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKLGA FIFIFYCVAK	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVK SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC RKIRBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFPLLG LCCGKLRLAE	120 180 240 300 360 420 480 540 600 720 780 840 900
50	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLI VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	LMDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLD LMFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLINLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MEIVVLVQLC FAIFNTLQGF VSSSNSLQS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 660 720 780 840
50	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLI VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	LMDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLD LMFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLINLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	SNETEKTKIT NGTLTGVLSI NGTLTGVLSQV VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLI VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN	LMDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLD LMFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLINLVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MEIVVLVQLC FAIFNTLQGF VSSSNSLQS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVPNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG	LMDVTLSLLP STVPQNQHIT NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGB PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50	PSSNEVETTS GEIMPQYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL LLIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO:	LMDVTLSLLP STVPQNQHIT INTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLE LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLMIVFLLDS YILKPCIVGW PCVIFLLNVS GPVNVIFMYL GLKKQTVNQG DVCLHDFTGK	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMPNEKEDS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac:	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLC LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LINIVFLLDS YILKPCIVGW PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	SNETEKTKIT NGTLTGVLSU AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac:	LMDVTLSLLP STVPQNQHIT INTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLE LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLMIVFLLDS YILKPCIVGW PCVIFLLNVS GPVNVIFMYL GLKKQTVNQG DVCLHDFTGK	SNETEKTKIT NGTLTGVLSU AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequ	LNDVTLSLLP STVPQNQHIT NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession uence: 37	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS Leence n #: NM_005	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	PSSNEVETTS GEIMPQYDKE TLNCTFTIKL VCLADHPRGP PQPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac:	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLC LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LINIVFLLDS YILKPCIVGW PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession	SNETEKTKIT NGTLTGVLSU AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTY1AF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVMNDCSVHA	SICNDSAFFR IMCATAEAGS IMCATAEAGS KIQCDLQDPI SPIGEIQPLS ANVNITISAPE QVSLETQAPE YVISSSVANL RKLNETICIC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG LCCGKLRLAE SGNGNASTER IEQM	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55 60	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VOTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL VKVFNTYIRK AVPYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequal	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLD LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNILVFLLDS YILKPCIVGW FCVIFLLNVS GCVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid accession lence: 37	SNETEKTKIT NGTLTGVLSU AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSI TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS #: NM_005 3117 21	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SF6SPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAGS KLQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLIGE LCCGKLRLAE SGNGNASTER IEQM	120 180 240 360 420 540 600 660 720 780 840 900 960
50 55	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFFITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequil AGCCAGCCCG	LNDVTLSLLP STVPQNQHIT NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGB PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession tence: 37 11	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS LEENCE n #: NM_005 3117 21 CGGCAGGTGT	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVMNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAGS KIQCDLQDPI SPIGEIQPLS ANVNITISAPE QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA	120 180 240 360 420 540 660 720 780 900 960
50 55 60	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFFITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequil AGCCAGCCCG	LNDVTLSLLP STVPQNQHIT NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGB PCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession tence: 37 11	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS LEENCE n #: NM_005 3117 21 CGGCAGGTGT	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVMNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAGS KIQCDLQDPI SPIGEIQPLS ANVNITISAPE QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA	120 180 240 360 420 540 660 720 780 900 960
50 55 60	PSSNEVETTS GEIMPOYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT ILLIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence AGCCAGCCCG CTCGGGGTCA	LNDVTLSLLP STVPQNQHIL NYMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW PCVIFLLNVS GPUNVIFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession cence: 37 11 AGGACGCGAG GGATGGTTTT	SNETEKTKIT NGTLTGVLSL NGTLTGVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LECCE 1 #: NM_005 3117 21 CGGGCAGGTGT CCGGCAGGTGT	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FTFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT GCACAGAGGT CAGTTIGGCC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVM SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA	120 180 240 360 420 540 660 720 780 840 960 960
50 55 60	PSSNEVETTS GEIMPOYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL LIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSPSVQNG Seq ID NO: Nucleic Ac: Coding sequ 1 AGCCAGCCCG CTCGCGGCCCG GTTTACTGA	LNDVTLSLLP STVPQNQHIT NNTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLG LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW PCVIFLLNVS GPUNVIFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession Lence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT	SNETEKTKIT NGTLTGVLSL NGTLTGVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE 1 #: NM_005 3117 21 CGGGCAGGTGT CTCTGTCAGG ATTCCTTGTC	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTIGTC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYLAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTL EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM S1 GTTTTCTGAA AACTGAAGAA TCTGGTAACA	120 180 240 360 420 540 660 720 780 840 960
50 55 60	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL OKVPNTYIRK AVPYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG CTCGCGGTCA TCCCTGGAAG	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq icid Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSIGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CTCTCTCAGG ATTCCTTGTC TAATTCCAGT	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGCC ATCATTIGTC TTGTCACCAC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCANGTCGT CACCTGCTAA	SICNDSAFFR IMCATAEAGS KIQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGGTAACA ATTATCTGTT	120 180 240 360 420 540 660 720 780 900 960
50 55 60	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Cocing sequency AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTGG	LNDVTLSLLP STVPQNQHIL NTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW PCVIPLLNVS GPVNVIFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession cence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGTA ACCCCCTCTC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE H #: NM_005 3117 21 CGGCAGGTGT CTGTCTGGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCA GAAACACAA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGCAG TCACTGCTAA	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFPLIG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA AATTATCTGTT	120 180 240 360 420 540 660 720 780 840 960 960
50556065	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Cocing sequency AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTGG	LNDVTLSLLP STVPQNQHIL NTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW PCVIPLLNVS GPVNVIFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession cence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGTA ACCCCCTCTC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE H #: NM_005 3117 21 CGGCAGGTGT CTGTCTGGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTGTC TTGTCACCA GAAACACAA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGCAG TCACTGCTAA	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFPLIG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA AATTATCTGTT	120 180 240 360 420 540 660 720 780 840 960 960
50 55 60	PSSNEVETTS GEIMPOYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL LLIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequil AGCCAGCCCG GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC	LMDVTLSLLP STVPQNQHIT INTMNACAAI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LMFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LIMIVFLLDS YILKPCIVGW PCVIFLLNVS GPUNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession Lence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AAGATACTGA ACCCCCTCCTC CTTCAAACGA	SNETEKTKIT NGTLTGVLSU NGTLTGVLSU VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LECCE n #: NM_005 3117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT TAATTCCAGT AACAGAAAAA	IVKTFNASGV SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC ACAAAAATCAA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCCAATGA CCTATGAAAA	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTL EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTPILG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGGTAACA ATTATCTGTT TGTTACTTTA	120 180 240 360 420 540 660 720 780 840 960 960
50556065	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLITSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL OKVPNTYIRK AVPYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG CTCGCGGTCA TCCCGGGTCA TCCCTGGAAG GTCTATTGA AGCTTACTCC AGCTTACTCC GCTTCAGGCG GCTTCAGGCCG	LNDVTLSLLP STVPQNQHIL STVPQNQHIL NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq icid Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CAGTTCAAGTA AAGATACTGA CCCCTTCAAACGA TCAAACCCA	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSIGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAAA AGGGAAATATC	IVLTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTIL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGC ATCATTGTC ATCATTGTC ATCATTGTC ATCATTAGTC TIGTCACCAC GAAACACAA ACTAAAATCA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGTGG CACCTGCTAA GCCTCAATGA CCTATAGTAGA CATCTATTTG	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RELNETICIC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGATGACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA	120 180 240 360 420 540 660 720 780 900 960 120 180 240 300 360 420
50556065	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLITSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL OKVPNTYIRK AVPYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG CTCGCGGTCA TCCCGGGTCA TCCCTGGAAG GTCTATTGA AGCTTACTCC AGCTTACTCC GCTTCAGGCG GCTTCAGGCCG	LNDVTLSLLP STVPQNQHIL STVPQNQHIL NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq icid Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CAGTTCAAGTA AAGATACTGA CCCCTTCAAACGA TCAAACCCA	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSIGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT AACAGAAAAA AGGGAAATATC	IVLTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTIL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGC ATCATTGTC ATCATTGTC ATCATTGTC ATCATTAGTC TIGTCACCAC GAAACACAA ACTAAAATCA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGTGG CACCTGCTAA GCCTCAATGA CCTATAGTAGA CATCTATTTG	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RELNETICIC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGATGACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA	120 180 240 360 420 540 660 720 780 900 960 120 180 240 300 360 420
50556065	PSSNEVETTS GEIMPQYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Acc Coding sequ 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCC GCATTTTTTA	LNDVTLSLLP STVPQNQHIT INTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession accecsion 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AGGATACTGA CCCCTCCTC CTTCAAACCCA TCAAACCCA	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVLSI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MFIVVLVI PAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE n #: NM_005 33117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTGTC TAATTCCAGT CAATTAGGGTT AACAGAAAAA GAGAAAATC CATGTTCAA	IVLTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPFVKA EPNLAGEMIN RVNASSFNTT FFETPALFOD DLGRNGGRG GIGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAAACAA ACTAAAATCA TGCAATTTGT TATGATAAAG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS SSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT TCACTGCTAA GCCTCAATGA GCTCAATGA CATATATTAA AAAGCACTGT AAAGCACTGT	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNITISAPE DWLAPLAQRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA AATTATCTGTT TGTTACTTT AACCTTCAAT TCATGCATCA TCATGATACT TCATGCATCA TCCCCAGAAT	120 180 240 360 420 540 660 720 780 840 900 960 180 240 300 360 420
50556065	PSSNEVETTS GEIMPOYDKE TLNCTFTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVI ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequ 1 AGCCAGCCCG GCTCGGGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTTA CAACATATAA	LNDVTLSLLP STVPQNQHIN NNTMNACATI PFSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLINLVFLLDS YILKFCIVGW PCVIFLLNVS GPUNVIFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid Accession cence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA AAGATACTGA TCAAACCCCA GAGGTGAGAT TCAAACCCCA GAGGTGAGAT CGAATGGCAC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW WIALYKMQGL GVPAVVVTII MPIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMPNEKEDS LENCE 1 #: NM_005 3117 21 CGGGCAGGTGT CAGGCAGGTGT TAATTCCAGG ATTCCTTGTC TAATTCCAGG ATTCCTTGTC TAATTCCAGG ATTCCTTGTC TAATTCCAGG ATTCCTTGTC TAATTCCAGG CATGTTTCAA CGAGAAAAA CGTTAACTGGA	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAACCAACAA ACTAAAATCA TGCAATTTGT TATGATAAAG GTCCTGTCTC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTTT ATGTTGGCAG TTCANGTCGT CACCTGCTAA GCCTCAATGA CCTATAGTAAA CATCTATTTG AAAGCACTGT TAAGTGAATT	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLTFLLG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGGTACTTT AACCTTCAAT CAATGACTCA TCCCCAGAT AARACGCTCA	120 180 240 360 420 540 660 720 780 840 960 960 120 180 240 300 420 420 420
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL ILIQLCAALL VKVFNTYIRK AVPYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Coding sequity AGCCAGCCCG CTCGCGGTCA TCCCGGGTCA TCCCTGGAAG GTCTACTCA AGCTTACTCA AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAAA GAGCTTACACA	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq ici Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA CCCCTCCTC CTTCAAACGC GAGGTGAGAT CCAAACCCCA GAGGTGAGAT CCAAACCCCA AAACCCTGCA	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGATAA AGGGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGCC ATCATTIGTC ATCATTIGTC ATCATTAGAT ACTAAAATCA TAGATATAAAG GTCTGTCTC GAGACTTACT GAGACTTACT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGCAG GCCTCAATGA GCCTCAATGA CACTTATTTG AAAGCACTGT TAAGTGAATT TTAATATGTG	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRINETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGATGACA ATCTGATGACA ATCTGATT TGTTACTTT AAACCTCCAT CAATGACTCA TCCCCAGAAT TAAAACGCTCA TGCTACAGCA	120 180 240 360 420 540 660 720 780 900 960 120 120 120 140 300 360 420 480 540
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL ILIQLCAALL VKVFNTYIRK AVPYITVVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Coding sequity AGCCAGCCCG CTCGCGGTCA TCCCGGGTCA TCCCTGGAAG GTCTACTCA AGCTTACTCA AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAAA GAGCTTACACA	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq ici Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA CCCCTCCTC CTTCAAACGC GAGGTGAGAT CCAAACCCCA GAGGTGAGAT CCAAACCCCA AAACCCTGCA	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MPIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGATAA AGGGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGCC ATCATTIGTC ATCATTIGTC ATCATTAGAT ACTAAAATCA TAGATATAAAG GTCCTGTCTC GAGACTTACT GAGACTTACT	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGCAG GCCTCAATGA GCCTCAATGA CACTTATTTG AAAGCACTGT TAAGTGAATT TTAATATGTG	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL RRINETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGATGACA ATCTGATGACA ATCTGATT TGTTACTTT AAACCTCCAT CAATGACTCA TCCCCAGAAT TAAAACGCTCA TGCTACAGCA	120 180 240 360 420 540 660 720 780 900 960 120 120 120 140 300 360 420 480 540
50556065	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVNGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Acc Coding sequ 1 AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTTA CAACATATAA GAGGCCCAAA	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession idence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGAT AGGATACTGA CCCCTCCTC CTTCAACGAA TCAAACCCCCA GAGGTGAGAT CGAATGGCAC AAACCCTGC AAACCCTGC AAACCCTAC AAACCCTACA AAACCTACA	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVLSI NGTLTGVLSI VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE n#: NM_005 3117 21 CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATTC	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFOD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGI ETIKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAAAACA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGG GRYGKFPNGG GRYGKFPNGG GRYKFQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CTATATGTAAAAGCACTGT TAAAGTGAATT TTATAAATGTG TGAATTAATTGT TGAATTAGTG	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNITISAPE DWLAPLAGRL QVSLETQAPE YVISSSVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA AATTATCTGTT TGTTACTTT TGTTACTTT AACCTTCAAT TCATGCAT TCATGCAT TCATGCAT AAAACGCTCA TGCTACAGCA TGCTACAGCA TGCTACAGCA TGCTACAGCA TATATCTGT	120 180 240 360 420 540 660 720 780 900 960 180 240 360 420 480 540 660
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVI ILLIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG GTTTACTGA GTCAGTTTTC AGCTTACTCC GCTTCAGGCG GCATTTTTA CGACTTACTCC GCATTTTTA CGACTTACTCC GCATTTTTA CGACTTACTCC GCATTTTTA CAACATATAA GAGCCCAAA TGTGCTGCAAA	LMDVTLSLLP STVPQNQHIN MNTMNACATI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIPLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA ACCCCTCTC CTTCAAACCA CTCAAACCCCA CGATGGTGAG CGATGGTGAG CGATGGCAC AAACCCTGCA AAAC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LENCE H#: NM_005 3217 321 CGGCAGGTGT CTGTTCAGG ATTCCTTGTC TAATTCCAGT CAATTAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATTC GGAAAGAGTA	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATTAAG GTCCTGTCTC GAGACTTACAC ACAATAAAC ACAATAACAC ACAATACAC ACAATTCGAC	KPQRNICNLS TLQTLSETYP FCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TVVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAAGTGAATT TTATAATGTG TGAATAATG CAATGGAACA CAATGGAACA CAATGGAACA	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFPLIG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGGAT AAAACGCTCA TCGTCACGCA AATGAATGCA CTGCTGCTGT	120 180 240 360 420 540 660 720 780 840 960 180 240 360 420 420 420 420 660 660 6720
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVI ILLIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG GTTTACTGA GTCAGTTTTC AGCTTACTCC GCTTCAGGCG GCATTTTTA CGACTTACTCC GCATTTTTA CGACTTACTCC GCATTTTTA CGACTTACTCC GCATTTTTA CAACATATAA GAGCCCAAA TGTGCTGCAAA	LMDVTLSLLP STVPQNQHIN MNTMNACATI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIPLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AAGATACTGA ACCCCTCTC CTTCAAACCA CTCAAACCCCA CGATGGTGAG CGATGGTGAG CGATGGCAC AAACCCTGCA AAAC	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFN WIALYKMQGL GVPAVVVTII MFIVVLVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LENCE H#: NM_005 3217 321 CGGCAGGTGT CTGTTCAGG ATTCCTTGTC TAATTCCAGT CAATTAGGTT AACAGAAAAA GAGAAATATC CATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATTC GGAAAGAGTA	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCCLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATTAAG GTCCTGTCTC GAGACTTACAC ACAATAAAC ACAATAACAC ACAATACAC ACAATTCGAC	KPQRNICNLS TLQTLSETYP FCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TVVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAAGTGAATT TTATAATGTG TGAATAATG CAATGGAACA CAATGGAACA CAATGGAACA	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNBTICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFPLIG LCCGKLRLAE SCNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGGAT AAAACGCTCA TCGTCACGCA AATGAATGCA CTGCTGCTGT	120 180 240 360 420 540 660 720 780 840 960 180 240 360 420 420 420 420 660 660 6720
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL ILIQLCAALL OKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequence 1 AGCCAGCCCG CTCGCGGTCA CTCGCGGTCA TCCCTGGAAG GTCTACTGA GGCTTACTGA GCTTACTGA AGCTTACTCC GCTTCAGGCG GCATTTTTTA CAACATATAA GAGGTCCAACA GAGGCCCAAA TGTGCTGCAA TCTGTCAGGAG TCTGTCAGGA	LNDVTLSLLP STVPQNQHIL STVPQNQHIL NTMNACAAI PFSSSQSIPV PAIDMPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKFCIVGW FCVIFILNVS GPVNVTFMYL GLKKQTVVNG DVCLHDFTGK 21 DNA seq id Accession id Accession id Accession carrier AGGACGCGAG GGATGGTTTA AGGATACTGA CCCCTTCAACGA TCAAACCCA GAGGTGAGAT CGAATGGAA CCGATTAAA TAGCCGCTT TACCCTGCCC	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS 117 21 CGGCAGGTGT CATCTTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGATA AGGAAAATAT CCATGTTTCAA CTTAACTGGA AACCCTAAGT TTGTACATGT TTGTACATCT TGGAAAGAGTT	IVLTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTTIGGC ATCATTGTC ATCATTGTC TTGTCACCAC GAAACTAAAA GCTCTGTCT GAGACTTACT GAGACTTACT ACAATAAAAC AAGATTCGC GAAAGTTCGC GAAGATTGGC GAAGATTGGC ACAATTAGAC AAGATTCGC GAGACTTGGC GAGAGTTGGC GAGAGT GAGAG	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS GYGKPPNGS GRYGKPPNGS GYKFPNGS TRANGER LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG GTCAATGAAA CACTTATTG AAAGCACTGT TAAGTAAAT TTAATATTG TAAATGAAT TTAATATTG TGAATAATAA CAATGAAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAATGGAAAC CAAATGAAAC CAAAGCATTCA	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL EKIREDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA ATCTGATGACA ATTATCTGTT TGTTACTTTA CACTGACTCA TCCCCAGAAT TAAAACGCTCA TCCCCAGAAT AAAACGCTCA TGCTACAGCA AATGAATGCA AATGAATGCA AATGAATGCA AATGAATGCA AATGAATGCA CTGCTACAGCA AATGAATGCA CTGCTACTGCTGT GTGTGACCTG	120 180 240 360 420 540 660 720 780 900 960 120 180 240 300 360 480 540 660 720 780
5055606570	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVNGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding sequity AGCCAGCCCG CTCGCGGTCA GTTTTACTGA GTCAGTTTTTACTGA GCTTACTGC GCTTCAGGGC GCATTTTTA CAACATATAA GAGCCCAAA TGTGCTGCAA TGTGTGCGAA TGTGTCTGCAA CAGGGCCCAAA TCTGTCAGGGA CAGGATCCCA	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGM FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequ id Accession ence: 37 11 AGGACGCGAG GGATGGTTTT CGTTCAAGGAA CCCCTCCTC CTTCAACGAA TCAAACCCTAC CAAACCCCAA ACCCTGCA AAACCCTGCA AAACCCTGCA AAACCCTGCA TCACCTGCC TTGTCTGTCTT TACCCTGCCC TTGTCTGTCTT	SNETEKTKIT NGTLTGVLSL NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC PAIFNTLQGF VSSSNSLQS QHMFNEKEDS LENCE LENCE LENCE CGGCAGGTGT CTCTGTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACAGAAAAA CGAGAAAAAA CGAGAAAAAA CGAGAAAAA CGTTAACTGGA ACCCTAAGT TTGTTCCAGT GGAAGAGTA TTCCTCCCCA TTGTCCCCCCA TTCCTCCCCAT TTCTCCCCCAT TTCCTCCCCAT TTCCTCCCCAT TTCCTCCCCAT TTCCTCCCCAT TTCCTCCCCAT TTCCTGCCCAT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFOD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGI RIKKKQLGA PIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGGCC ATCATTGTC TATGATAAAC ACTAAAATCA TGCAATTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAAAC AAGATTCGAC GAGAGTTGGC CACGTGGCC CCACGTGGCC CCACGTGGCC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT TCACTCGTAA GCCTCAATGA CCTCTATATGAATT TTATATATGT TAAAGTGAATT TTATATATGT TGAATGAA	SICNDSAFFR IMCATAEAGS KIQCDLODPI SPIGEIQPLS ANVNITISAPE DWLAPLAQRL QVSLETQAPE YVISSSVANL RILNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA TCTGGTAACA TCTTCGTTACTTT TGTTACTTTA AACCTTCAAT TCAATGACTCA TCACAGCAA TAAAACGCTCA TCACAGCAA TAAAACGCTCA TGCTGACGCA TGCTGACTGGTGACC TGCTGCTGTT TGTTGCCTGTGTCCTGTT TGTTGCCTGTGTCCTGTTCCAGCCAA	120 180 240 360 420 540 660 720 780 960 120 180 240 360 420 540 660 720 780 840
505560657075	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG GTTTACTGA GTCAGCGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTTTTTT	LNDVTLSLLP STVPQNQHIN NTMNACATI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSC DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AGATACTGA CCCCTCCTC CTTCAAACGA TCAAACCCTGCA GAGGTGAGAT GAGGTGAGAT GAATGGCAC CGATGGCAC CGATGGCAC TCACCTGCC TTGCTCTCTCT TACCCTGCCC TTGTCTGCTT TGGTGCCTCGCTTCGTTCTGTTCTTGTTTTTTTT	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN MELASRVQFN MELASRVQFN WIALYKMQGL GVPAVVVTII WIALYKMQGL GVPAVVVTII WFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LENCE 1 #: NM_005 3117 321 CGGCAGGTGT CTGTCCAGG ATTCCTTGTC TAATTCCAGT CAATTAAGTGTT AACAGAAAAA GAGAAATATC CATGTITCAA CTTAACTGGA AACCCTAAGT TTGTACATT TGGAAAGAGTA TTCCTCCCCA TGTTCCCCCA TGTTCCCCCA TGTGACCAT TGGCAACTGTG GGCAACTGTG GGCAACTGTG GGCCACTGTG GGCCACTGT GGCACTGT GGCCACTGT GGCCACT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRG GIGCSLSSIFL CISVAVFLHY LTISPDNYGL RIKKRQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATTAAAG GTCCTGTCTC GAGACTTACAC ACAGAGTTGGC AAGATTAGGC AAGATTGGC AAGATTGGC CAAGAGTTGGC CAGGGCC CCTTTCCCAGG	KPQRNICNLS TLQTLSETLY FCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TVVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTGT TAAGTGAATT TTATAATGTG GAAAGCTTCA CAATGGAACT CACCATTTCC TCCCCAAAGC TCCCCAAAGC CACCATTTCC TCCCCAAAGC TTCCCCCAAAGC	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SCHGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGTCA TCCCCAGAAT AAAACGCTCA TCCCCAGAAT AAAACGCTCA TCCCTGCTGT GTTGACCTG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCCAA TTCCCCCCCAG TTCCAGCCCAA TACCTCTTTT	120 180 240 360 420 540 660 720 780 840 960 180 240 420 420 420 420 420 420 420 420 42
505560657075	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITWGFAFFAW NSDWSKTATN NGVSFSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG GTTTACTGA GTCAGCGGTCA GTTTTACTGA GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTTTTTT	LNDVTLSLLP STVPQNQHIN NTMNACATI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD VTLKHINPSC DLSRTSVLPA LLNLVFLLDS YILKFCIVGW GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession Lence: 37 11 AGGACGCGAG GGATGGTTT CGTTCAAGAT AGATACTGA CCCCTCCTC CTTCAAACGA TCAAACCCTGCA GAGGTGAGAT GAGGTGAGAT GAATGGCAC CGATGGCAC CGATGGCAC TCACCTGCC TTGCTCTCTCT TACCCTGCCC TTGTCTGCTT TGGTGCCTCGCTTCGTTCTGTTCTTGTTTTTTTT	SNETEKTKIT NGTLTGVLSI NGTLTGVLSI NGTLTGVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN MELASRVQFN MELASRVQFN WIALYKMQGL GVPAVVVTII WIALYKMQGL GVPAVVVTII WFIVULVQLC FAIFNTLQGF VSSSSNSLQS QHMFNEKEDS LENCE 1 #: NM_005 3117 321 CGGCAGGTGT CTGTCCAGG ATTCCTTGTC TAATTCCAGT CAATTAAGTGTT AACAGAAAAA GAGAAATATC CATGTITCAA CTTAACTGGA AACCCTAAGT TTGTACATT TGGAAAGAGTA TTCCTCCCCA TGTTCCCCCA TGTTCCCCCA TGTGACCAT TGGCAACTGTG GGCAACTGTG GGCAACTGTG GGCCACTGTG GGCCACTGT GGCACTGT GGCCACTGT GGCCACT	IVKTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRG GIGCSLSSIFL CISVAVFLHY LTISPDNYGL RIKKRQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGCC ATCATTTGTC TTGTCACCAC GAAACAACAA ACTAAAATCA TGCAATTTGT TATGATTAAAG GTCCTGTCTC GAGACTTACAC ACAGAGTTGGC AAGATTAGGC AAGATTGGC AAGATTGGC CAAGAGTTGGC CAGGGCC CCTTTCCCAGG	KPQRNICNLS TLQTLSETLY FCPSSPEELG DYSPVTHNVP SFSSPTVSAP QVSRLLHSPP TVVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKFPNGS GRYTSIQDLR ENVRQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGT CACCTGCTAA GCCTCAATGA CATCTATTGT TAAGTGAATT TTATAATGTG GAAAGCTTCA CAATGGAACT CACCATTTCC TCCCCAAAGC TCCCCAAAGC CACCATTTCC TCCCCAAAGC TTCCCCCAAAGC	SICNDSAFFR IMCATAEAGS KLQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSYVANL RRLNETICTC EKIRRDYPSK LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SCHGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACAA ATTATCTGTT TGTTACTTTA AACCTTCAAT AAACGTCA TCCCCAGAAT AAAACGCTCA TCCCCAGAAT AAAACGCTCA TCCCTGCTGT GTTGACCTG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCAA TTCCCCCCAG TTCCAGCCCAA TTCCCCCCCAG TTCCAGCCCAA TACCTCTTTT	120 180 240 360 420 540 660 720 780 840 960 180 240 420 420 420 420 420 420 420 420 42
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505560657075	PSSNEVETTS GEIMPOYDUS GEIMPOYDUS TINCTPTIKL VCLADHPRGP POPSAPIASS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SHLTSFGVLL ILIQLCAALL ILIQLCAALL VKVFNTYIRK AVFYITVVGY ITMGFAFFAW NSDWSKTATN NGVSPSVQNG Seq ID NO: Nucleic Ac: Coding seq 1 AGCCAGCCCG TCAGGGCC CTCCGGGTCA AGCCCAGTCAG TCCCTGGAAG GTCTAATTAA GAGCTCAACA GAGGCCCAAA TGTGTCAGGA TCCTGCAGGC CAGGATCCCA TCCATCCCAG TCCACCCTT CCACAGCTC CCACAGTCT CCACAGTCT CCACAGTCTC CCCTGGAAAG	LNDVTLSLLP STVPQNQHIL STVPQNQHIL PSTVPQNQHIL PSSSQSIPV PAIDMPPQSS ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LINIVFLLDS YILKPCIVGW FCVIFLLNVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA sequid ACCESSION LEDCE: 37 11 AGGACGCGAG GGATGGTTT CGTTCATGTT TGTTCTATGT TGAAACCAC TCAAACCAC TCAAACCAC CCAACACAC ACACCTGCAC TTGCTGCCT TGGTGCCTC TGGTGCCTC CAACCACTCCAACCAC CAACCATTATTC CACCCCAGCC AAACCATTCC CACCCCAGCC AAACCATTCC CACCCCAGCC CAACCATTCC CCCCATCTC CCCCATCT CCCCATCTC CCCCATCTC CCCCATCTC CCCCATCT CCCCCATCT CCCCCATCT CCCCATCT CCCCATC CCCCATCT CCCCATCT CCCCATCT CCCCATCT CCCCATCT CCCCATCT CCCCATCT CCCCATCT CCCCCATC CCCCATCT CCCCATCT CCCCATCT CCCCCATC CCCCCATC C	SNETEKTKIT NGTLTGVLSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSIGSL TSPSLALAVI MELASRVGFN QMMALTFITY WIALYKMQGL GVPAVVTII MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QCHMFNEKEDS LENCE M #: NM_005 3117 21 CGGCAGGTGT CTCTGTCAGG AATCAGGTT TAATTCCAGT CAATGAGAAAA GAGAAATAA GAGAAATAA GAGAAATAA GTAAACTGGA AACCCTAAGT TTCTCCCCCA TGCTGCCCCA TGCTGTCCCCA TCCTCCCCAC TTCAGCTCCC TTCAGCTCCC TTCAGCTCCC TTCAGCTCCC TTCAGCTCCC TTCAGCTCCC TTCAGCTCCC TTCCCCCAC TTCCCCCAC TTCCCCCAC TTCCCCCAC TTCCCCCAC TTCCCCCAC TTCCCCCAC	IVLTFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD LIGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKKQLGA FIFIFYCVAK SSNSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGGC ATCATTTGTC TTGTCACCAC GAAACACAA ACTANAAACA TGCAATTTGT TATGATAAAG GTCCTGTCTC GAGACTTACT ACAATAAACC CACATGGGC CTTTCCCAGG CACATGTGC CATCACTCCAGC CTTCCCCAG CCCAAACCC GTGTCTCCC GTGTCTCCCC GTGTCTCCC	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS WSDNGCSVKD SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS QRKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTGGTG CACCTGCTAA GCCTCAATGA CATCTATTTG AAAGCACTGT TAAGTGAATT TTAAGTGTAATATAC CAATGTAATATAC CACCATTTTC CACCAAAGC CCTCTCCAAATGC CCTCTCCAATGCCCTCCCATATGTCTCCCG CCTGCCAATGT CTGCCAATGT	SICNDSAFFR IMCATAEAQS KIQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL REAFHMYLAL EAFHMYLAL EDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGCAT TCCCAGCAT TCTCAGCCA AATGAATGCCT TTCCAGCCAA ATTACTGTT TGTGACCTG TTCCAGCCAA ATTACTGTT TGTGACCTG TTCCAGCCAA ATTACTGTT TGACATGCCC CACCCCACCC	120 180 240 360 420 540 660 720 780 840 960 120 180 240 300 420 420 420 420 780 960 1020 1020 1040
50 55 60 65 70 75	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL VKVFNTYIRK AVFYITVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac. Coding sequity AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA TCGTCAGGA TCGTCCAGG GCTGTCAACA GGGCCCAAA TCTGTCAGGA TCCATCCCAG GCTGAGCCTC CCACCCTTT CCACACTCTG CCACACCTCT CCACACCCTTT CCACACCCCTTT CCACACCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCTCT CCACACCCCTTT CCACACCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCCTC CCACCCCCCCTC CCACCCCCCTC CCACCCCCCCC	LNDVTLSLLP STVPQNQHIL STVPQNQHIL NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession id Accession id Accession cence: 37 11 AGGACGCGGA GGATGGTTT CGTTCAAGGA CCCCTCCTC CTTCAACGA TCAACGAA CCAATGATC GAATGATC GAATGATC GAATGATC GAATGATC CCTGCC TTGTCTGTCT TGGTGCCTC CACCCCAGCC AAACGATTTC CCTCCCTCC CCCCCCCAGCC CAACCCAGCC CCCCCCCCCC	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LEENCE n #: NM_005 3117 21 CGGCAGGTGT CTCTTCTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACACAAAAA ACCCTAAGT TTGTACATGG AACCCTAAGT TTGTACATGG ACCTGTAGC TTCCCCCA TTCCCCCA TTCCCCCA TTCCCCTATG CTTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA AGACATCTCC AGACATCTC AGACATCT AGACATC AGACATCT AGACATC AGACATC AGACATC AGACATC AGACATC AGACATC AGACATCT AGACATC AGACA	IVETFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGCC ATCATTTGTC TTGTCACCAC GAAACAAAAAAAAAA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CATTATTTG AAAGCACTGT TAAATGAATT TATATATGT TGAATAATAC CAATGGAACA CAATGTAATTG GAAAGCTTCA CACCATTTTC TCCCCAAAGC CCTCTCCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCTTGCCAAT GCCTGCCAAT GCCTGCCAAT GCCTGCCAT GTATTTCTGA	SICNDSAFFR IMCATAEAQS KAQCDLODPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL LEAFHMYLAL PDDFCWINNN SIAGLIFFLIG LCCGKLRLAE SGNGNASTER IEQM S1 GTTTTCTGAA AACTGAAGAA AACTGAAGAA AATGAACTACATTA CAATGACTA TCATGGTAACA AATGATCTGTT TGTTACTTTA CAATGACTA TCATGGTAACA ATGATCTGTT TGTTACTTTA CAATGACTCA TCCCAGAAT AAAACGCTCA TCCCAGCAAT AAAACGCTCA TCCTCAGCCA TCCCAGCCAA TACCTCTTTT AGGGGAGATT TGGTGAGCCC CACCCCCACCT CAACACTACC CTCTCAGCCA CTCTCAGCCA CTCCCCCCCCCC	120 180 240 360 420 540 660 720 780 840 960 120 180 360 420 480 540 660 720 780 840 900 900 9108 1080 1140
505560657075	PSSNEVETTS GEIMPOYDKE TINCTPTIKL VCLADHPRGP POPSAPIASS VQTDIVNTSS LKVVDDIGLQ NSIGTITLPS TVRNLTRNVT SKLTSFGVLL ILIQLCAALL ILIQLCAALL ILIQLCAALL VKVFNTYIRK AVFYITVGY ITWGFAFFAW NSDWSKTATIN NGVSFSVQNG Seq ID NO: Nucleic Ac. Coding sequity AGCCAGCCCG CTCGCGGTCA GTTTTACTGA TCCCTGGAAG GTCAGTTTTG AGCTTACTCC GCTTCAGGCG GCATTTTTA CAACATATAA TCGTCAGGA TCGTCCAGG GCTGTCAACA GGGCCCAAA TCTGTCAGGA TCCATCCCAG GCTGAGCCTC CCACCCTTT CCACACTCTG CCACACCTCT CCACACCCTTT CCACACCCCTTT CCACACCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCCCTTT CCACACCTCT CCACACCCCTTT CCACACCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCCTC CCACCCCCTC CCACCCCCTC CCACCCCCCTC CCACCCCCCCTC CCACCCCCCTC CCACCCCCCCC	LNDVTLSLLP STVPQNQHIL STVPQNQHIL NTMNACAAI PFSSSQSIPV PAIDMPPQSE ISDLENQVLQ LNFSNTTISL SLMNNLPAHD UTLKHINPSQ DLSRTSVLPA LLNLVFLLDS YILKPCIVGW FCVIFILINVS GPVNVTFMYL GLKKQTVNQG DVCLHDFTGK 21 DNA seq id Accession id Accession id Accession cence: 37 11 AGGACGCGGA GGATGGTTT CGTTCAAGGA CCCCTCCTC CTTCAACGA TCAACGAA CCAATGATC GAATGATC GAATGATC GAATGATC GAATGATC CCTGCC TTGTCTGTCT TGGTGCCTC CACCCCAGCC AAACGATTTC CCTCCCTCC CCCCCCCAGCC CAACCCAGCC CCCCCCCCCC	SNETEKTKIT NGTLTGVUSL AALERVKIRP VPRATVLSQV TISSPMPQTH MEKALSLGSL TSPSLALAVI MELASRVQFN DELTVRCVFW QMMALTFITY WIALYKMQGL GVPAVVVTI MFIVVLVQLC FAIFNTLQGF VSSSNSLQS QHMFNEKEDS LEENCE n #: NM_005 3117 21 CGGCAGGTGT CTCTTCTCAGG ATTCCTTGTC TAATTCCAGT CAATGAGGTT AACACAAAAA ACCCTAAGT TTGTACATGG AACCCTAAGT TTGTACATGG ACCTGTAGC TTCCCCCA TTCCCCCA TTCCCCCA TTCCCCTATG CTTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA TTCCCCTATG CTCTCCCCCA AGACATCTCC AGACATCTC AGACATCT AGACATC AGACATCT AGACATC AGACATC AGACATC AGACATC AGACATC AGACATC AGACATCT AGACATC AGACA	IVETFNASGY SELKRSELNK MEHCCCSVRI PKATSFAEPP VSGTPPPVKA EPNLAGEMIN RVNASSFNTT FFETPALFQD DLGRNGGRGG IGCGLSSIFL CISVAVFLHY LTISPDNYGL RIKKKQLGA FIFIFYCVAK SENSTNSTTL CNGKGRMALR 756.1 31 GCACAGAGGT CAGTGTGCC ATCATTTGTC TTGTCACCAC GAAACAAAAAAAAAA	KPQRNICNLS TLQTLSETYF PCPSSPEELG DYSPVTHNVP SFSSPTVSAP OVSRLHSPP TFVAQDPANL PSLENLSLIS SVTLVTYIAF FLLVSFTWMG GSYGKPPNGS ORKTSIQDLR ENVRKQWRRY LVNNDCSVHA RTSKRGSLHF 41 TCTCCACTTT ATGTTGGCAG TTCATGTCGT CACCTGCTAA GCCTCAATGA CATTATTTG AAAGCACTGT TAAATGAATT TATATATGT TGAATAATAC CAATGGAACA CAATGTAATTG GAAAGCTTCA CACCATTTTC TCCCCAAAGC CCTCTCCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCCTGCCAAT GCCTTGCCAAT GCCTGCCAAT GCCTGCCAAT GCCTGCCAT GTATTTCTGA	SICNDSAFFR IMCATAEAQS KIQCDLQDPI SPIGEIQPLS ANVNTTSAPP DMLAPLAQRL QVSLETQAPE YVISSSVANL REAFHMYLAL EAFHMYLAL EDDFCWINNN SIAGLTFLLG LCCGKLRLAE SGNGNASTER IEQM 51 GTTTTCTGAA AACTGAAGAA TCTGGTAACA ATTATCTGTT TGTTACTTTA AACCTTCAAT CAATGACTCA TCCCCAGCAT TCCCAGCAT TCTCAGCCA AATGAATGCCT TTCCAGCCAA ATTACTGTT TGTGACCTG TTCCAGCCAA ATTACTGTT TGTGACCTG TTCCAGCCAA ATTACTGTT TGACATGCCC CACCCCACCC	120 180 240 360 420 540 660 720 780 900 960 120 180 360 420 360 420 780 660 720 780 660 720 780 181 900 900 910 181 181 181 181 181 181 181 181 181 1

			CAGACTCCTT				1320
	GCTCAAAGAT	TGCTGAAAGT	AGTGGATGAC	ATTGGCCTAC	AGCTGAACTT	TTCAAACACG	1380
	ACTATAAGTC	TAACCTCCCC	TTCTTTGGCT GGCCCAAGAC	CTGGCTGTGA	TCAGAGIGAA	TCTGGAAACC	1440 1500
5	CAAGCTCCTG	AGAACAGTAT	TGGCACAATT	ACTOTTCCTT	CATCGCTGAT	GAATAATTTA	1560
			AGCTTCCAGG				1620
			GGAGAACCTC				1680
			GAACTTGACA				1740
10	AACCCGAGCC	AGGATGAGTT	AACAGTGAGA	TGTGTATTTT	GGGACTTGGG	CAGAAATGGT	1800
10	GGCAGAGGAG	GCTGGTCAGA	CAATGGCTGC AACAAGCTTC	TCTGTCAAAG	ACAGGAGATT	GAATGAAACC	1860 1920
			GGCTCTGACG				1980
	TCAATTTTTC	TGTCAGTGAC	TCTTGTAACC	TACATAGCTT	TTGAAAAGAT	CCGGAGGGAT	2040
	TACCCTTCCA	AAATCCTCAT	CCAGCTGTGT	GCTGCTCTGC	TTCTGCTGAA	CCTGGTCTTC	2100
15	CTCCTGGACT	CGTGGATTGC	TCTGTATAAG	ATGCAAGGCC	TCTGCATCTC	AGTGGCTGTA	2160
	TTTCTTCATT	ATTTTCTCTT	GGTCTCATTC	ACATGGATGG	GCCTAGAAGC	ATTCCATATG	2220
			ATTTAATACT				2280 2340
	ATTGTCGGTT	GGGGGGTACC	AGCTGTGGTT TGGGAAATTC	CCCAACCATCA	CACCCCATGA	CTTCTCCTCC	2400
20	ATCAACAACA	ATGCAGTATT	CTACATTACG	GTGGTGGGAT	ATTTCTGTGT	GATATTTTTG	2460
			TGTGGTCCTG				2520
	CAACTGGGAG	CCCAGCGAAA	AACCAGTATT	CAAGACCTCA	GGAGTATCGC	TGGCCTTACA	2580
	TTTTTACTGG	GAATAACTTG	GGGCTTTGCC	TTCTTTGCCT	GGGGACCAGT	TAACGTGACC	2640
25			CTTTAATACC				2700
25			CAGGAAGCAA CTGGAGTAAA				2760 2820
	CGGCTGGCTG	GACTETCEA	CTCTTCAAAT	TOTTACACT	CARCCAGTAA	CTCCACTAAC	2880
	TCCACCACAC	TGCTAGTGAA	TAATGATTGC	TCAGTACACG	CAAGCGGGAA	TGGAAATGCT	2940
	TCTACAGAGA	GGAATGGGGT	CTCTTTTAGT	GTTCAGAATG	GAGATGTGTG	CCTTCACGAT	3000
30			GTTTAACGAG				3060
			AAAGCGGGGA				3120
			ATGATGCTTG				3180
	CACAATGTGA	GATGTATGAA	AATCAACTCA TTATTATTAC	ANGRAGARA	CARCACATUT	CACCATGGTT	3240 3300
35	TTTAGACATT	TCTGATTTGG	TTTCTTATCT	TTCATTTTAT	AAGAAGGTTG	GTTTTAAACA	3360
-			ATAAAGAAAA				3420
	TTTAAAGAGG	CTAAGTTATC	TTTGATAACA	TCATATAAAG	CAACTGTTGA	CTTCAGCCTG	3480
			TGCCTTTGTT				3540
40			ATTTTTTTGT				3600
40			TGTCTCACGT GAGATGATAT				3660 3720
			CCAGACTGAG				3780
	TCATACAGTG	CCTTTGAGCA	AGTTAGGAAA	AGATGCCCCC	ACTGGGCAGA	CACAGCCCTA	3840
			AGAGTGAGAG				3900
45	GTGCACGACC	TGTACAGCCA	AACACAGCAT	CCAATATGAA	TACCCATCCC	CTGACCGCAT	3960
	CCCCAGTAGT	CAGATTATAG	AATCTGCACC	AAGATGTTTA	GCTTTATACC	TTGGCCACAG	4020
	AGAGGGATGA	ACTGTCATCC	AGACCATGTG TCCCCAGAGC	TCAGGAAAAT	TGTGAACGTA	DOTACONTEC	4080
			ATATATGGAA				4200
50	ACTGCATGGT	ACATTGTTGA	TTGTTATGAC	TGGTACACTC	TGGCCCAGCC	AGAGCTATAA	4260
_	TTGTTTTTTA	AATGTGTCTT	GAAGAATGCA	CAGTGACAAG	GGGAGTAGCT	ATTGGGAACA	4320
	GGGAACTGTC	CTACACTGCT	ATTGTTGCTA	CATGTATCGA	GCCTTGATTG	CTCCTAGTTA	4380
	TATACAGGGT	CTATCTTGCT	TCCTACCTAC	ATCTGCTTGA	GCAGTGCCTC	AAGTACATCC	4440
55			CCCTTTTAGT CTCAGACTAA				4500 4560
55			TTCTTTTCTG				4620
			CAATGAAATA				
<i>c</i> 0		22 Protein					
60		cession #:					
	1	11	21	31	41	51	
	J.	 VCDTEEVILLT	PETERNITICS.	HUM.WTSLEE	DTDNSSI.SPP	PAKLSVVSFA	60
	PSSNEVETTS	LNDVTLSLLP	SNETGVKPQR	NICNLSSICN	DSAFFRGEIM	FOYDKESTVP	120
65	ONOHITNGTL	TGVLSLSELK	RSELNKTLQT	LSETYFIMCA	TAEAQSTLNC	TFTIKLNNTM	180
	NACAVIAALE	RVKIRPMEHC	CCSVRIPCPS	SPEELEKLQC	DLQDPIVCLA	DHPRGPPFSS	240
			SFAEPPDYSP				300
	MPPQSETISS	PMPQTHVSGT	PPPVKASFSS	PTVSAPANVN	TTSAPPVQTD	IVNTSSISDL	360
70	ENQVLQMEKA	LSLGSLEPNL	AGEMINQVSR SSFNTTTFVA	ODDANT OVEL	PLAQRILKVV	TITI.DCCI.MN	420 480
70			PALFQDPSLE				540
			NGGRGGWSDN				600
	TSVLPAQMMA	LTFITYIGCG	LSSIFLSVTL	VTYIAFEKIR	RDYPSKILIQ	LCAALLLLNL	660
76						NTYIRKYILK	720
75			PDNYGLGSYG				780
	FLLNVSMFIV	VLVQLCRIKK	KKQLGAQRKT	SIQUERSIAG	LIFLLGIIWG	SKTATNGLKK	840 900
						PSVQNGDVCL	960
			GRMALRRTSK				500
80							
		23 DNA sec					
			n #: NM_001	565.1			
		nuence: 67		31	41	51	
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					28	52	

		TCAATTGCTT					60
	AGCACCATGA	ATCAAACTGC	GATTCTGATT	TGCTGCCTTA	TCTTTCTGAC	TCTAAGTGGC	120
	ATTCAAGGAG	TACCTCTCTC	TAGAACCGTA	CGCTGTACCT	GCATCAGCAT	TAGTAATCAA	180
_		CAAGGTCTTT					240
5	CGTGTTGAGA	TCATTGCTAC	aatgaaaaag	AAGGGTGAGA	AGAGATGTCT	GAATCCAGAA	300
		TCAAGAATTT					360
		GGGGAGCAAA					420
		CACTTCCCTA					480
10		AAGGTGACCA					540
10		CATCATCCTA					600
		GGTGCTATGT					660
		TCTTCCAAGG					720
		AAATAACTAA					780
16	ACTTCATGGA	CTTCCACTGC	CATCCTCCCA	AGGGGCCCAA	ATTCTTTCAG	TGGCTACCTA	840
15	CATACAATTC	CAAACACATA	CAGGAAGGTA	GAAATATCTG	AAAATGTATG	TGTAAGTATT	900
	CTTATTTAAT	GAAAGACTGT	ACAAAGTATA	AGTCTTAGAT	GTATATATTT	CCTATATTGT	960
	TTTCAGTGTA	CATGGAATAA	CATGTAATTA	AGTACTATGT	ATCAATGAGT	AACAGGAAAA	1020
		ACAGATAGAT			AAGATAAATG	TGCTGAATGG	1080
20	TTTTCAAATA	AAAATGAGGT	ACTOTOCTGG	AAATATTAAG			
20	0 70 110	04 2					
		24 Protein					
		ession #: N	21 .	31	41	51	
	1,	11	Z	31	1	1	
25	NOVOMB TI TOO	LIFLTLSGIQ	CONTRACTOR	TOTOTONODU	MODEL PRICE	I DA CORCEDU	60
23		EKRCLNPESK			MERGHERMET	I PADQL CPRV	
	ETTATPIKKKG	EARCLINFESA	AIRMULIKAVS	KENSKKSF			
	Sea ID NO.	25 DNA sequ	ience				
		id Accession		559			
30		uence: 11					
50	1	11	21	31	41	51	
	î.	ī	ī	ĭ	ī	ī	
	ATGAACCGCA	GCCACCGGCA	CGGGGCGGGC	AGCGGCTGCC	TGGGCACTAT	GGAGGTGAAG	60
		GAGCTGAATT					120
35		ATGGATTACT					180
••		ACATCCATGG					240
	GCTGTTTCAA	CGGCCAATCC	ACTGCTTAGG	ATATTTATAC	AAAAGAAGGA	AGAAGCAGAC	300
	TACAGTGCCT	TTGGTACAGA	CACGCTAATA	AAGAAGAAGA	ATGTTTTAAC	CAACGTATTG	360
	CGTCCTGACA	ACCATAGAAA	AAAGCCACAT	ATAGTCATTA	GTATGCCCCA	AGACTTTAGA	420
40	CCTGTGTCTT	CTATTATAGA	CGTGGATATT	CTCCCAGAAA	CGCATCGTAG	GGTACGTCTT	480
	TACAAATACG	GCACGGAGAA	ACCCCTAGGA	TTCTACATCC	GGGATGGCTC	CAGTGTCAGG	540
	GTAACACCAC	ATGGCTTAGA	AAAGGTTCCA	GGGATCTTTA	TATCCAGGCT	TGTCCCAGGA	600
	GGTCTGGCTC	AAAGTACAGG	ACTATTAGCT	GTTAATGATG	AAGTTTTAGA	AGTTAATGGC	660
4.5		CAGGGAAGAG					720
45	AACCTCATCA	TAACAGTGAG	ACCGGCAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTCGG	780
		GTTCCGGTCA					840
		TTGAGCCAGA					900
		CACAGCAGAT					960
50	ACACAGATAG	AGCTAAGCTT	TGAGTCTGGA	CAGAATGGCT	TTATTCCCTC	TAATGAAGTG	1020
50		CCATAGCAAG			AAACACATGC	TCCAGATCAA	1080
	AAACTCTTAG	AAGAAGATGG	AACAATCATA	ACATTATGA			
		26 Protein					
55		cession #: :		21	41	51	
22	1	11	21	31	41	1	
		SGCLGTMEVK	CKECYNDDD	OI EDENDONE	PERVELLOR	INTERMINATION	60
		PINNDDNYHK					120
		IVISMPQDFR					180
60	WEDWALEKAD	GIFISRLVPG	GI.AOSTGI.I.A	UNDEVIEUNG	TEVSGKSI-DO	VTDMMIANSR	240
00	MITTTUDDAN	QRNNVVRNSR	TSGSSGOSTD	NSLLGYPOOI	EPSFEPEDED	SEEDDIIIED	300
	NGVDOOTPKA	VPNTESLESL	TOTELSPESG	ONGFIRSNEY	SLAATASSSN	TEFETHAPDO	360
	KLLEEDGTII		1610001 000	Sucr zz pun	021212000		•
		•••					
65	Sea ID NO:	27 DNA seq	uence				
		id Accessio		667.1			
		uence: 12					
	1	11	21	31	41	51	
	1	1		1	1	1	
70	ATGGACACCT	CCCGGCTCGG	TGTGCTCCTG	TCCTTGCCTG	TGCTGCTGCA	GCTGGCGACC	60
	GGGGGCAGCT	CTCCCAGGTC	TGGTGTGTTG	CTGAGGGGCT	GCCCCACACA	CTGTCATTGC	120
						CTCGGAGCTG	180
						CATCAGTCAG	240
75						TGCGGGAAAC	300
75	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCTTT	ACAGTCTTAA	AGTTCTTATG	360
						GCGAAGCCTT	420
						TTTCAGTGGC	480
	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	TAACAGAAAT	CCCCGTCCAG	540
0.0	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	CCCTGAACAA	AATACACCAC	600
80						CCATAACAAT	660
						GACTTTAGAT	720
						CAACCTTAAA	780
						TCAACATTTA	840
0.5						TCCTGATTTA	900
85	ACTGGAACTG	CAAACCTGGA	GAGTCTGACT	TTAACTGGAG	CACAGATCTC	ATCTCTTCCT	960

					ATCTGTCTTA		1020
	GAAGATTTAC	CCAGTTTTTC	AGTCTGCCAA	AAGCTTCAGA	AAATTGACCT	AAGACATAAT	1080
					TTAGCCTCCG		1140
	GAAAICIACG	AMAIIAAAGI	TOACACITIC	CAGCAGITOC	TINGCCI CCG	ACCOUNT COOMS	
_	TTGGCTTGGA	ACAAAATTGC	TATTATTCAC	CCCAATGCAT	TTTCCACTTT	GCCATCCCTA	1200
5	ATAAAGCTGG	ACCTATOGTO	CAACCTCCTG	TCGTCTTTTC	CTATAACTGG	GTTACATGGT	1260
					GCTTGATATC		1320
							1380
					AGTGCTGTGC		
	TGTGAGAATG	CCTATAAGAT	TTCTAATCAA	TGGAATAAAG	GTGACAACAG	CAGTATGGAC	1440
	CACCTTCATA	ACABACATOO	TICCS STOTT	CAGGCTCAAG	ATGAACGTGA	CCTTGAAGAT	1500
10							1560
10	TTCCTGCTTG	ACTITGAGGA	AGACCTGAAA	GCCCTTCATT	CAGTGCAGTG	TTCACCTTCC	
	CCAGGCCCCT	TCAAACCCTG	TGAACACCTG	CTTGATGGCT	GGCTGATCAG	AATTGGAGTG	1620
	TOGACCATAG	CACTTCTCCC	ACTTACTTCT	AATGCTTTGG	TGACTTCAAC	AGTTTTCAGA	1680
	TOUNCUNTAG	T-CT-CT-CC-C	~~~~~	May y marcaca	TONTOCONCO	ACTCA ACATC	1740
	Tececterer	ACATTTCCCC	CATTAAACTG	TTAATTGGGG	TCATCGCAGC	AGIGAACAIG	
					CGTTCACTTT		1800
15	CCACCACATG	GTGCCTGGTG	GGAGAATGGG	GTTGGTTGCC	ATGTCATTGG	TTTTTTGTCC	1860
10	3000000000000	CICCICCIC	BORROW COMO	COURT COURT CO	Checectecan	CCCCCCCCCC	1920
	ATTTTTGCTT	CAGAATCATC	TGTTTTCCTG	CTTACTCTGG	CAGCCCTGGA	GCG1GGG11C	
					TTTCTAGCCT		1980
	ValuabelClasser	GTGCCCTGCT	GGCCTTGACC	ATGGCCGCAG	TTCCCCTGCT	GGGTGGCAGC	2040
					GGGAGCCCAG		2100
00							
20	TACATGGTCG	CTCTCATCTT	GCTCAATTCC	CTTTGCTTCC	TCATGATGAC	CATTGCCTAC	2160
	ACCARGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTTGGGA	CTGCTCTATG	2220
	CERT 2 2 C C C C	TO COCOTO	COMPONED CC	NACTOCATOC	TAAACTGCCC	小によらていかから	2280
	GTAAAACACA	TIGCCCIGIT	GCTCTTCACC	MACIGCAICC	IMMCIGCCC	IGIGGCIIIC	
	TTGTCCTTCT	CCTCTTTAAT	AAACCTTACA	TTTATCAGTC	CTGAAGTAAT	TAAGITTATC	2340
	CTTCTGGTGG	TAGTCCCACT	TCCTGCATGT	CTCAATCCCC	TTCTCTACAT	CTTGTTCAAT	2400
25					CCTACGTCTG		2460
23	CCTCACTTIA	AGGAGGAICI	GGIGNGCCIG	MOMMMOCANA	CCIACGICIG	GACAAGATCA	
	AAACACCCAA	GCTTGATGTC	AATTAACTCT	GATGATGTCG	AAAAACAGTC	CTGTGACTCA	2520
	ACTCAAGCCT	TGGTAACCTT	TACCAGCTCC	AGCATCACTT	ATGACCTGCC	TCCCAGTTCC	2580
	CHICAGO TO CO	CACCOMMATCC	A CINCA CINCA C	A COTCCCATC	TTTCCTCTGT	CCCATTCTC	2640
			MGIGMCIGMG	MOCIGCOMIC	IIICCICIGI	GGGATIIGIC	
	CCATGTCTTA	A					
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		28 Protein					
	Protein Acc	cession #: 1	NP_003658.1				
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25	·	1	1		1	DOCUMENT OF COL	60
35	MDTSRLGVLL	SLPVLLQLAT	GGSSPRSGVL	LRGCPTHCHC	EPDGRMLLRV	DCSDTGTSET	60
	PSNLSVFTSY	LDLSMNNISO	LLPNPLPSLR	FLEELRLAGN	ALTYIPKGAF	TGLYSLKVLM	120
	TOMMOT.PHT/P	TENIONI.PSI.	OST-RT-DANHT	SYVPPSCFSG	LHSLRHLWLD	DNALTEIPVO	180
							240
					RIHSLGKKCF		
	LNYNNLDEFP	TAIRTLSNLK	ELHFYDNPIQ	FVGRSAFQHL	PELRTLTLNG	ASQITEPPDL	300
40					EDLPSFSVCQ		360
70	IGIANDESDI	DIGNOTODE	& TANKS AND THE	2112222112	TYPETONE	CCRDIMOTIO	420
	EIYEIKVDTF	QQLLSLRSLN	LAWNKIAI IH	PNAFSTLPSL	IKLDLSSNLL	SSFFITGLING	
							480
	LTHLKLTGNH	ALOSLISSEN	FPELKVIEMP	YAYQCCAFGV	CENAYKISNQ	MINGORNASAM	400
	LTHLKLTGNH	ALQSLISSEN	FPELKVIEMP	YAYQCCAFGV	CENAYKISNQ DCDEKDCEVI	INCUITATEU	
	DLHKKDAGMF	QAQDERDLED	FLLDFEEDLK	ALHSVQCSPS	PGPFKPCEHL	LDGWLIRIGV	540
	DLHKKDAGMF WTIAVLALTC	QAQDERDLED NALVTSTVFR	FLLDFEEDLK SPLYISPIKL	ALHSVQCSPS LIGVIAAVNM	PGPFKPCEHL LTGVSSAVLA	LDGWLIRIGV GVDAFTFGSF	
45	DLHKKDAGMF WTIAVLALTC	QAQDERDLED NALVTSTVFR	FLLDFEEDLK SPLYISPIKL	ALHSVQCSPS LIGVIAAVNM	PGPFKPCEHL LTGVSSAVLA	LDGWLIRIGV GVDAFTFGSF	540 600
45	DLHKKDAGMF WTIAVLALTC ARHGAWWENG	QAQDERDLED NALVTSTVFR VGCHVIGFLS	FLLDFEEDLK SPLYISPIKL IPASESSVFL	ALHSVQCSPS LIGVIAAVNM LTLAALERGF	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI	540 600 660
45	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPFGEPSTMG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY	540 600 660 720
45	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPFGEPSTMG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY	540 600 660
45	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720
45	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
45 50	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS	FLLDFEEDLK SPLYISPIKL IFASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
	DLHKKDAGMF WTIAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO:	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequ	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
	DLHKKDAGMF WTIAVLALTC ARHGAWWEND ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac:	QAQDERDLED NALVTSTVFR VGCHVIGFLS VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
	DLHKKDAGMF WTIAVLALTC ARHGAWWEND ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac:	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequ	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKPI DDVEKQSCDS	540 600 660 720 780
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA segr id Accession uence: 135.	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVST VPSPAYPVTE UECICE n #: NM_002 .1472	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI	540 600 660 720 780
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50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession LUBERT CONTROL CONTROL LUBERT CONTROL LU	FLLDFEEDLK SPLYISPIK IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVST VPSPAYPVTE Uence uence uence 1472 21 GTCAGTGCTG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGGCT	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS	540 600 660 720 780 840
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession LUBERT	FLLDFEEDLK SPLYISPIK IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVST VPSPAYPVTE Uence uence uence 1472 21 GTCAGTGCTG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGGCT	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS	540 600 660 720 780 840
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1 	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession uence: 135. 11 GGGGTGGCGG CCTGGAGCTC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLIFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSPSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKPI DDVEKQSCDS	540 600 660 720 780 840
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG ILLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ GGCACGAGTA GTTCCTGGTC GCGACTGGCC	QAQDERDLED NALVISTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN SITYDLPPSS 29 DNA sequid Accession LECTOR 11 GGGGTGGCGG GCCTGGAGCTC GGCCATGCCTT GGCCATGCCTT	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHPKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG GCGACTTGGC TCCCGGGCTG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS	60 120 180
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50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN STTYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCCT CGGCCATGCCT	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VESPAYPVTE uence n #: NM_0021472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAGATCC	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG GCGCAACCTG GGGGATAGAA GGAGGAAGAG GGAGAAGAG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT	60 120 180
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequil GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA seq id Accession uence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGCCCTTGC TGACTATGGC TGACTATGGC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVST VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGGCT GCGCAACCTG AGGACTATGA AGGTAAGAG AAGCTGAGAA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTTGTAC TGATGGCAAG ACAGATGCTT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKPI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG	60 120 120 300 840
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding seq 1 GGCACGAGTA GTTCCTGGTC GGGACTGGCC CAGGCTCCTA GGAAGAACT TGBATTGCTT	QAQDERDLED NALVISTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCCT CGGCCGTGC TGACTATGGC TTGATATGGC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGC TCCCGGGCTG CAGAAGATCC TCCATGACAG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA AACATCGGTAA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATATTG	600 120 780 840 60 120 180 240 300 360
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1 GGCACGAGTA GTTCCTGGTC GGGACTGGCC CAGGCTCCTA GGAAGAACT TGAATTTGCT ACCGGACCAA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNFLLYLLFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCT TGACTATGGC TCGTGAACTG TACAACACTG	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA ATACATTGTAA	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA GGAGGAAGAG AAGCTGAGAA ACATCGTTCG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA	60 120 180 240 300 420
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50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequing GGCACGAGGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAATAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC GGCCATGCCTT TGACTATGGC TCGTGAACTG TAAACACACTG AAAGGGAACC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVST VPSPAYPVTE UEENCE G#: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CGCAGAGTCC TCCATGACAG AAACATCCAA AAGGAAAGGC	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGAGGAGAGA AAGCTGAGAA ACATGGTCG TGGAATATTG AATACTTAGA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGAAGGAAG ACAGATGCTT TTACTATGAT TTGAAGGAGG TGAAGAGGTT TGAAGGAGGT TGAAGGAGGT TGAAGGAGGT TGAAGAGGT TGAAGAGGT TGAAGAGGT TGAAGAGTT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGGACTCTG ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGTA GATCTTCGAG GATCTCGAA	60 120 180 240 300 420
50 55 60	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG ILLVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequil GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCCTGGAGCTC CGGCGCTGCC TGACTATGGC TGACTATGGC TGCTGAACTG AAAGGGAACC GTTGACTCTG GTTGACTCTG GTTGACTCTG	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHLALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGG AGGCAGGG GCCCTGAAGG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGCTAAGAA AACATCGTTCG TGGAATATTG AATACTTAGA AATACCTAGA AATACCTAGA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILINS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGGAGGTT ACGAAGGATGTT ACGAAGTGTT ACGAAGTGTT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GTTCTTCTAGAG GGTGGTCATA	60 120 180 840 60 120 180 240 360 420 480 540
50	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ GGCACGAGTA GTTCCTGGTC GGGACTGGCC CAGGCTCCTA GGAAGAACT TGAATTTGCT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA CCGTATTGCA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNFLLYLIFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCT CGGCCATGCT TGACTATGGC TTACAACACTG AAAGGGAACTG TCGGGATCTC TCGGGCATCTT	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAGGG AAACATCCAA AAGGAAAGGG AAACCAGCCA	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG AGGACTATGA AGGACTATGA AGACTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGTTTTCCT	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGGCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA GCGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CCGATTATTG GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA CAAAACGTCA	60 120 300 420 480 480 540 540
50 55 60	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TOALVTFTSS Seq ID NO: Nucleic Ac: Coding sequity GGCACGGGC GGCACGGGC CAGGGCTCCTA GGAAAGAACT TGAAATTGCT ACCGGACCGA TGCCTAATTGC TGATGACTCA CCGTATTGCA AGCTTGGAGA	QAQDERDLED NALVTSTVF VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC GGCCATGCCT CGGCCGCTGC TGACTATGGC TGACTATGGC TGACAACTG AAAGGGAACCT GTGAACTGT CTTTGGGCTA	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VPSPAYPVTE UEEnce n #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCT TCCATGACAG AAACATCCAA AAGAAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGC GCCCTGAAGG AAACCAGCA AAACCAGCA GCTAGAATAT	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG GCGCAACCTG AGGACTATGA AGGAGGAAGAG AAGCTGAGAA ACATCGTCG TGGAATATTG AATACTTAGA AATGCCACAG ATGCTTCCC TAAACCATGA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGAATGCTAT TTACTATGAT TTACTATGAT TGAAGGAGG TGAAGAGTTT ACGAAGTGTT ACGAAGTGTT ACGAAGTGTT CGAATGCAAG CACAGTTTT	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATT GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTGGCTA GATCTCGAG GGTGGTCATA CAAAACGTCA GCAAAACAT	540 600 720 780 840 120 120 240 300 360 420 480 540 660
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50 55 60	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG ILLVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequil GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA CCGTATTGCA AGCTTGGAGA AGCTTGGAGA ATTGTTGGCA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNFLLYILFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCGTGC TGACTATGGC TGACTATGGC TGACACACT ACAGGGAACT CGTTGACTCT CTTGGGCTTC CTTGGGCTTCT ACAGGGAACT ACCTTATTACACTACAC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHLALLLFT PHFKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG GCGCACTTGGC TCCCGGGCTG CAGAAGATCA TACATTGTAA AAGGAAAGGC AAACCAGCA AAACCAGCA AAACCAGCA AACTAGAACA AACTAGAACA AACTAGAACA AACTAGAACA AACTAGAATAT AATGTCTCCTG	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GGGAACCTG AGGACTATGA AGGACTATGA AACCTGATGA AATGCTACGA ATGTTTCCT TAAACCATGG AAACAATGAA AACAAATGAA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILINS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAG ACAGTGCTT TTACTATGAT TGAAGGAGGT TGAAGGAGGTT ACGAAGTGTT ACGAAGTGTT ACGAAGTGTT TCGATGCAG CACGAGTTTT TCGCATGCC	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTGAAG CGGATTATTG GATCTGGCTA GATCTGGCTA CAAAACGTCA GCAAAAACAT TACAATGAGA	60 120 180 840 60 120 180 240 360 420 540 600 720
50 55 60	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequil GCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TAGATTTGCT ACCGGACCAA GTGTAATTGCT TGATTTGCA AGCTTGGAC AGCTTGACA AGCTTGGAC AGCTTGAC AGCTTGGAC AGCTTGAC AGCTTGGAC AGCTTGGAC AGCTTGGAC AGCTTGGAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTTGCAC AGCTT	QAQDERDLED NALVISTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYILFN SITYDLPPSS 29 DNA seq id Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCCT CGGCCATGCCT TGACTATGGC TCGTCAACTG TACAACACTG TACAACACTG TACAACACTG TACAACACTG TACACACTG TACACACTG TACACTCTACTACTC CTTTGGGCTACTTC CTTTGGGCTACTTC CTTGTCATTTACCTC ACCTTACTTAC	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHPKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG GCGACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA TACATTGTAA AAGGAAAAGGCA GCCTGAAGG AAACCAGCCA GCTTAGAATGT ATGTTCTCTG GGCTGGTTGC	ALHSVQCSPS LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWTRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GGGACTGT AGGACTATGA AGGACTATGA ACATCGTTCG TGGATATTC AATACTTAGA AATGCCACAG ATGTTTTCCT TAAACCATGA AACAAATGAA ATGTATGAGTT	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCCAAG ACAGATGCTT TTACTATGAT TGAAGGAGGG TGAAGAGTTT ACGAAGTGAT ACGAAGTGAT CGCATGCAAG CACGAGTTTT TCGCATGCC ATGTGCATTA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA ACCATTGGCA ATATTAGTTT GTTTCTGAAG GGTGGTCATA GGTGGTCATA GGTGGTCATA CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCTCCAT	540 600 720 780 840 60 120 180 240 300 420 480 540 600 650 720 780
50 55 60 65	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA CCGTATTGCAA CCGTATTGCAA AGCTTGGAGA ATTACAGATAT TTACAGCTTT	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN STTYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGCTGGCGG CCTGGAGCTC CGGCCGTGC TGACTATGGC TTACAACACTG AAAGGGAACC GTTGACTCTG ACCTGTGACTC CGTGGGCTT CCTGGGCTACCTG ACCTGTGACTCTT CTTGTGGCTA ACCTTATTAC CTTGTGTCATTT TAGCCAGAAA	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VESPAYPVTE USENCE #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCAGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGAT AAGGAAAGGC AGCTGAAGG AACCACCAA GCTGAAGGC AGCTGAAGGC AGCTGAAGGC GCCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGCTGC GGCTGCTTGC GGACTCCTG	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACTGA AGATTATGA AACATCGTTCG TAAACCATGA AACAATGAA TGTATGAGTT GGAAAATCAG GGAAAATCAG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG ACGATTGTAC TGATGGCAAG ACAGATGTT TTACTATGAT TGAAGGAGGG TGAAGAGTAT ACGAAGTGTT TCGCATGCCAAG CACGAGTTTT TCGCATGCCAAG CACGAGTTTT TCGCATGCCAAT AGAAGGCAAA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ATATTAGTTT GTTTCTGAAG GCGATTATC GATCTGGCTA GTTCTTCGAG GGTGGTCAT GTTCTTCGAG GGTGGTCAT CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT	540 600 720 780 840 120 240 300 360 480 540 660 720 780 840
50 55 60 65	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequ 1 GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA CCGTATTGCAA CCGTATTGCAA AGCTTGGAGA ATTACAGATAT TTACAGCTTT	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN STTYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGCTGGCGG CCTGGAGCTC CGGCCGTGC TGACTATGGC TTACAACACTG AAAGGGAACC GTTGACTCTG ACCTGTGACTC CGTGGGCTT CCTGGGCTACCTG ACCTGTGACTCTT CTTGTGGCTA ACCTTATTAC CTTGTGTCATTT TAGCCAGAAA	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHFKEDLVSL VESPAYPVTE USENCE #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCAGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGAT AAGGAAAGGC AGCTGAAGG AACCACCAA GCTGAAGGC AGCTGAAGGC AGCTGAAGGC GCCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGAAGGC AGCTGCTGC GGCTGCTTGC GGACTCCTG	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACCTG GCGCAACTGA AGATTATGA AACATCGTTCG TAAACCATGA AACAATGAA TGTATGAGTT GGAAAATCAG GGAAAATCAG	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG ACGATTGTAC TGATGGCAAG ACAGATGTT TTACTATGAT TGAAGGAGGG TGAAGAGTAT ACGAAGTGTT TCGCATGCCAAG CACGAGTTTT TCGCATGCCAAG CACGAGTTTT TCGCATGCCAAT AGAAGGCAAA	LDGWLIRIGV GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ATATTAGTTT GTTTCTGAAG GCGATTATC GATCTGGCTA GTTCTTCGAG GGTGGTCAT GTTCTTCGAG GGTGGTCAT CAAAACGTCA GCAAAAACAT TACAATGAGA ATGCCTCCAT	540 600 720 780 840 60 120 180 240 300 420 480 540 600 650 720 780
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50 55 60 65	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG ILLVAVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding sequil GGCACGAGTA GTTCCTGGTC GGGACTGGCC CAGGCTCCTA GGAAAGAACT TGAATTTGCT ACCGGACCAA GTGTAATTGCT ACCGTATTGCA AGCTTGGGAC AGCTTGGGAC AGCTTGGAGA TTGTTGGCAC AGCTTAGAGT TTCATACCA TTCATACCA TTCATACCA ATCATCCATACCG ATTACCATCG	QAQDERDLED NALVISTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNPLLYLLFN SITYDLPPSS 29 DNA sequid Accession Lence: 135. 11 GGGGTGGCGG CCTGGAGCTC CGGCCATGCCT CGGCCATGCCT TACAACACTG AAAGGGAACC GTTGACTCT CTTGGGCTTC CTTGGGTTCATTG CTTGGGTTATTA ACCTTATTATACCTGGATTA TTACCTGGAT TACACCAGAAA TTACTCTGAT ACCTTCTGTT	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHLALLLFT PHPKEDLVSL VPSPAYPVTE uence n #: NM_002 .1472 21 GTCAGTGCTG GCGCACTGGC TCCAGGCGTG CAGAAGATCCA AAACATCCAA TACATTGTAA AAGGAAAGGC GCCTGCAAGG AAACCAGCCA GCTAGAATGA TACATTGTAA AAGGAAAGGC GCCTGCAAGG AAACCAGCCA GCTAGAATGA TACATTGTAA AAGGAAATGCT GGCTTGCT GGCTTGCT GGCTTGCT GGATGATGATAATGAATGAATGAATGAATGAATGAATG	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RCQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT AGGACTATGA AGGACTATGA AGGACTATGA AAGCTGAGA AATACTTAGA ATGCTCACAG ATGTTTCCT TAAACCATGA ATGTTTCCT TAAACCATGA ACAATGAT AGGAATCAG AAGTATAGATTAGA AAATTATTAC AAATTATTAC AAATTATTAC TTGAGGAACCC	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG AGTGTTGTAC TGATGCAAG ACAGATGCT TTACTATGAT TGAAGGAGGG TGAAGAGTTT TACGAAGTGTT TGCGATGCAAG CACGATTTT TCGCATTGTAC ATGTGCATTA AGAAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA AGAGGCAAA TTTAATAGCA	EDGWLIRIGY GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGGACTCTG ACCATTGGCA ATATTAGTTT GTTTCTCGAAG CGGATTATTC GATCTGGCTA GCTCTCTCTCAGC GCAAAAACAT TACAATGAGA ATGCTCCAT TTCAGGCGAA AACTTAAAGG ATGCTTCAGGCGAA AACTTAAAGG	60 120 180 240 300 420 480 560 780 840 960
50 55 60 65	DLHKKDAGMF WTTAVLALTC ARHGAWWENG ILLCALLALT TKLYCNLDKG LLVVVPLPAC TQALVTFTSS Seq ID NO: Nucleic Ac: Coding seq I GGCACGAGTA GTTCCTGGTC GCGACTGGCC CAGGCTCCTA GGAAGAACT TGAATTTGCT TGAATTTGCT ACCGGACCAA GTGTAATTAC TGATGACTCA AGCTTGGAGA TTGTTGGAGA TTGTTGGAGA TTGTTGGAGA ATCAGATAT TTACAACTTT TTCCATACCG ATTACCATC CAGACCAGCA CAGACCACA CAGACCACAC CAGACCACACA	QAQDERDLED NALVTSTVFR VGCHVIGFLS MAAVPLLGGS DLENIWDCSM LNFLLYLLFN SITYDLPPSS 29 DNA sequid Accession LNFLYLLFN GGGGTGGCGG CCTGGAGCTC CGGCCATGCCT CGGCCATGCCT TGACTATGGC TTGACTATGC TTGACTATTACC CTTGGTCATT TAGCCAGAAA TTACTCTGAT ACCTTCTTT AAGARGAAAT	FLLDFEEDLK SPLYISPIKL IPASESSVFL KYGASPLCLP VKHIALLLFT PHEKEDLVSL VPSPAYPVTE UCCCC #: NM_002 .1472 21 GTCAGTGCTG CGCACTTGGC TCCCGGGCTG CAGAAGATCC TCCATGACAG AAACATCCAA AAGGAAAGGCA AACATCCAA AAGGAAAGGCA AACCAGCCA AACCAGCCA GCTGAGATAT ATGTCTTCCTG GGACTTGCCTG GGACTTGACCAG GGACTGCCTG GGACTCGCTG GAATTGAATG CGACTTGACAGAATG CGACTTGACAGAATTC CTTGAGAGAAATG	ALHSVQCSPE LIGVIAAVNM LTLAALERGF LPPGEPSTMG NCILNCPVAF RKQTYVWIRS SCHLSSVAFV 497.1 31 CTCGGGGGCT GCGCAACCTG GCGCAACCTG GAGGATATGA AGGTGAGAA ACATCGTTCG TGGAATATTG AATACTTAGA ATGCTACAG AACTAGAT AACAATGATT GGAAAATCAG TTAAACCATGA TGTATAGATTC GGAAAATCAG CGAGGGGCACA	PGPFKPCEHL LTGVSSAVLA SVKYSAKFET YMVALILLNS LSFSSLINLT KHPSLMSINS PCL 41 TCTCCATCCA CGTGAGGCAG ACAGTGCTT TTACTATGAT TTACTATGAT TGAAGGAGGT GGAAGGAGTTTT ACGAAGTGTT TCGCATGCCA CACGAGTTTT TCGCATGCCA AGAGTGAT AGAAGGATTA AGAAGGCAAA AGAAGCAAA AGAAGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA AGAAGGCAAA ATTAGGAAGAG	LDGWLIRIGY GVDAFTFGSF KAPFSSLKVI LCFLMMTIAY FISPEVIKFI DDVEKQSCDS 51 GGTCCCTGGA CGCGACTCTG ACCATTGGCTA ATATTAGTTT GTTTCTGAAG GGTGGTCATA GGTGGCTA GGTGGTCATA GGTGGCTA GTCCTCGAC GGATATTCGACA GGATATTCGACA GGTGGTCATA TACAATAGAC TACAATAGAC TTCAGGCGAA AACTTAAAGG GATTTTGGTTG CCAGAAAAAT	540 600 720 780 840 120 120 300 360 360 480 540 660 720 840 900 900 900 1020
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	PVLSELKLKE	IQLQERERAL	KAREERLEQK	EQELCVRERL	AEDKLARAEN	LLKNYSLLKE	360
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	GTCTAACCAA	CCAAGTAATG	AAGGTGATGC	CATCAAAGTT	TTTGTGCGAA	TTCGTCCTCC	180
30					TGCTTATCTG TTCACGTTTG		240 300
50	AGATGTGGAT	ACCACTCAGG	AATCTGTATT	TGCAACTGTG	GCTAAAAGCA	TTGTGGAGTC	360
					CAGACTGGCT CATAACCTGA		420 480
2.5	CCCACGAAGT	TTTGAATATT	TGTTTTCCTT	AATTGATCGT	GAAAAAGAAA	AGGCTGGAGC	540
35	TGGAAAGAGT	TTCCTTTGTA	AGTGTTCCTT	TATTGAAATC	TACAACGAGC CATATCAAGA	AGATATATGA AGGGAGTCTT	600 660
	TGTTGTTGGT	GCGGTGGAGC	AGGTGGTAAC	CTCAGCTGCT	GAAGCCTATC	AGGTGCTGTC	720
	TGGAGGATGG	AGGAATAGAC	GTGTGGCATC	AACATCAATG	AACAGAGAAT AGTAATGAGA	CGTCTAGGTC	780 840
40	ACGGACCTCC	CTACTCAACC	TGGTGGATTT	AGCAGGATCT	GAAAGGCAAA	AAGATACCCA	900
	TGCAGAAGGG	ATGAGATTGA	AGGAAGCAGG	TAACATAAAT	CGATCATTGA CAGAGACATG	GCTGCCTGGG	960 1020
	AGACTCCAAA	CTTACCTTCT	TACTACGGGA	TTCCCTTGGA	GGTAATGCCA	AAACAGCCAT	1080
45	AATTGCAAAT	GTTCATCCTG	GATCCAGGTG	TTTTGGGGAA GGCAGTAGTA	ACCCTATCAA AATGAAGACA	CCCAAGGAAA	1140 1200
	TGTGAGCCAG	CTCCAAGCTG	AAGTGAAGAG	GCTCAAAGAA	CAACTGGCGG	AGCTTGCTTC	1260
	AGGACAGACA GTATTTCCAG	GAAGCAATGT	TATTCTTTAA	GAAATCTGAA	AAGAAGACTA CAGGAAAAGA	AGTCTCTGAT	1320 1380
50	AGAAAAAGTT	ACCCAATTAG	AAGACCTCAC	CCTCAAAAAG	GAAAAATTTA	TTCAATCTAA	1440
30	TAAAATGATT	GTGAAATTCC	GAGAGGATCA CTGAGGAGCA	GGATCGTTTG	TTGGAAAAGC CTCTCAGAAT	TAAGGAATGA	1500 1560
	GATTCAAACT	CTGCGAGAAC	AAATAGAGCA	CCACCCCAGA	GTTGCAAAGT	ATGCTATGGA	1620
	AAATCATTCC	CTCAGGGAGG GATGCCCAGA	AGAATAGAAG CCATTGCAAA	ACTGAGATTA ACTAGAAAAA	TTAGAGCCTG GCTTTCTCTG	AAATAAGTGG	1680 1740
55	CATGGAGAAA	AGTGACAAAA	ATCAGCAAGG	ATTTTCACCT	AAAGCTCAGA	AAGAGCCATG	1800
	TTTGTTTGCA	AACACTGAGA CAAGAATATG	AGTTAAAAGC AAGAATTCAA	ACAACTCCTG	CAAATTCAGA AGGAAAAGGC	AGCTAGAATT	1860 1920
	GGAATCAGAG	CTTCAGTCTT	TGCAAAAAGC	GAACCTTAAT	CTTGAAAACC	TTTTGGAAGC	1980
60	TANGATTATA	TGCAAGCGGC ACTACACCAA	AAGAAGTTTC	CCAACTTCAT	AAAATTCATG TCCCGACCAG	TACCAAAATT	2040 2100
	AAGCCCTGAA	ATGGGAAGCT	TTGGCTCTCT	ATACACTCAG	AATTCTAGCA	TATTAGATAA	2160
	TGATATATTA	AATGAGCCAG AGAACAGTGC	AGGAACAAAT	GATGAATGAA	CAAGCTTTTG CAAGCCAAAC	TGGATGAAGA	2220 2280
65	AGAGCATAAA	AACCTAAAGC	TTCAGCAGCA	TGTTGAÇAAA	. CTGGAACATC	ATTCTACCCA	2340
65						AAGAGCTTCT ATGACTTTTT	2400 2460
	GAAAAGTGAG	GTACATGACC	TGCGAGTAGT	CCTTCATTCT	GCTGACAAGG	AGCTTTCTTC	2520 2580
_						ACAAACTTTC ACGAAAAGCT	2640
70	GCTTGAGAGC	AAAGCCTGCC	TACAGGATTO	CTATGACAAC	TTACAAGAAA	TAATGAAATT	2700 2760
	ATCTGATCTC	AATAATTTGA	TGGAGCTTCT	TGAGGCAGAA	AAAGAACGCA	AAACTCTGAA ATAACAAATT	2820
	ATCATTACAG	TTTGAAGAAG	ATAAAGAAAA	CAGTTCTAAA	GAAATCTTAA	AAGTTCTTGA	2880 2940
75	ACAGAAACTA	GAAGAGAGCT	TGCTTGCTAC	TGAAAAAGTG	ATCAGTTCCC	TGGCAAAAGTC	3000
	TAGAGATTCT	GATAAGAAAG	TTGTAGCTGA	CCTCATGAAC	CAGATCCAGG	AGCTAAGAAC	3060 3120
	TTGCAAATAC	: AACTCTGCTT	TGGTTGACAC	AGAAGAGAG	: AGAGTGTTGA	AGGACATAAA TCAAGAAGCA	3120
80	GGAAGTGGAT	ATTCTGGATC	TGAAAGAAAC	CCTTAGGCTG	AGAATACTTT	CTGAGGACAT	3240 3300
6 0	AGAGGCCTC	AAAAAACACT	CGGGGCTGCT	GCAGTCTGCC	CAGGAAGAAC	ACATGCTCAC TGACCAAGAA	3360
	GGAAGCCCTC	ATTCAGGAAC	TTCAGCACA	GCTAAACCA	AAGAAAGAGG	AAGTAGAACA	3420 3480
	TGAGGATCC	CAGAGTCCTA	AGACACCACC	TCACTTTCA	ACACATTTGG	ATTCTGCTGC CAAAACTCCT	3540
85	GGAAACACA	A GAACAAGAG	TAGAAGATG	AAGAGCCTCT	r aagacttctt	TGGAACACCT	3600

	TGTAACAAAG	CTAAATGAAG	ACAGAGAAGT	CAAAAATGCT	GAAATCCTCA	gaatgaagga	3660
	GCAGTTGCGT	GAAATGGAAA	ACCTACGCCT	GGAAAGTCAG	CAGTTAATAG .	AGAAAAACTG	3720
		GGTCAGCTGG					3780
		CAACAGCTGA					3840
5							
5		GTTGAAGAAA					3900
		AAAGAGATGG					3960
	TTTGGAGTCT	AAAGCATTCC	AGGAAAAAGA	ACAACTGAGA	TCAAAGCTGG	AAGAAATGTA	4020
		GAGAGAACAT					4080
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10		AATGGAAAGT					
10	AGTGCGACTA	AAGAAGGAAA	ATGTCAGGCT	TGCTGAGGAG	ACAGAAAAGT	TGCGTGCCGA	4200
	AAATGTATTT	TTAAAAGAAA	AGAAAAGAAG	TGAATCTTGA	GGATTCCGGT	CAGCTACCTA	4260
		TGTTTGAAGA					4320
		TGAATTTATG					4380
	TTAGGAGAGC	TGAATTTATG	GACCITAATT	MIIMAMIGII	TATAAGGTGG	TGGTANCCAC	
4 -	CTCAAGTTTC	TGATGAACAT	TCTGCATCCA	TATACACCCT	GTGACAGTCA	GCAGTCTGCT	4440
15	ATTAAGTGGC	CTACTTCAAG	GCTTTGAATC	AACTTAAGGG	AAAACCTTTT	GTCTTTGTAA	4500
	AAATAAAAGC	CTGTAGCTAA	GGTTTACAGT	GGACATTAGC	CAGATCATTT	TCTTCTTAGA	4560
		ATCTCCTTTG					4620
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		GTTTAATGAC					
	GATTATTTTT	GTATTCTTAC	TTTAGGTATT	TTACTTGAGC	ATTTTCCATG	ACTGTAAATA	4740
20	AAGCCATTTT	TTAAGATAAA	ААААААААА	AAAAA			
	Com ID NO.	32 Protein	500010000				
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	MADGCKTRI.D	SVTNGQSNQP	SNEGDATKUT	VRIRPPAERS	GSADGEONLC	LSVLSSTSLR	60
	T WENDSDUMPS	TFDHVADVDT	TOPEUPATION	KSTVECOMEC	YNGTIRAYCO	TGSGKTETMM	120
							180
		NLRGVIPRSF					
20		IKKGVFVVGA					240
30		NEIVNIRTSL					300
	AT.VDVGNGKO	RHVCYRDSKL	TFLLRDSLGG	NAKTAIIANV	HPGSRCFGET	LSTLNFAQRA	360
	TT TOTAL	EDTQGNVSQL	OPERADI REO	TARTACCOTO	DESET.TENKK	KUNAMBABUB	420
	KUIKWKAVN	EDIQGRV3QD	Suparities A	VIIIONINGTI	VEDEDOTTEL	DAI BABGBGG	480
		EKKSLIEKVT					
~ ~		SELRNEIQTL					540
35	AOTIAKLEKA	PSEISGMEKS	DKNQQGFSPK	AQKEPCLFAN	TEKLKAQLLQ	iqtelnnskq	600
	EVEEFKELTE	KRQLELESEL	OSLOKANLNL	ENLLEATKAC	KROEVSOLNK	IHAETLKIIT	660
	TOTAL VOLUE	RPVPKLSPEM	GEEGEL VTON	SSTLONDILN	EDADDEMNEO	APEATSEELR	720
							780
	TVQEQMSALQ	AKLDEEEHKN	TYTYQUE	PUTPIONO	FOREKIDNIK	QQCCDD3QD0	
40		TKNDFLKSEV					840
40		LENEKLLESK					900
	NUMBILIEAEK	ERNNKLSLQF	EEDKENSSKE	ILKVLEAVRO	EKOKETAKCE	QQMAKVQKLE	960
	POLLATEVAL	SSLEKSRDSD	CKANADIMNO	TORTRYSVCE	KTETTOTIKO	ELKDINCKYN	1020
	ESULATARVI	OSUEKSKUOD	TOTAL AND THE	TI CERTERON	TODY NUMBER	OT MMT TENEY	1080
		AFIKKÕEADI					
4.5		EELTKKEALI					1140
45	SPKTPPHFQT	HLAKLLETQE	QEIEDGRASK	TSLEHLVTKL	NEDREVKNAE	ILRMKEQLRE	1200
	MENURLESOO	LIEKNWLLQG	OLDDIKROKE	NSDONHPDNO	OLKNEOEESI	KERLAKSKIV	1260
	PEMT.KMKADI.	EEVQSALYNK	EMECLEMENT	VERTOTLESK	AFORKEOLRS	KLEEMYEERE	1320
	DECORMENT D	KQVECLAEEN	CAL ACAOMI'A	OKTOVINDIK	KENUDI AEET	EKI DAENURI.	1380
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	AGAGACATTA	AAAATAAGTT	TAAAAATGAA	GACCTTACTG	ATGAACTAAG	CTTGAATAAA	120
	AGAGACATTA	AAAATAAGTT	TAAAAATGAA	GACCTTACTG	ATGAACTAAG	CTTGAATAAA	
	ATTTCTGCTG	AAAATAAGTT ATACTACAGA	TAAAAATGAA TAACTCGGGA	GACCTTACTG ACTGTTAACC	ATGAACTAAG AAATTATGAT	CTTGAATAAA GATGGCAAAC	120 180
60	ATTTCTGCTG AACCCAGAGG	AAAATAAGTT ATACTACAGA ACTGGTTGAG	TAAAAATGAA TAACTCGGGA TTTGTTGCTC	GACCTTACTG ACTGTTAACC AAACTAGAGA	ATGAACTAAG AAATTATGAT AAAACAGTGT	CTTGAATAAA GATGGCAAAC TCCGCTAAGT	120 180 240
60	ATTTCTGCTG AACCCAGAGG GATGCTCTTT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT	TAAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA	120 180 240 300
60	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG	AAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA	TAAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA	120 180 240 300 360
60	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA	TAAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAG	120 180 240 300 360 420
60	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA	TAAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAG	120 180 240 300 360
60	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT	TAAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC ATCTTTTGCA	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA	120 180 240 300 360 420
	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC ATCTTTTGCA AAAAGCTGTA	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGGAG	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGCAAA AGAAATGCTG	120 180 240 300 360 420 480 540
60 65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTGCCC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGGAATTT	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAAACCTCCAA	GACCTTACTG ACTGTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGGAG AAAAAGCAGC	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG	120 180 240 300 360 420 480 540
	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTGCCC AAGAATTTAT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GACTTTTGCT TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAACCTCAA GGTATTAACT	GACCTTACTG ACTOTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGGAG AAAAAGCAGG GCCCAAGAAT	ATGAACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTCCGG	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG	120 180 240 300 360 420 480 540 600 660
	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTTGCCC AAGAATTTAT CATTTACAGA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA ATTGTTCATAT TACTTCATAT TGCGGAATTT CAGCATCTAC ATAGGAACAA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTCGT GAGTTTTGCT TGCACGTGA ATCTTTTGCA AAAACCTGTA AAACCTCCAA AGGTATTAACT CAGTTGTGAT	GACCTTACTG ACTOTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAG CAATTTGAAC GAACGTGGAG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC	ATGAACTAGA ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGTCCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCCGG AGACTACTAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT	120 180 240 300 360 420 480 540 600 660 720
	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTTGCCC AAGAATTTAT CATTTACAGA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTCGT GAGTTTTGCT TGCACGTGA ATCTTTTGCA AAAACCTGTA AAACCTCCAA AGGTATTAACT CAGTTGTGAT	GACCTTACTG ACTOTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAG CAATTTGAAC GAACGTGGAG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC	ATGAACTAGA ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGTCCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCCGG AGACTACTAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT	120 180 240 300 360 420 480 540 600 660
65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTGCCC AAGAATTTATAT CATTTACAGA TTATATGGAG	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAAACCTCCAA GGTATTAACCT CAGTTGTGAT ACCACAAGAT ACCACAAGAT	GACCTTACTG ACTOTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGGAG AAAAAGCAGC GCCCAAGAAT TCCCAAGAGAC GCAAGAAT	ATGAACTAAG ANATTATGAT ANAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGG CAGTACCACT TGCTTTCAGA CATTTTCCGG AGACTACTAA GTTACCGGAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA	120 180 240 300 360 420 480 540 600 660 720
65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTGCCC AAGAATTTAT CATTTACAGA TTATATGGAG CAAACTAACA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC AAACTAAACA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCA ATCTTTTGCA AAAGCTGTA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT GTCATGCCA	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAACTGGAG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTTGGAAGAGAGT	ATGACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCCGG AGACTACTAA GTTACCGGAA TCCCAGTTAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TCCATTGAGA CCTTCTAAAAT	120 180 240 300 360 420 480 540 600 660 720 780 840
	ATTTCTGCTG AACCCAGGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTATC CATTTACAGA TTATATGAGA CAAACTAACA AGCCCAGATT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA ATGGTTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC AAACTAAACA GTGATGTGAA	TAAAATGAA TAACTCGGGG TTTGTTGCT GATTGGTCGT GCACGTGAC ACCTCGACA AAAAGCTGTA AAAACCTCCAA AAAACCTCCAA CGGTATTAACT CAGTTGTGAT ACCACAAGAT ACCACAAGAT GTCATGCACA GACAGATGAT	GACCTTACTG ACTOTTAACC ARACTAGGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGGAG AAAAGCAGG GCCCAAGACT TCCAGAGGAC TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGCCCAGAGC CAGTACCACT TGCTTTCAGA CATTTTCCGG AGACTACTAA GTTACCGGAA TCCCAGTTAA CCTGTTTTAT	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAC TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAGACAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCATG AAATTTGCT AAAAGTAAAC GAAATTTGCCC AAGAATTTACACA ATTATACAGA TTATATAGAG CAAACTAACA AGCCCAGATT ACCTCTAGAT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGGTCATAT AACTTCTTCA TGCGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC AAACTAAACA GTGATGGAA CAGAATGCCG	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTCGT GAGTTTTGCT TGCACGTGAA AAAGCTGTA AAAACCTCTA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT ACCACAAGAT ACACACAAGAT AGACTGTGAT AGACTTTGCCCA	GACCTTACTG ACTOTTAACC AAACTAGAGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTCGAG AAAAAGCAGC GCCCAAGAAT TCCACAGGAAT TCTCGAAGAG TTTTGGAAGAG TTTGGAAGAG GTGCTTGTAC GTGCCTGGAT	ATGAACTAAG ANATTATGAT ANANCAGTET CANTTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTTCCGG AGACTACTAAA GTTACCGGAA TCCCAGTTAA CTTGTTTTAT CTAAACCAAG	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TTAATGCAAA AGAATGCTAG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT TGAAAAGACAA TGGAAATGAT	120 180 240 300 360 420 480 540 660 720 780 840 900 960
65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTGCCC AAGAATTTACAA TTATATGAGA CAAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA ATAGGAATAT AGAATCAC ATAGGAACAA AGAACATGCC AAACTAAACA GTGATTGAA CAGAATGCT TAAGAAATTT	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCA ATCTTTTGCA AAAAGCTGTA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT GTCATGCCAA GGTATTAACT ACCACAAGAT ACACACAAGAT AGATTTGGTT AAAGTTTGGTT AAAGTCTGTT	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAACTGGAG GCCCAAGAAT TCCAGAGGAC GCAGAATAG TTTGGAAGAG TCAGTTGAAG GTGCCTGGAT CAAATAGTC	ATGACTAAG ANATTATGAT ANACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCAGA CATTTTCAGA GTTACCGGAA TCCCAGTTAA CTTGTTTTAT CTAAACCAAG ATTCCAAGG ATTCCAAGGA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAAGACAA TGGAAATGAT ACCTCTGGTG	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
65	ATTTCTGCTG AACCCAGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCT AAAAGTAAAC AAGAATTTAT CATTTACAGA TTATATGGAG CAACTAACA AGCCCAGATT ACCTCTAGAT TCCGTGTAAAT TCCAGTAAAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA TGGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC AAACTAAACA GTGATGTGAA CAGAATGCG TAAGAAATTT AGAGATTCTGA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCTAA AAACCTCTAA ACCTCCAA CGTATTAACT CAGTTGTGAT ACCACAAGAT GTCATGCCCA GACAGATGAT AGATTTGGTT AAAGTCTGTT AAAGTCTGTT AAAGTCTGTT ACTTATTATT	GACCTTACTG ACTGTTAACC ARACTAGGA TACAGTCAAG TACAGTCAAG TACTTCAAA CAATTTGAAC GAACGTGAGG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTCGAGAGGAC TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC GTGCTGGAT CAAAATAGTC ACTGATTCAA	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTCCGG AGACTACTAA GTTACCGGAA CTCGTTTTAC CTGATTACCGAA CTTGTTTTAT CTAAACCAAG ATTTCAAGA ATTTCAAGA ATTTCAAGA ATTTCAAGGA ATTCCAAGGA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAATGAT ACCTCTGGTG GAAATGAT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
65 70	ATTTCTGCTG AACCCAGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCT AAAAGTAAAC AAGAATTTAT CATTTACAGA TTATATGGAG CAACTAACA AGCCCAGATT ACCTCTAGAT TCCGTGTAAAT TCCAGTAAAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA TGGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC AAACTAAACA GTGATGTGAA CAGAATGCG TAAGAAATTT AGAGATTCTGA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCTAA AAACCTCTAA ACCTCCAA CGTATTAACT CAGTTGTGAT ACCACAAGAT GTCATGCCCA GACAGATGAT AGATTTGGTT AAAGTCTGTT AAAGTCTGTT AAAGTCTGTT ACTTATTATT	GACCTTACTG ACTGTTAACC ARACTAGGA TACAGTCAAG TACAGTCAAG TACTTCAAA CAATTTGAAC GAACGTGAGG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTCGAGAGGAC TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC GTGCTGGAT CAAAATAGTC ACTGATTCAA	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTCCGG AGACTACTAA GTTACCGGAA CTCGTTTTAC CTGATTACCGAA CTTGTTTTAT CTAAACCAAG ATTTCAAGA ATTTCAAGA ATTTCAAGA ATTTCAAGGA ATTCCAAGGA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAATGAT ACCTCTGGTG GAAATGAT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
65 70	ATTTCTGCTG AACCCABAGE GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAGAATTTAC CATTTACAGA TTATATGGAG CAAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT TCAGATGAAA CAGATCAAAA GAATCAAGA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA ATGGTTCATAT TAACTTCTTCA TGCGGAATTAT CAGCATCTAC ATAGGAACAA AGAACATGAC AAACTAACC AAACTAACC AAACTAACC TAAGAAATTC TAGGAATTT CAGCATTCAC AAACTAACC AAACTAACC TAAGAAATTT AGAGTTCTGA	TAAAATGAA TAACTCGGGG TTTGCTC GATTGCTC GAGTTTTGCT TGCACGTGAC AAAAGCTGTA AAAACCTCCAA AGGTATTAACT CAGTTGTGAT ACCACAAGAT ACCACAAGAT ACCACAAGAT ACACACAGTTATTACT AAAGTTGTTATACT AAAGTTTGTTAACT AAAGTTTGTTAACT ACTTATTATT ACTTATTATT	GACCTTACTG ACTOTTAACC ARACTAGGA TACAGTCAAG TACAGTCAAG TACTTCAAA CAATTTGAAC GAACGTGGAG AAAAAGCAGC GCCAAGAAT TCCAGAGGAC TTCGAAGAG TTTGGAAGAG TTAGGAAGAG TCAGTTGTAC GTGCTGGAT ACTGATTGA ACTAAAGAGT	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGCCCAGAGC CAGTACCACT TGCTTTCAGA CATTTCCGG AGACTACTAA TCCCAGTTAA CTTACCAGTTAA CTTATTTTAT CTAAACCAAG ATTTCAAGGA ATTACACGAAA ATCAAGAAC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAAGACAA TGGAAATGATA ACCTCTGGTG AGCAGATTAAC AGAGGTTCCA AGAGGTTCCA	120 180 240 360 420 480 660 720 780 840 900 960 1020 1140
65	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTTGCCC AAGAATTTACAG TTATAATGAG CAACTAACA AGCCCAGATT ACCTCAGAT TCCTGTGAAT TCCTGTGAAT TCAGATGAAC GAATCAAGTC GAGAGTAACC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGAATGA TTGTTCATAT AACTTCTTCA ATAGGAACTA AGAACAATGCC AAACTAACA GTGATTGAACA GTGATTGAA CAGAATGCC TAAGAAATTT AGGATATT AGGATTCTGA TTGTTCTAGCTAA ATTCTGACTAA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCA ATCTTTTGCA AAAAGCTGTA AAACCTGTA AGGTATTAACT CAGTTGTGAT GCCAAAGAT GTCATGCCA GACAGATGAT AGATTTGGTT ACTTATATT ATTAGAAGAA AGCAATTTAACT ACTTATATAT ATTAGAAGAA GCAATTTAAG	GACCTTACTG ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAACTGAGG GCCCAAGAAT TCCAGAGGAC GCAGAATAGAGG TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC GTGCCTGGAT CAAAATAGTC ACTGATTCAA ACTAAAGAGT AGAAACTCAG	ATGACTAAG AAATTATGAT AAAACAGTGT CAATTGAAGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCAGA CATTTTCAGA CATTTTCAGA CATTTTCAGA TCCCAGTTAA TCCAGTAA ATCAAGG ATTCCAGGA ATTTCAAGGA ATTTCAAGGA ATCAAGAAC ATGAACAAG ATTATAAACAAG ATTATAAACAAG ATTATAAAACA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTAAA AGAAATGCTAA TCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAAGACAA TGGAAATGAT ACCTCTGGTG GAATAAAAC ACCTCTGGTG GAATAAAAC AGAGGTTCCA CCAGAATCCT	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020 1080 1140 1200
65 70	ATTTCTGCTG AACCCAGGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC AAGAATTGCCC AAGAATTTAC CATTTACAGA TTATATGGAG CAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT TCAGATCAAA GAATCAAGA GAATCAAGA GAATCAAGA GAATCAAGA GAATCAAGA GAATCAAGA GAATCAAGA GAATCAAGA GAGTAACC GCTGCATCTT	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGGGAATTA CAGGAACTAC ATAGGAACAA GGAACATGCC AAACTAAACA GTGATGTGAA CAGAATGCCG TAAGAAATTT AGAGTTCTGA TTCTAGCAAA AGAAACAGTG CAAATCACTG	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAAGCTGTA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT ACCACAAGAT ACACACAGAT ACACTCCAA GACAGTTGGTT AAAGTCTGTT AAAGTCTGTT AAAGTCTGTT ATTAGAGAA GCAATCTAAG GCAGATTCCG	GACCTTACTE ACTGTTAACC ARACTAGGA TACAGTCAAG TACAGTCAAG TACATTCAAG CAACTGGAG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC GCAGAAATAG TTCAGAGGAC TCAGTTGAAG TTCAGAAGAG TCAGTTGAAC TCAGATTACAA ACTAAAGAGT ACTAAAGAGT AAAAGTCAG GAGTTAGCCC	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA GATTACCGA AGTACCAGT TCCTTTAT CTAAACCAAG ATTTCAGA ATTTCAGA ATTTCAGA ATTTCAGA ATTCAAGAA ATCAAGAACC AGTGATATAA AGGAAAGTTAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAAGACAA TGGAAATGAT ACCTCTGGTG GAATAAACG AAGGGTTCCA ACAGGTTCCA ACAGGTTCCA ACAGGTTCCA ACAGGTTCCA ACAGGTTCCA ACAGGTTCCA TACAGAGCAG	120 180 240 300 420 420 600 660 720 780 840 900 1020 1080 1140 1260
65 70	ATTTCTGCTG AACCCABGEG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAGAATTTAT CATTTACAGA TTATATGGAG CAAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT TCAGATGAAA GAATCAAGT GAGAGTAAC GAGAGTAACCG GCTGCAACTA AACCACCAACA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA TGCGAAATTA ATAGGAACAA AGAACATGCC AAACTAAACA GTGATTGTGAA CAGAATTGTA AGAGATTCTGAA TTCTAGCAATTCTC AAACTAAACA GTGATTCTGAA CAGAATCACT AGAATCACT AGAATCACT CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CATTTTGAGCA	TAAAATGAA TAACTCGGGG TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAAGCTGTA AAAACTCCAA AGGTATTAACT CAGTTGTGAT ACCACAAGAT ACCACAAGAT AGATTTGGT AAAGTCTGTT AAAGTCTGTT AAAGTCTGTT AAAGTCTGTT AATTTAGT ACTTATTATT ACTTATTATT ATTAGAAGAA GCAATCTAAG GCAGATTCAG	GACCTTACTG ACTOTTAACC ARACTAGGA TACAGTCAAG TACAGTCAAG TACTTCAAA CAATTGAAC GAACGTGGAG TTCCAGAGGAC TCCAGAGGAC TCCAGAGGAC TCAGAGAGAT TCGAAGAGA TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGATTGAA ACTAAAGAGT ACTAAAGAGT AGAAAGTCAG GAGTTACAG GGATTACAG TCAGATTCAGA ACTAAAGAGT ACGAAAGTCAGG GAGTTACAG	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC CAGTACCACT TGCTTTCAGA CATTTTCAGA ATCACGGTAA CTTGTTTACCGGAAC ACTTTTACCGAAC ATCACAGAAC ATTTCAAGA ATCAAGAACC AGTATAAACCAAG ATTACAGAAACTCACC AGAAAAGTTAAA AAAAGTTAAC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GCAGGAAAT TTCACTTGAGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAATGAT GAAAATGAT GAAAATGAT GAAAATGAT ACCTTCTGAT ACCTCTGTGT ACAAACAC AGAGGTTCCA CCAGAATCCT TACAGAGCCAG ACCAAATATCA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1260 1320
65 70	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTTGCCC AAGAATTTACAG TTATTACAGA TTATTATGAG CAAACTAACA AGCCCAGATT TCCTGTGAAT TCCTGTGAAT TCAGATCAAA GAATCAAGTC GAGAGTAACC GCTGCATCTT AAACATACCA AACATACCA AACATACAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGAATGA TTGTTCATAT AACTTCTTCA ATAGGAACAT CAGCATCTAC ATAGGAACAT GCGAACTTAC ATAGGAACAT GTGATCTGAA CAGAATGCC TAAGAATGTC TAAGATTCTGA TTCTGCTAA TTCTAGCTAA CAGAATCCTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CGTTTTGAGCAC GGTTTGAGCAC	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTCGT GAGTTTTGCA TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAAACCTGTA GGTATTAACT CAGTTGTGAT GCACAAGAT GTCATGCCCA GACAGATGAT AGATTTGGTT ACTTATATT ATTAGAAGAA GCAATTTAGT ATTAGAAGAA GCAGATTCCG ACCTGTCTTAAA	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAATTTGAAC GAACGTGAAG GCCCAAGAAT TCCAGAGGAC TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC CAGTTTGAA ACTAAAGAGT AGAAATTCAG GGGGTAACACC CAGTTTCAA TGATTCAG TCAGTTTCAA TGATTCAG TCAGTTTCAA	ATGACTAAG AAATTATGAT AAACAGTGT CAATTGAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCAGA GTTACCGGAA TCCCAGTTAA CCTGATTAA ATCAAGGA ATTCAAGGA ATCAAGGAA ATCAAGGAA ATCAAGGAA ATCAAGGAA CGTGATTATAA CAAGTAAC CAAGCAGCACAA	CTTGAATAAA GATGGCAAAA TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GCAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAAGACAA TGGAAATGAT ACCTCTGGTG GAATAAAAC AGAATAAAC AGAGGTTCCA CCAGAATCCT TACAGAGGCA TACCATAATCA TACCTTGGAT	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1260 1320
65 70 75	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC GAAATTTGCCC AAGAATTTACAG TTATTACAGA TTATTATGAG CAAACTAACA AGCCCAGATT TCCTGTGAAT TCCTGTGAAT TCAGATCAAA GAATCAAGTC GAGAGTAACC GCTGCATCTT AAACATACCA AACATACCA AACATACAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGAATGA TTGTTCATAT AACTTCTTCA ATAGGAACAT CAGCATCTAC ATAGGAACAT GCGAACTTAC ATAGGAACAT GTGATCTGAA CAGAATGCC TAAGAATGTC TAAGATTCTGA TTCTGCTAA TTCTAGCTAA CAGAATCCTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CAAATCACTG CGTTTTGAGCAC GGTTTGAGCAC	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTCGT GAGTTTTGCA TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAAACCTGTA GGTATTAACT CAGTTGTGAT GCACAAGAT GTCATGCCCA GACAGATGAT AGATTTGGTT ACTTATATT ATTAGAAGAA GCAATTTAGT ATTAGAAGAA GCAGATTCCG ACCTGTCTTAAA	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAATTTGAAC GAACGTGAAG GCCCAAGAAT TCCAGAGGAC TTTGGAAGAG TTTGGAAGAG TCAGTTGTAC CAGTTTGAA ACTAAAGAGT AGAAATTCAG GGGGTAACACC CAGTTTCAA TGATTCAG TCAGTTTCAA TGATTCAG TCAGTTTCAA	ATGACTAAG AAATTATGAT AAACAGTGT CAATTGAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCAGA GTTACCGGAA TCCCAGTTAA CCTGATTAA ATCAAGGA ATTCAAGGA ATCAAGGAA ATCAAGGAA ATCAAGGAA ATCAAGGAA CGTGATTATAA CAAGTAAC CAAGCAGCACAA	CTTGAATAAA GATGGCAAAA TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GCAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAT GAAAAGACAA TGGAAATGAT ACCTCTGGTG GAATAAAAC AGAATAAAC AGAGGTTCCA CCAGAATCCT TACAGAGGCA TACCATAATCA TACCTTGGAT	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1200 1260 1320
65 70 75	ATTTCTGCTG AACCCAGAGG GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC AAGAATTGCCC AGAAATTGCCC AGAAATTACAGA TTATATGGAG CAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT TCAGATCAAA GAATCAAAC GAAGAGTAACC GCTGCATCTT AAACATACCA ACATCTAAAT GATTACATGA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA TGGGAATTT CAGCATCTAC ATAGGAACAA AGAACATGCC ATAGTACAC GTGATGTGAA TAGGAACATC CAGAATCCGG TTAGGAAATT AGAGTTCTGA TTCTAGCTAA AGAACAGTG CAAATCACTG CAAATCACTG CTTTTCAGCA GTTTTCAGCA GTGTTTTAG	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC ATCTTTTGCA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAGAT ACCACAGAT ACCACAGAT ACACAGAT ACATTGGTT ACTTATTGTT ACTTATTATT ATTAGAGAA GCAATCTAAG GCAGATCCG ACCTGTCTTT AAAATCTATT AAAATCTATT AAAATCTATT AAAATCTATT AAACTCCAGTT	GACCTTACTE ACTGTTAACC ARACTAGGA TACAGTCAAG AGAATTCAAG TACATTGAAC GAACGTGGAG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTTGGAAGAG TTAGATTGAAC ACTGATTCAA ACTAAAGAGT ACTAAAGAGT AGAAAGTCAG GGGTTAGCC TCAGTTTCAA ACTAAAGAGT GGGTTAGCCC TCAGTTTCAA TGTAAGACAC GGTAAAGACCC	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAC TGAGATTTGC TGGCCAGAGC TGTCACAAGG AGATTACCAGA TGCTTTCAGA ATTACCAGAA TCCCAGTTAA CTTATTACCAGA ATTACCAGAA TCCCAGTTAA CTTATTAT CTAAACCAAG ATTTCAAGAA ATTACAAGAACC AGTGTATTAA GARAAGTTAA AACAGTCACC CAAGCAGCAA ACTTTCCACC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAC TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAAGACAA TGGAAATGAC ACCTCTGGTG GAATAAACG ACAGGTTCCA ACAGGTTCCA TACAGAGCAC TACAGAGCAC TACAGAGCAC TACCTTGGAT TACAGAGCAC TACCTTGGAT TGCTTGTCAG	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1380
65 70	ATTTCTGCTG AACCCAGGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAACTAACA TTATATGAGA TTATATGAGA TTATATGAGA TCCTGTGAAT TCCAGTGAAT TCAGTAGAA GCACAGAT ACGCTGCATCT AACCACAC GCTGCATCT AACCACAC ACATCACAC ACATC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA ATAGGAACTA AGAACATGAC AAACTAAACA GTGATCTGAA CAGAATGAC TAGGAACTAC CAGAATGCC TAAGAACAT CAGAATCACC CTATTGACA CAGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTTTTGACCA CTTTTGACCA CTTTTGACCA CTTTTTGACCA CGCTGTTTTGACCC CTTTTGACCA	TAAAATGAA TAACTCGGGG GATTGTGCT GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCCAA AAACCTCCAA CGTATTACT CAGTTGTGAT ACCACAAGAT GCATTGGT ACAGATGAT ACATTACT ACTTATTATT ATTAGAAGAA GCAATCTAAG GCAGATCCAG ACCTGTTTT AAAATCTATT AACTCCATT AAAATCTATT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT AACTCCAGT ACTGCCTGT	GACCTTACTG ACTOTTAACC ARACTAGGA TACAGTCAAG AGAATTCAAG TACTTTCAAA CAATTTGAAC GAACGTGAGG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTCGAGAGAG TTGGAAGAG TCAGTTGTAC GTGCTGGAT ACTAAAGAGT CAAAATAGT CAAAATAGT ACTAAAGAGT TCAGTTCAA TGTAAGACAC TCAGTTTCAA TGTAAGACAC TCAGTTTCAA TGTAAGACAC TCAGTTTCAA	ATGAACTAAG ANATTATGAT ANAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG AGATTACCGAA ACTACCAGT ACCAGTTACCGAA ACTACCAGT ATTACCGGAA ACTACCAGT ATCAAACCAAG ATTCAAGA ATTCAAGAA ACTATTACAGAA ACAGTACACC AACAGCAACAA ACTTTCACC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGT CCTTCTAAAAT GAAAATGAT ACCTCTGGTG GAATAAAACG AGAGGTTCCA CCAGAATCCT TACCAGAGCAG ACCATATCA TACCTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGGAT ACCTTTGTAAT ACCTTTGTAAT ACATTTGCCT	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1440 1500
65 70 75	ATTTCTGCTG AACCCAGGG GATGCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAACTAACA TTATACAGA TTATACAGA TTATACAGA TCAGATCAAAC AGCCCAGATT ACCTCTAGAT TCAGATCAAAC GAAACTAACA GAATCAAGT CAGATCAACA GAACTAACA GAACTAACA CACACCACAT AAACATACCA CACTCTAGAT AAACATACCA CACTCTAGAT AAACATACCA CACTCCACTTC AATCCAACTAAAT CATTCCAACTACA CACTCCACTTC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGAATGA TTGTTCATAT AACTTCTCA ATAGGAACAT CAGCATCTAC ATAGGAACAT GGATCTAC ATAGGAACAT GTGATTGAA CAGAATGCC TAAGAATGCC TAAGAATTCT AGAGTTCTGA ATTCTAGCTAA AGAAACATGC CAAATCACTG CAAATCACTG CATTTTGAGCCA GTTTTTGAGCCA GGTTTTTAGCCA AGATTTTAGCCA AGATTTTAGCCA AGAATTTACA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGTGCTC GATTGTGCT TGCACGTGAC ATCTTTTGCA AAAAGCTGTA AAACCTCCAA GGTATTAACT CAGTTGTGAT GCCACAAGAT GTCATGCCCA GACAGATGAT AGATTTGGTT ACTTATATT ATTAGAAGAA GCAATCTAAG GCAGATTCCG ACCTGTCTTT AAAATCTATAT TAAAATCTATT AAAATCTATT AAAATCTATT AAACTCCAGTT ACCTGCCTTT ACCTGCCTTT ACCTGCCTTT ACCTGCCTTT ACCTGCCTTTGT ACCTGCCTTTGT ACCTGCCTTTGT ACCTGCCTTTGT ACCTGCCTTTGT ACCTGCCTTTGT ACCTGCCTTTGT GGTTTTAGCA	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG CAATTTGAAC CAATTTGAAC CAACCTGGAG GCCCAAGAAT TCCAGAGGAC TTTGGAAGAG TTTGCAGAGAG TTAGTTGAA CAGTTGAG GTGCTGGAT ACTGATTCAA ACTAAAGAGT AGAAATCAG TGAGTTCAG TGAGTTCAG TGAGTTCAG TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TGTAAAGACT TTCAGCTTCTAG	ATGACTAAG AAATTATGAT AAAACAGTGT CAATTGAGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTTCAGA CATTTTCAGA CATTTTCAGA CATTTTCAGA ATCACAGT TCACAGGTAA ATCAAGGAACAAAACCAAGA ATTACAAGGAACAAAAACTCAAC ACTTTCCACC AACAGCAATAC ACTTCCACC AACAGCAATAC CAAATGAATG	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTAA AGAAATGCTAA TCACTTGGG AGCCAGGTTT TCATTGAGA CCTTCTAAAT GAAAAGACAA AGCAATATCA ACCTCTGGTG GAATAAACCA CCAGAATCCT TACAGAGCAG ACCAATATCA TACCTTGGTA TACCTTGGTA AAACTTGCA AATACTTGCC CATTTCGGTT CATTCGGTT CCATTTCGGTT CCATTTCGGTT CCATTTCGGTT CCATTTCGGTT CCATTTCGGTT CCATTTCGGTT	120 180 240 300 360 420 540 600 720 780 900 960 1020 1140 1260 1320 1380 1440 1560
65 70 75	ATTTCTGCTG AACCCAGGGG GATGCTTT GATAAATATG GCTATTCAAG AAATTGCTC AAAAGTAAAC AAGAATTGCCC AGAAATTGCCC AGAAATTACAGA TTATATGGAG CAACTAACA AGCCCAGATT ACCTCTAGAT TCAGTGAAT TCAGTGAAAT GAGTAACA ACACTCAAAT GATGAACA ACATCTAAAT GATTACAGA TTGCTCACTCT AAACATACAA ACTCCACTCC	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTTCA ATGGGAATTT CAGCATCTAC ATAGGAACAA GGAACATGCC AAACTAACA GTGATGTGAA TAGGAACATCC TAGGAAACTC TAGGAACATCC TAGGAACATCC CAGATTCTGA TTTTTTCAGCCA GGTTTTAGCAA GGTTTTAGCCA CTTTTTAGCCA CTTTTTAGCCA CTTTTTAGCCA CTTTTTAGCCA CTTTTTAGCCA TTTTTTTAGCCA TTTTTTTAGCCA TTTTTTTAGCCA TTTTTTTAGCCA TTTTTTTCAT	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GACTTTTGCA ATCTTTTGCA AAACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT GTCATGGCCA GACAGATGAT ACTATTGGTT ACTTATTATT ATTAGAAGAA GCAATCTTAG GCAGATCCGT ACCTGTCTT AAATCTATT AAATCTATT AACTCCAGTT AACTCCAGTT AACTCCAGTT ACCTGCTGT ACCTGCTGT ACCTGCCTGT ACCTGCCTGT ACCTGCCTGT ACCTGCCTGT TTTAAAGCAG TTTAAACTAT TTAAACTAT TTTAAACTAT TTAAACTAT TTAAATTAT TTAAATTAT TTAATTAT TTAATTAT TTAATTAT TTAATTAT TTAATTAT TTAATTAT TTAATTAT TTAATTAT T	GACCTTACTE ACTGTTAACC ARACTAGAGA TACAGTCAAG AGAATTCAAG TACATTGAAC CAACTGGAG AAAAGCAGC GCCCAAGAAT TCCAGAGAAC TCAGATTGAAC GTAGATTGAAC ACTAATAGTC ACTAATAGTC ACTAATAGTC ACTAATAGTC TCAGATTCAA ACTAAAGAGT AGAAAGTCAG GAGTTAGCC TCAGTTTCAA TGTAAGACAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGTTTCAC TTCAGCAGC TCTTCTTCTCAG TTCTTCTTCAG TTCAGGAACTC	ATGACTAAG ANATTATGAT ANACAGTGT CAATTGAGC TGAGATTTGC TGGCCAGAGC TGTCACAAGG CAGTACCACT TGCTTCAGA ATTACCGGA ATCCAGTAC TCAGTACTAAA CTTGTTTAT CTAAACCAG ATTACAGAA ATCAAGAACC AGGTATATAA AACAGTCACC CAAGCAGCAA ACTTTCCACC AACAGCATCAC ACAGCATCAC ACAGCATCAC ACAGCATCACC CAACAGCATCAC ACAGCATCAC ACAGCATCAC ACAGCATCAC ACAGCATCAC ACAGCATCAC ACAGCATCAC CAACAGCATCAC CAACAGCATCACAC CAACAGCATCACAC CAACAGCATCACAC	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GCAGGAAAAG TTCACTTGGG AGCCAGGTTT TCCATTGAGA CCTTCTAAAA TGGAAATGAA TGGAAATGAA TGGAAATGAA TCCCTTGGTG GAATAAACG AAAGGTTCCA TACAGAGCAG TCCAGAATCCT TACAGAGCAG TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGTTCAGA TACCTTTGTCAG AATACTTCCC CATTTCCGGTT CAAGGTATTT	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1440 1500 1500
65 70 75	ATTTCTGCTG AACCCAGGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAATTATC ATTATATGAGA TTATATGAGA TTATATGAGA TTATATGAGA TTATATGAGA TCCTGTGAAT TCAGTAGAA GAATCAAC GCTGCATCTT AACATACCA ACATCAAC ACAGAAGAAC ACAGCACT AAAGGAAC ACAGGAGTTAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA ATGGGAACTA AGAACATGC AAACTAAACA GTGATGTGAA CAGAATGCG TAAGAAATTT AGAGTTCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTTTTGAGCA CTTTTTGAGCA CTTTTTGACCA AAATTTACCAT ATGAAAAGAA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCCAA AAACCTCCAA ACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT ACACACAAGAT ACACACAAGAT ACACACAAGAT ACTCTAT ACTTATATT ATTAGAAGAA GCAATTCAGG GCAGATTCAG GCAGATTCAG ACCTGCTTT AACTCCAGTT AACTCCAGTT ACCTGCTGT ACCTGCT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCT ACCTCT ACCTGCT ACC	GACCTTACTE ACTGTTAACE ACTGTTAACE ARACTAGGA TACAGTCAAG TACAGTCAAG TACATTCAAA CAATTGAAC GAACGTGAGG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTCGAGAGGAC TCAGTTGTAC GTGCTGGAT ACTAAATAGTC ACTAATCAA ACTAAAGAGT TCAGATTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCTAGTACCC TCAGTTTCAA TGTAAGAAGT TCTAGGAAGT TTCCAGCAGC TCTTCTAGGAGC TTCTTCTAGG TTCTTCTAGGAGT TTCTTCTTAGGAGT TTCTTTAGGAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTTTAGGAAGT TTCTTTTAGGAAGT TTCTTTAGGAAGT TTCTTTAGGAAGT TTTTTTAGGAAGT TTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTT	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAC CAGTACCACT TGCCACAAG CAGTACCACT TGCTTTCAGA CATTTCCGG AGACTACTAA CTTACCGGAA CTTACCGGAA CTTACCGGAA CTTACCGGAA CTTACCGGAA CTTACCGGAA CTTACCGGAA ATCAAGAACCAGAA ATCAAGAACCA AGGATACTAA AACAGTCACC CAAGCAGCAA ACCTCCACC AACAGCATCA CAAATGAATCA CAAATGAATCA CAAATGAATCA CAAATGAATCA CAAATGAATCA AACGGTTCAAC AACGGTTCAAG ATGTGAACTTA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAATGATA ACCTCTGGTG GAATAAAACG AGAGGTTCCA ACCAGAATCCT TACCAGAGCAG ACCAGAATCCT TACCTTGGAG ACCATTTCCT TACAGAGCAG ACCATTTCCT CAAGAGTATTC CAAGAGTATTC CAAGAGTATTT CAAGAGAACCA	120 180 240 300 360 480 540 660 720 780 960 1080 1140 1260 1380 1560 1560 1680
65 70 75 80	ATTTCTGCTG AACCCAGGGG GATGCTGTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAATTATC ATTATATGAGA TTATATGAGA TTATATGAGA TTATATGAGA TTATATGAGA TCCTGTGAAT TCAGTAGAA GAATCAAC GCTGCATCTT AACATACCA ACATCAAC ACAGAAGAAC ACAGCACT AAAGGAAC ACAGGAGTTAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA ATGGGAACTA AGAACATGC AAACTAAACA GTGATGTGAA CAGAATGCG TAAGAAATTT AGAGTTCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTGATCTGA CTTTTGAGCA CTTTTTGAGCA CTTTTTGACCA AAATTTACCAT ATGAAAAGAA	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCCAA AAACCTCCAA ACCTCCAA GGTATTAACT CAGTTGTGAT ACCACAAGAT ACACACAAGAT ACACACAAGAT ACACACAAGAT ACTCTAT ACTTATATT ATTAGAAGAA GCAATTCAGG GCAGATTCAG GCAGATTCAG ACCTGCTTT AACTCCAGTT AACTCCAGTT ACCTGCTGT ACCTGCT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCTGT ACCTGCT ACCTCT ACCTGCT ACC	GACCTTACTE ACTGTTAACE ACTGTTAACE ARACTAGGA TACAGTCAAG TACAGTCAAG TACATTCAAA CAATTGAAC GAACGTGAGG AAAAAGCAGC GCCCAAGAAT TCCAGAGGAC TTCGAGAGGAC TCAGTTGTAC GTGCTGGAT ACTAAATAGTC ACTAATCAA ACTAAAGAGT TCAGATTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCAGTTTCAA TGTAAGAGT TCTAGTACCC TCAGTTTCAA TGTAAGAAGT TCTAGGAAGT TTCCAGCAGC TCTTCTAGGAGC TTCTTCTAGG TTCTTCTAGGAGT TTCTTCTTAGGAGT TTCTTTAGGAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTTAGGAAGT TTCTTAGGAAGT TTCTTTAGGAAGT TTCTTTTAGGAAGT TTCTTTTAGGAAGT TTCTTTAGGAAGT TTCTTTAGGAAGT TTTTTTAGGAAGT TTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTAGGAAGT TTTTTTAGGAAGT TTTTTTTT	ATGAACTAAG ANATTATGAT ANANCAGTGT CAATTGAAC CAGTACCACT TGCCACAAG CAGTACCACT TGCTTTCAGA CATTTCCGG AGACTACTAA CTTACCGGAA CTTGCTTTAT CTAAACCAGA ATTCAAGAA ATTCAAGAA ATTCAAGAA ATCAGGAA ACAGCATCAC AACAGCATCA CAAATCAACA ACTTCCACC AACAGCATCA CAAATCAAAT	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAG TAATGTCAAA AGAAATGCTG GGAGGAAAAG TTCACTTGGG AGCCAGGTTT TTCATTGAGA CCTTCTAAAAT GAAAATGATA ACCTCTGGTG GAATAAAACG AGAGGTTCCA ACCAGAATCCT TACCAGAGCAG ACCAGAATCCT TACCTTGGAG ACCATTTCCT TACAGAGCAG ACCATTTCCT CAAGAGTATTC CAAGAGTATTC CAAGAGTATTT CAAGAGAACCA	120 180 240 300 360 420 540 660 720 780 960 1080 1140 1260 1380 1560 1560 1680
65 70 75	ATTTCTGCTG AACCCABAGE GATGCTCTTT GATAAATATG GCTATTCAAG AAATTTGCTT AAAAGTAAAC CAAACTAACA TTATATGGAG CAAACTAACA AGCCCAGATT ACCTCTAGAT TCCTGTGAAT TCAGATGAAA GAATCAACA GAACTAACA AGAATTACAGA TTATATGGAG ACCTCTAGAT ACCTCTAGAT ACATCAAAT GAATCAACAC ACACCTCAACTC AACACACACAC ACTCCACTTC AAAGGAACAA CAGTGTTAA	AAAATAAGTT ATACTACAGA ACTGGTTGAG TAAATAAATT GCCAAAATGA AGCCAGATGA TTGTTCATAT AACTTCTCA ATAGGAACAA AGAACATGAC AAACTAAACA GTGATTCTGAA TCTGGCAAATTTCAGCATTCTGAAATCAA CAGAATGCCG TAAGAAATTTCTAGCTAA AGAACAGTG CATTTGAGCA CTTTTGAGCA CTTTTTGAGCA AAAATTATCAA TTTTTTTTTT	TAAAATGAA TAACTCGGGA TTTGTTGCTC GATTGGTCGT GAGTTTTGCT TGCACGTGAC AAAACCTCCAA AAAACCTCCAA ACCTCCAA CAGTTGTGAT ACCACAAGAT ACCACAAGAT AGATTTGGT AAAACTCGTA AGATTTGGT AAAATCTGTT ATTAGAAGAA GCAATTTAACT ACTGATTTACT AAAATCTATT AAAATCTATT AACTCCAGTT AAAATCTATT ACTGCCTGT GGTTTTAGCA TTTAAAAGCAA TTTAAAAGCAA TTTAAAAGCAA TTTAAAAGCAA TTTAAAAGCAA TTTAAAAGCAA	GACCTTACTG ACTOTTAACC ACACTCAAG AGAATTCAAG TACTTCAAA AGAATTGAAC GAACGTGGAG TTCCAGAGGAC TCCAGAGGAC TCAGAGAATTAGAC GAGAAATAGCAG TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGAGAGAC TCAGATTCAA ACTAAAGAGT AGAAACTCAG GAGATTAGAC TCAGAGAGC TCAGATTCAA TGTAAGACT TCAGAGAGC TCAGTTTCAA TGTAAGAACT TTCAGCAGC TCAGTTTCAA TGTAAGAACT TTCAGCAGC TCAGTTTCAAC TTCAGCAGC TTCAGCAGC TTCAGTTCAAC TTCAGCAGC TTCAGCAGC TCTCTTCAGCAGC TTCAGCAGC TCTTCTTCAGC TTCAGCAGC TCTTCTTCAGC TTCAGCAGC TCTTCTTCAGC TTCAGCAGC TCTTCTTCAGC TTCAGCAGC TCTTCTTCAGC TCTTTCTTCAGC TCTTTCTTCAGC TCTTCTTCAGC TCTTCTTCAGC TCTTTCAGC TCTTTCTTCAGC TCTTTCAGC TCTT	ATGAACTAAG ANATTATGAT ANAACAGTGT CAATTGAAGC TGAGATTTGC TGGCCAGAGC TGTTCACAAGG AGATTTCAGA ACATTTCAGA ACTTACCGATA ATCAGATTAAC ATTTCAGA ATTTCAGA ATTTCAGA ATTTCAGA ATTTCAGA ATTACAGAAA ATAACATAAA AACAGTAACC CAAGCAGCAA ACTTTCCAGG CAACAGCATCA CAATGAATGA ATGAATGAATGA ACTTCACC AACAGCATCA CAATGAATGA ATGAATGAATGA ATTTCAAGT ATTTCAAGT ACTTCACC AACAGCATCA CAATGAATGA ATGTGAACTT ATTTGAATAA	CTTGAATAAA GATGGCAAAC TCCGCTAAGT GCTTCCCCA TGAATTAAAA AAACTGCAAA AGAAATGCTG GCAGGAAAAG TTCACTTGGG AGCCAGGTTT TCCATTGAGA CCTTCTAAAA TGGAAATGAA TGGAAATGAA TGGAAATGAA TCCCTTGGTG GAATAAACG AAAGGTTCCA TACAGAGCAG TCCAGAATCCT TACAGAGCAG TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGGTA TCCTTGTTCAGA TACCTTTGTCAG AATACTTCCC CATTTCCGGTT CAAGGTATTT	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1740

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	CCATGGGAAC						1920
	CATGGCATTG						1980
	AAGCTAATTG						2040
	GATTCTCAGG						2100
5	TCCAGAGAGA						2160
	GGATGTATTT	AIGGGAAAIC	CA COURT COCC	ALAAGCCCCA	TTCACCACAT	BATTAATCAG	2220
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	ATTTCTAAAT						
10	GAGAAAGATC	TTCAAGATGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
10	TCCATTCCTG						2400
	ATGGCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
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20	NPEDWLSLLL	TITE TENNE	DALLMALTCD	VECNTENTED	DEACONECES	DIOVERABLE	120
20	NAEDMESTER	KTEKNAALD	DALLENKIIGK	TOUTENDER	DRIGORNOLL	EDGSUDI EMI	180
	AIQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQGNVK	KSKQLLQKAV	CRGAVPLEMD	
	EIALRNLNLQ						240
	LYGENMPPQD						300
25	TSRSECRDLV						360
25	ESSLLAKLEE						420
		SVSKQSPPIS					480
		FQQQQHQILA					540
	OVLNEKKOIY	AIKYVNLEEA	DNQTLDSYRN	EIAYLNKLQQ	HSDKIIRLYD	YEITDQYIYM	600
	VMECGNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHO	HGIVHSDLKP	ANFLIVDGML	660
30	KLIDEGIANO	MQPDTTSVVK	DSOVGTVŇYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
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		CCGCCCTCGG					180
	CCCTCGAGGA	CCCTGGCTGG	AGAGACAGGG	CAGGAGGCTG	CACCCCTGGA	CGGAGTCCTG	240
4 =		CTAACATTTC					300
45	GAGGTGTCCG	GCCTGAGCAC	GGAGCGTGTC	CGGGAGCTGG	CTGTGGCCTT	GGCACAGAAG	360
	AATGTCAAGC	TCTCAACAGA	GCAGCTGCGC	TGTCTGGCTC	ACCGGCTCTC	TGAGCCCCCC	420
	GAGGACCTGG	ACGCCCTCCC	ATTGGACCTG	CTGCTATTCC	TCAACCCAGA	TGCGTTCTCG	480
		CCTGCACCCG					540
	CCGAGGGGGG	CTCCCGAGCG	ACAGCGGCTG	CTGCCTGCGG	CTCTGGCCTG	CTGGGGTGTG	600
50	CGGGGGTCTC	TGCTGAGCGA	GGCTGATGTG	CGGGCTCTGG	GAGGCCTGGC	TTGCGACCTG	660
		TTGTGGCCGA					720
		ACCAGGACCA					780
		CCCCGTCGAC					840
		GCCAGCCCAT					900
55		CTCGGGACCC					960
33	THE COCCCCC	AAGTGGAGAA	CACACCCTCT	CCTTCACCCA	AGAAGGCCCG	CGAGATAGAC	1020
	110000000	WARRANCE CAN	CDACMCCCIGI	CALCUSTANCE	GCGTGGATGC	GGCCCTGCTG.	
	GAGAGCCICA	TCTTCTACAA	CARCICCARC	CIGGRAGCCI	ACCAGCAGCT	GGACGTCCTA	1140
	GCCACCCAGA	TGGACCGCGT	CONCOCCATO	CCCTTCACCT	VCGUCACAGCT.	COUCCICCIA	1200
60	AAGCATAAAC	TGGATGAGCT	CIACCCACAA	GGTTACCCCG	AGICIGIGAL	CAGCACCIG	1260
UU	GGCTACCTCT	AGGCTTTGCT	GAUCCUTGAG	SACATTCGCA	VOTOGRAPHOL.	GACGTCCCTG	1320
	GAGACCCTGA	ACCGCTTTGT	CANGTONAC	CCCCICCACG	WWIGWGICC	TOTAL CALCA	1380
	ACCCTGATCG	ACCGCTTTGT	GAAGGGAAGG	GGCCAGCTAG	ACAMAGACAC	CLINGACACC	
	CTGACCGCCT	TCTACCCTGG	GTACCTGTGC	TCCCTCAGCC	CCGAGGAGCT	GAGCTCCGIG	1440
65	CCCCCCAGCA	GCATCTGGGC	GGTCAGGCCC	CAGGACCTGG	ACACGTGTGA	CCCAAGGCAG	1500
65						GTCCGAATAC	1560
						GGCGCTCAGT	1620
						TGCGGTGCTG	1680
	CCGTTGACTG	TGGCTGAGGT	GCAGAAACTT	CTGGGACCCC	ACGTGGAGGG	CCTGAAGGCG	1740
	GAGGAGCGGC	ACCGCCCGGT	GCGGGACTGG	ATCCTACGGC	AGCGGCAGGA	CGACCTGGAC	1800
70	ACGCTGGGGC	TGGGGCTACA	GGGCGGCATC	CCCAACGGCT	ACCTGGTCCT	AGACCTCAGC	1860
						TCTCACCGTC	1920
	CTGGCACTGC	TCCTAGCCTC	CACCCTGGCC	TGAGGGCCCC	ACTCCCTTGC	TGGCCCCAGC	1980
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	LSPRQLLGFP	CAEVSGLSTE	KVKELAVALA	QKNVKLSTEQ	LKCLAHKLSE	PPEDLDALPL	120
	DLLLFLNPDA	FSGPQACTRF	ISRITKANVO	LLPRGAPERQ	KLLPAALACW	GVRGSLLSEA	180
	DVRALGGLAC	DLPGRFVAES	AEVLLPRLVS	CPGPLDQDQQ	EAARAALQGG	GPPYGPPSTW	240
0.5	SVSTMDALRG	LLPVLGQPII	RSIPQGIVAA	WRQRSSRDPS	WRQPERTILE	PRFRREVEKT	300
85	ACPSGKKARE	IDESLIFYKK	WELEACVDAA	LLATQMDRVN	AIPFTYEQLE	AFKHKTDEFA	360
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	GRGQLDKDTL RLAFQNMNGS	HLGYLFLKMS DTLTAFYPGY EYFVKIQSFL KAEERHRPVR	LCSLSPEELS GGAPTEDLKA	SVPPSSIWAV LSQQNVSMDL	RPQDLDTCDP ATFMKLRTDA	RQLDVLYPKA VLPLTVAEVQ	420 480 540 600
5		TVLALLLAST					
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		TCAACAGAGC					420
20		GCCCTCCCAT					480
20		TGCACCCGTT					540
		CCCGAGCGAC					600 660
		CTGAGCGAGG GTGGCCGAGT					720
		CAGGACCAGC					780
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		CAGCCCATCA					900
		CGGGACCCAT					960
		GTGGAGAAGA					1020
30		TTCTACAAGA					1080 1140
20		GACCGCGTGA GATGAGCTCT					1200
		CTCAAGATGA					1260
		GCTTTGCTTG					1320
~ ~		CCACAGGTGG					1380
35		ACCCTAGACA					1440
		CTGAGCTCCG					1500
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		GGGTCCGAAT AAGGCGCTCA					1620 1680
40		GATGCGGTGC					1740
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		GACGACCTGG					1860
		CTAGACCTCA					1920
15		GTTCTCACCG					1980
45		GCTGGCCCCA					2040
	GTGATCCCCG GACACGT	TTCCACCCCA	AGAGAACTCG	CGCTCAGTAA	ACGGGAACAT	GCCCCCTGCA	2100
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	MDT.ORT.DRCW	SCGDRPGSLL	FLLESLGWVH	PARTLAGETG	TESAPLGGVL	TTPHNISSLS	60
		EVSGLSTERV					120
55		GPQACTRFFS					180
		PGRFVAESAE					240
		PVLGQPIIRS					300
		ESLIFYKKWE					360
60	GYPESVIQHL	GYLFLKMSPE LDKDTLDTLT	DIRKWNVISL	ELPKYTPEAD	CCTWAVPDOD	LDTCDPROLD	420 480
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70	ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC		TCATTGATCA	CAGTCATGTC	60
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	TTCGTGATGG	GCCTTCTGGG	GAACAGCGTC	ACCATTCGGG	TCACCCAGGT	GCTGCAGAAG	180
	AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240 300
75		CATCGGCAT ACACCCTGTC				TCCCCTGACC	360
15						CTGTCACCCC	420
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	GTCACCTCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCCTG	540
90						CCACCACGAG	600
80	CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
	CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTCGTGG	AGGGCTCTC	CGTAGCCTTC GGCCGGGGGC	720 780
	ACGCGGCCTC	CGCAGCTGAG	GAAGTCCGAC	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	
	ACCATCATCI	TCCTGAGGCT	GATTGTTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900
85	ATTCGGAGGA	TCATGGCTGC	GGCÇAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960

5	CCGCTCCTGT TGCCGCCTGT ACCACCGACA TCTGCAAGGA TCTAAGTCCC AATTCTGCTG	ACACGGTGTC CGCTGCAGCA GCGCCCGCTT GAACTGAGAA AGTCATTGAG CAGAGAATGG	CTCGCAGCAG CGCCAACCAC TGTGCAGCGC GATTTTCTTA TCTCGAGTCA TTTTCAGGAG	ACGTTTTTCT TTTCGGCGGG GAGAAGCGCC CCGTTGCTCT AGCACTTTTC CTAGAGCCCA CATGAAGTTT	TGTTCGTGCA TGCGCGTACA TCGCGTCCCG AGAGCGAGGC ACTCAGGCGC	GGTGCTGTGC TGCGCACTCC GCGCCAGTCC CGAGCCCCAG	1020 1080 1140 1200 1260 1320
10		40 Protein ession #: N 11		31	41	51	
15	KGYLQKEVTD ATLLHVLTLS VNVPSHRGLT MCWNMMQVLM	HMVSLACSDI FERYIAICHP CNRSSTRHHE KSQKGSLAGG	LVFLIGMPME FRYKAVSGPC QPETSNMSIC TRPPQLRKSE	ITLILVYLII FYSIIWNPLT QVKLLIGFVW TNLSSRWTVF SEESRTARRQ TFFYLSSVIN	TSSYTLSCKL VTSALVALPL QSSIFGAFVV TIIFLRLIVV	HTFLFEACSY LFAMGTEYPL YLVVLLSVAF TLAVCWMPNQ	60 120 180 240 300 360
20	CRLSLQHANH SKSQSLSLES	EKRLRVHAHS	TTDSARFVQR	PLLFASRRQS	SARRTEKIFL	STFQSEAEPQ	420
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30	CGCCATGCGG GCTGGTGGGC	AGGCCGAGCG GCTGCTGTCT	TGCGCGCGGC TCGACGCGCT	TTGGGACCGC CGGGCTGGTC CGAGTCCGAG GAGGAAGTTC	CTGTGCACCC GCGGAAAGCG	TGTGTTACCT	120 180 240
	GTTCCCCGGC CGCGCCGGGT	TCCTTCTACT ACGGACTCCG	TCGCCATCAC GCAAGGTCTT	TGAGCCCCAC CGTCATCACT CTGCATGTTC CGAACGGCTG	ACCATCGGGT TACGCGCTCC	ACGGCCACGC TGGGCATCCC	300 360 420 480
35	CCTGTTGGCG GGTGGTGGCC GCACTTCGAG CATCGGCTTC	GCCAAGTGCT GGGCTGCTGG GGCTGGACCT GGCGACTTCG	GCCTGGGCCT CGTGTGCCGC TCTTCCACGC TGGCACTGCA	GCGGTGGACG CACCCTGGCC CTACTACTAC GAGCGGCGAG	TGCGTGTCCA CTCGGGGCCG TGCTTCATCA GCGCTGCAGA	CGGAGAACCT TCGCCTTCTC CCCTCACCAC GGAAGCTCCC	540 600 660 720
40	CAACCTGGTG CCCCCCAGC CCCGGCCCGC CGCCCGCGAC	GTCCTGCGCT CCGCGCCCCC TCCGTGGGCT AACCTGGGCT	TCCTCGTTGC CGGGGGGGCCC CCGCCTCTGT TTTCGCCCCC	CCTGGGGCTC CAGCGCCGAC CGAGAGCCGT CTTCTGCCAC CTCGAGCCCG	TGGCCCGAGC GGCCTCTGGC GTGCACAAGC GGGGTCGTGC	GCGCTGCCG TGCCCCGCCG TGGAGAGGTG GTGGCGGGCA	780 840 900 960 1020
45	AATCTGGAAT GGATGACGGG AAGTCCCCTC	GGGAGGGTCT	GGCTTCAGCT GTCTTCTGCC AAAAATATAT	CATCTGACAA ATCAGGGCAC ACGAGCAGTT TACAGTCACA	CCTCCCCAGG	GCCAGGGTCG GATTGGAAAC GTCTGTGGCT AAAAAAAAA	1080 1140 1200 1260
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65	GGAAACATGA	TCCAGCTGAA	GGACTGATTG	CAGGAAAACT GAAGGTGTGA	TGGCAGCTCC GCAGTGGCCA	CCAACCTTGG CGAGAGGCAG	60 120
70	GCTGGCTGGG TGAGCACTCG	ACATGAGGTT GAGGCACTCC	GGCAGAGGGC TATGCTTGGA	: AGGCAAGCTG L AAGCTCGCTA	GCCCTTGGTG	GGCCTCGCCC GGTCCAGCAG	180 240
70	AACACCACCA GGTGTGCGCC TATGCCATCC	GGCCCGCTCT CCGTGAGGGA CTCAACGTGGA	GCTGAGGCTG CTGGAGGAAG TGAGAAGAAT	TCGGATTACC CCAACCACCG CAGGTGCTGA	TTTTGACCAA TATCCATTGA CCACCTACAT	GAGGAGCCGA CTACAGGAAG CGTCATTGTC CTGGTACCGG	360 420 480
75	TTGTCCATCO GTGGGGAAGT	CCACGGACAG CTCCAAATAT TTCAGGTGGT	CATCTGGGTC CCCGTACGTC	CCGGACATTO TATATTCGGO AGCCTCGACA	TCATCAATGE ATCAAGGCGE ATCTACAACTT	CATCACCAAG COTTCAGAAC COCCTTCGAT CATCAACATC	600 660 720
80	TCTTTGTGGC GAGTGGGAGT TACTATGCAG AGCCTGCTAG	GCTTGCCAGA TGCTGGGGGT AAATGAAGTT TGCCCAGCAT	AAAGGTGAAA GCTGCCCTAC CTATGTGGTC CTTCCTCATC	TCCGACAGGA TTTCGGGAGT ATCCGCCGGG GTCATGGACA	A GTGTCTTCAT T TCAGCATGGA C GGCCCCTCTT A TCGTGGGCTT	GAACCAGGGA AAGCAGTAAC CTATGTGGTC CTACCTGCCC	840 900 960 1020
85	CCCAACAGTC	GCGAGAGGG	CTCTTTCAAC	ATTACACTCO	C TCCTGGGCTI	CTCGGTCTTC CATTGGTGTC CTTCATTGTG	1080 1140

	CGGCTGGTGC	ACAAGCAAGA	CCTGCAGCAG	CCCGTGCCTG	CTTGGCTGCG	TCACCTGGTT	1260
	CTGGAGAGAA						1320
	GCCACCTCCC						1380
	ATGGGAGGAC	CCCAGGACTT	CGAGAAGAGC	CCGAGGGACA	GATGTAGCCC	TCCCCCACCA	1440
5		CCTCGCTGGC					1500
•		AGCGGGATGA					1560
		AGCTGCTATT					1620
		TCTGGTCCAT					1680
		CTGGTTAGGT					1740
10							1800
10		GACATTTTCA					
		AATCACAAGC					1860
		CTTGTCCCAC					1920
		ACTCGGGCAC					1980
1.5		ATAAGGGACT					2040
15	GAAGGCAAAA	CCAACTCTCT	ACTACACAGG	CCTGATAACT	CTGTACGAGG	CTTCTCTAAC	2100
	CCCTAGTGTC	TTTTTTTTCT	TCACCTCACT	TGTGGCAGCT	TCCCTGAACA	CTCATCCCCC	2160
	ATCAGATGAT	GGGAGTGGGA	AGAATAAAAT	GCAGTGAAAC	CC		
	Seg ID NO:	44 Protein	sequence				
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	MITEMPROOFIE	ALLLPTLLAQ	CENDDODNITT	PDAT.T.PT.STV	LLTNYPKGVR	PVRDWRKPTT	60
		LNVDEKNQVL					120
25							180
23		SPNIPYVYIR					240
		RLPEKVKSDR					
		LPSIPLMVMD					300
		VCMALLVISL					360
20		QATKTDDCSA					420
30	ELSSIRQFLE	KRDEIREVAR	DWLRVGSVLD	KLLFHIYLLA	VLAYSITLVM	LWSIWQYA	
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	CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCCTCCCC	AGGCCGCGAG	60
	CGCCCCTGCC	GCGGTGCCTG	GCCTCCCCTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
40	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCCTCTGC	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
		CCAGTGCAAG					360
		GAACTAAACT					420
		CATGCGAACC					480
45		CAGGATACAC					540
10		CATGCCAACA					600
	CTCLCTCCCC	ACATGCTCAT	CCCACATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	AMANACTORC	AGTACAGCTG	TENACACACA	CARCARGEC	CACAGTGCCT	CTCTCCATCC	720
	MINANCIGIC	GCCTGGCCCC	A A A TOO A A CA	CACTCTCTAC	ATATTCATCA	ATCTCCCTCT	780
50	I CAGGACICC	TCTGTCCCTA	ANATOGNAGA	GUCTOTCING	CATTTCCAAC	CTACTACTCC	840
50	GGTAAAGTCA	TTGGTTTCGA	CAN I COMMON	ATCACTCCAC	CATITGGAAG	TATACATATA	900
	AAAIGICACA	CTATGGATAG	ACTOCAATAT	ATCAGIGGAC	CCNATTCCTT	CNATACCCAA	960
		AGTGTAAATG					1020
	GGGTCCTTCA	ATTCTGTGAA	CANGUAGGGA	1A1AAAGGCA	CENCCATCA	ACACACAATC	1080
55		TTGCTCACAA					1140
55	AAGAAGTTGC	TIGCICACAA	AAACAGCA1G	AAAAAGAAGG	CAMMATIAN	CTATCAACAC	1200
	CCAGAACCCA	CCAGGACTCC	CHCCCCTAAG	GIGAACTIGC	AGCCCTTCAA	CIVICUMOUS	1260
	ATAGITTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	ACAMIGAAGA	AUNUATOWNY	1320
						AGAGGAGCGA	1320
ćn		GAGATGTGTT					
60		GGAAAGCGCT					1440
		TCAATCATGG					1500
	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	A COCCUTTUGUA	1560
						ACCCCAAAGC	1620
65	AACTTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
65	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAAAATTCA	GTTGTATCAA	GGAACTGATG	LTACCAAAAG	CATCATTTTT	1800
	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
	TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
70						CTCTGGCATT	1980
70	TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
	TCTTGTATAA	GATATGCCAA	TATTTGCTTT	' AAATATCATA	TCACTGTATC	TTCTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	AAATTATAA	ATATGGAAAT	GTCAGTTTAT	CTCCCCTCCT	2160
	CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
	TAGAAAAAA	AGCACAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
75						TAGCCAAACT	2340
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	"IE NE MOTIVITA	TIPOU A LOGI	BCEBGALGEL	CSUDAMECON	KPRPCOHRCU	NTHGSYKCFC	120
	T COUNT MODE	TOPCIONING	TNOOVEGED	EEGDUCT.CDG	SGLRI.ADNOR	DCLDIDECAS	180
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5	SLRGDVFFPK WNPADRDNAI	VNLQPFNYEE VNEAGEFGLI GFYMAVPALA WEKTTSEDEK	IVSRGGNSHG LVQRKALTSK GHKKDIGRLK	GKKGNEEKMK LEHKDLNISV LLLPDLQPQS	egledekree DCSFNHGICD NFCLLFDYRL	KALKNDIEER WKQDREDDFD AGDKVGKLRV	300 360 420 480 540
10	Nucleic Aci	47 DNA sequid Accession	#: NM_0050	46			
10	1	11	21	31	41	51	
		GCTCCATGGC	7700000		TCCNCNTCCT	ACTGCTATCC	60
15	TTAGCCTTGG TGTGCAAGAG GGAGGCGTCC TACACCGTGC	AAACTGCAGG GCTCCCACCC TGGTCAATGA ACCTGGGCAG TCCGCCACCC	AGAAGAAGCC ATGGCAGGTG GCGCTGGGTG TGATACGCTG	CAGGGTGACA GCCCTGCTCA CTCACTGCCG GGCGACAGGA	AGATTATTGA GTGGCAATCA CCCACTGCAA GAGCTCAGAG	TGGCGCCCA GCTCCACTGC GATGAATGAG GATCAAGGCC	120 180 240 300 360
		ATAGCCAGGC					420
20	CGCTGCGAAC GATGTGACCT	CCCCTGGAAC TTCCCTCTGA TTTACAAGGA	CACCTGTACT CCTCATGTGC	GTCTCCGGCT GTGGATGTCA	GGGGCACTAC AGCTCATCTC	CACGAGCCCA CCCCCAGGAC	480 540 600
	TCCAAGAAAA	ACGCCTGCAA	TGGTGACTCA	GGGGGACCGT	TGGTGTGCAG	AGGTACCCTG	660
25		TGTCCTGGGG GCAAGTTCAC					720 780
.23	CACACTGAGT	TAATTAACTG	TGTGCTTCCA	ACAGAAAATG	CACAGGAGTG	AGGACGCCGA	840
	TGACCTATGA	AGTCAAATTT	GACTTTACCT	TTCCTCAAAG	ATATATTTAA	ACCTCATGCC	900
	CTGTTGATAA AACCCTCAA	ACCAATCAAA	TTGGTAAAGA	CCTAAAACCA	AAACAAATAA	AGAAACACAA	960
30	AACCCICAA						
		48 Protein					
	Protein Acc	cession #: 1 11	NP_005037 21	31	41	51	
	1	1	1	1	1	1	
35		ILLLSLALET					60
		CKMNEYTVHL VRLPSRCEPP					120 180
		AGIPDSKKNA					240
40	FTKWINDTMK	KHR					
40	Seg ID NO:	49 DNA seq	uence				
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45	[GAATTCGGCG	 ATGCCTCACA	ACTCCATCAG	ATCTGGCCAT	 GGAGGGCTGA	 ACCAGCTGGG	60
45	GAATTCGGCG AGGGGCCTTT	 ATGCCTCACA GTGAATGGCA	ACTCCATCAG GACCTCTGCC	ATCTGGCCAT GGAAGTGGTC	 GGAGGGCTGA CGCCAGCGCA	ACCAGCTGGG TCGTAGACCT	120
	GAATTCGGCG AGGGGCCTTT GGCCCACCAG	 ATGCCTCACA GTGAATGGCA GGTGTAAGGC	ACTCCATCAG GACCTCTGCC CCTGCGACAT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA	ACCAGCTGGG TCGTAGACCT GCCATGGTTG	
4550	GAATTCGGCG AGGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG	120 180 240 300
	GAATTCGGCG AGGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG CCAGAACCCT	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG CTCCTGGCTG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GACTGATAGG ACTACAAACG AGGGCGTCTG	120 180 240 300 360
	GAATTCGGCG GGATTCGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGGTCTG CCAAAGTGCA GTCCCGGACA	120 180 240 300
50	GAATTCGGCG AGGGCCTTT GGCCCACCAG CGTCAGCAAG GGGCTCCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC	ATGCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTCCCTA ACCTCCCTA CCCAGCTCAG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GGTGGTGGAG CCGAGACCGG CATTAATAG CGTGGCCACC CCCGGAGTCA	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGGTCTG CCAAAGTGCA ATTCCCTGGG	120 180 240 300 360 420 480 540
	GAATTCGGCG AGGGCCTTT GGCCCACCAG CGTCAGCAAG CGTCAGCAAG CCAGAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA CCCAAGGTGG ACCATGTTTG ACTGTGCCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG	ACTCCATCAG GACCTCTGCC CCTGGGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GCTGGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCACC CCCGGGAGTCA CATCGCTCAG	GAAGGGCTGA CGCAAGCGCA CTCCGCGTCA ATCCGGCTG AAGATTGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA	120 180 240 300 360 420 480 540
50	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGCAAG CCAGAACCCT TGACAATGAC GCACACCATTC CACGCTGATC CTCACCTAC AATGGATGAC CGGACCCCGA	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGTGATCAGA AAGCACTTC	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCG GCACGGATGC	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC CGTGGTGGAG CCGAGACCGG CATTAATAGA CGTCGCCACC CCCGGAGTCA CATCGCTCAG ACTAAGCATT CTTCAGCCAG	GGAGGGCTGA CGCCAGCGCA CTCCGCGTCA ATCCGGCTG ATCATCGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACAGA CACCACCTCG	ACCAGCTGGG ACCAGCTGGGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAAGAGGAAA GCAGCAGCAG AGCCGCTGA	120 180 240 300 360 420 480 540 600 660 720
50	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGCAAG GCACCATTC TGACAATGAC GCAACCATTC CACCTGATC CTCCACCTAC AATGGATGAC CGGACCCCGA GTGCCCCGAGTGCCCGAGTGCCCGAGTGTC	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCATGTTTG ACTGTGCCA AACCTCCCTA ACCCTCCATCATCATCATCATCATCATCATCATCATCATC	ACTCCATCAG GACCTCTGCC CCTGGGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTG CTGTAACTCC GGCTCCTGGG ATAGCTGCCG GCACGGATGC ACTACCCAGA	ATCTGGCCAT GGAAGTGGTC GGATGGCAG GACTGGCAG GCGAGACCGG CATTAATAGA CCTCGCTCAG CATCGCTCAG CATCAGCAC GATTAATGCATCAGCAG GGCCTATGCCAG GGCCTATGCC	GGAGGGCTGA GGCAGGGCA CTCCGCGTCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA ACCTCCGGCGG CCTGGCAGCG GACTCACAGG CCCCACTCG TCCCCCAGCCG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCTGGGA ACTACAGGGAA GCAGCAGCAGCAGAAGAGAA ACCCCAAAGG	120 180 240 300 360 420 480 540 600 660 720
50 55	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGAAG CGTCAGAACCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGACCCGTA GGGCCCATTT CGAGCAGGGC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA ACCTGTTTG ACTGTGCCA AACCTCCCTA ACCTCCCTA TCCATCAG TCCATCAG AGGACCTCAG CCAGCTCAG CCAGCCCAGC	ACTCCATCAG GACCTCTGCC CCTGGACAT GGTACTACGA CCACCCCCAA CCTGGGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATAGCTGCG GCACGGATGCA ACTACCCAGA TGCCCTTGCT	ATCTGGCCAT GGAAGTGGTC GGTGGCAGG GACTGGCAGG CCGTGGCGAG CCGGAGTCA CATCACTCAG ACTAAGCAT CTTCAGCCAG GGCCTATGCC CAACAGCACC CAACAGCACC	GAAGGGCTGA CGCAAGCGCA ATCCGGCTG AAATTGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCTCCAGTCGG CCTGGCAGTCGG CCTGGCAGCCG GACTCACAGA CACCACCTCG TCCCCCAGCC	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG ACTCCCGGACA ATTCCCTGGG ACTAGAGGAAA GCAGCAGCAG AGCCGCTCAA AGCCCGTCAA	120 180 240 300 360 420 480 540 600 660 720
50	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGCAAG GGGTCCCAAG GCAACCCT TGACAATGAC CCACCTGAC CACCTGAC CCGACCCGA GTGCCCCGA GTGCCCCATTC CGAGCAGGC CCTGACCCCGA GTGCCCCATTC CGAGCAGGC CCTGACCCCGA GTGCCCATTT CGAGCAGGGC CCTGACCCCCT	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCATGTTTG ACTGTGCCA AACCTCCTTA ACTGATCAGT TCCATCAATG AGGACTTCAG AGGACCTTC GAGCGGCAGC TCCAACAGC CCTCAACAGC CCTCAACAGC	ACTCCATCAG GACCTCTGGCACAT GGTACTACGA CCTGGGAGAT CCTGGGAGAT CTGGACAGCTC GGCTCCTGGG ATAGCTCC GGCTCCTGGG ATAGCTCC GCCCCAAC TGCCCTGGG ATAGCTCCCAGA TGCCCTGGG CACTGCCCAGA TGCCCTGGC CACTGCGCAC	ATCTGGCCAT GGAAGTGGTC GGACTGGCAG GACTGGCAG CCGAGACCGG CATTAATAGA CCTCGCCAGAGTCA CATCGCTCAG ACTAAGCATC CTCAGCCAG GGCCTATGCC CAACAGCACC CAACAGCACC AAACCAGGAA	GGAGGGCTGA GGCAGGGCA CTCCGGGTCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGATCCCTGG CCTGGCAGCG GACTCACAGCA CACCACCTCG CCCGAGCG ACTCACCAGCA ACTCACCAGCA ACTCACCAGGA	ACCAGCTGGG ACCAGCTTGGGAGCACT GCCATGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 300 420 480 540 600 660 720 780 900 960
50 55	GAATTCGGCG AGGGCCTTT GGCCCACGA GGTCAGCAAG GGCTCCAAG GGAACCATT CACACTAGC CTCACCTAC AATGGATGAC AGGACCCGA AGGACCCTT CGAGCAGGC CCGACCCCGA CTGACCATTC CGAGCAGGC CTGACCATT	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTTTGGCA ACCTCCTA ACCTCCCTA ACCTCCAGCTCAG TCCATCAAGA CGAGCGCAGC CTCACCACCCC CTCCACCACCCCC CCTCACCCCCC CCTCACCCCCC CCTCACCCCCC CCTCCACCCCC CCTCCCCCTC	ACTCCATCAG GACCTCTGCC CCTGGGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTG GCTCTCGGG ATAGCTGCG GCACGGATG ACTACCCAGA TGCCCTTGCT CACTGGGGCG CCTTCGCCAT	ATCTGGCCAT GGAAGTGGTC GGATGGCAG GACTGGCAG GCCGAGACCGG CATTAATAGA CGTGGCCAC CACCGCACT CTTCAGCCAG GGCCTTATGCC CAACAGCACC AACACCTCTCG AAACAGGAA CGCCTTTTG	GAAGGGCTGA GGCAGGCGCA CTCCGCGTCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGCGG GACTCACCAGCC CTGGACGACG CTGGACGACG CTGGACGACG ACTCACCAGGC CTGGACGACG GACTCACCAGGC CTGGACGACG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA ATTCCCTGGA ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 300 420 480 540 660 720 780 900 960 1020
50 55 60	GAATTOGGCG AGGGCCTTT GGCCCACCAG GGCTCCAAG GGGCTCCAAG GGGCTCCAAG GCAACCCT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGACCCCGA GTGCCCATT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCAGC CGGGTCCCGG	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA ACCTCGCTA ACCTCCCTA CCCAGCTCAG TCCATCATG AGGACTCAG AGGCACCTTC GAGCGCAGC TCCAACACGC TCCAACACGC CCTCTACCCGC CCTCACTCACC CCTTCCTCTC	ACTCCATCAG GACCTCTGCC CCTGGACAT GGTACTACGA CCACCCCAA GCTGCAGAT GTGTCAGCTC TGGACAGCTC TGGACAGCTG GCTCCTGGG ATAGCTGCG GCACGGATGC ACTACCCAGA TGCCCTTGCT CACTGGGGCG CCTTCGCCAT TATCTAGCTC CCCTTTCCCCA	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAGC GATTGATGAG CCGGAGTCA CATCGCCACC CACAGCACC CACAGCACC CAACACCC CAACACCACC CAACCTCTCG AAAGCAGCAA CGCCTTTTTG TGCTGCCTCC	GAAGGGCTGA CTCCGCGTCA ATCCGGCTG ATCCGGCTG ATCATCCGGA ATCATCCGGA AAGTCCCTGA ACCCAGTCGG CCTGGCAGCG GACTCACAGA CCCCCAGGC TCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGG GATCACCAGG	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG ACTACAAACG ACGCGTCGA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCACCAAAGG GGAAGCACA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTCC AGTTCCAGGG AGTTCACGGG AGTTCACGGG AGTTCACGGG AGTTCACGGG	120 180 240 300 420 480 540 600 660 720 780 900 960
50 55	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGCAG GGTCAGCAG GGAACCCT TGACAATGAC CACCTGACCACTAC CACCTGACCACTAC CAGCCCGAC CAGCCCCAG CAGCCCCAG CCGAGCCCCAG CCGAGCCCCCA CGAGCAGCC CGGGGTCCCG CGGGGTCCCG CAGCCCCTC CAGCCCCTC CATCCCCACC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTCCTTA ACTGTGCCA AACCTCCTA AGTGATCAGG TCCATCAATG TCCATCAATG CTCACCAGGC CTCTACCGC CTCACACGC CCTCACTCAC CCTTCCTCT CCCTTCAATG CTCTCAGGGC AGCGCAGGC AGCGCAGGC AGCGCAGGC AGCGCAGGC CTCTCACTGACGC CTCTCACTGACGC CTCTCACTGACGC AGCGGACAGG	ACTCCATCAG GACCTCTGGACAGT GGTACTAGGACAGT GGTCTCGGGAGAT GGGTCCTGGG ATAGCTCCCCAA CCTGGGACAGT GGCTCCTGGG ATAGCTCCCCAGA TGCCCTGGG TGCCCTGGGT TGCCCTGGGT TGCCCTGGGT TGCCCTGGGT TGCCCTTGCT CACTGGGGATGC CCTTTCGCCAT TATCTAGCTC CCTTTCCCCAGA GGAGATGGT GCAGCTATGG	ATCTGGCCAT GGAAGTGGTC GGAAGTGGAG CCGAGACCGG CATTAATAGA CGTGGCCAC CATCAGCAG CATCAGCAG CATCAGCAG CATCAGCAG CATCAGCAG CATCAGCAG CAACAGCACC CAACAGCACC CAACCTCTCG CAACAGCACC CAACCTCTCG CAACGCACG CGCCTTTTTG GGGGCCACG CGGGCCACG	GGAGGGCTGA GGCAGGGCA CTCCGCGTCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGATTCCTGGA CCCCAGTCGG CCTGGCAGCG GACTCACAGA ACCCCCAGCC CTGGACGACG GATCTACCAGGA ACCCCCAGGC GATCTACCAGGA CTCACCAGG GATCTACCAGGA CTCACCAGGA CTCACCAGGA ACCCCCAGGAC GATCTCCAGGA ACCCCCAGGAC CTGCCCGGAT ATCGCAGGAC	ACCAGCTGGG ACCAAGGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 360 420 480 660 720 780 900 960 1020 1020 1140 1200
50 55 60	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGAAG GGGCTCCAAG GGACCATT TGACAATGAC GCAACCATTC CACGCTGATC CTCCACCTAC AATGGATGAC GGACCCCGA GTGCCCATT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTTCCACC CAGGCCCCC CAGGCCCCT CATCCCCACC AAGTGAATAC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGCA ATCCTTGGCA ACCTCCTTA ACTGTGCCCA AACCTCCCTA ACCTCACATCA TCCAACATCA GAGCACCTTCC GAGCGCAGC CCTCACCTAC CCTTCACTCAC CCTTCACTCAC CCTTCACTCAC	ACTCCATCAG GACCTCTGCC CCTGGGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATAGCTGCCG GCACCGATG TGCCCTGGT TGCCCTGCT CACTGCGGCGG CCTTCGCCAT TATCTAGCTC CCTTTCGCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT GCAGCTATGCCCA	ATCTGGCCAT GGAAGTGGTC GGAGCGGGCCACC CATTAATAGA CGTGGCCACC CATCAGCACC CATCAGCACC CAACATCTCAG AACAGCACC AACAGCACC CAACCTCTCG CAACAGCACC CAACCTCTCG CAACCTCTCG CAACCTCCC CACCCCCACC CACCCCCCCCCC	GAAGGGCTGA CGCAGCGCA ATCCGGCTCA ATCCGGCTG AAATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA ACCCCAGTCGG CCTGGCAGTCGG CCCCCAGCC CTGGACCAGCC CTGGACGAGC GATCACCAGA ACCCCCAGGC CTGGACGAGC GTGTACGGGC GTGTACGGGC CTGCCCGGAT ATCCCCGGAT ATCCCCGGAT ATCCCCGGAT	ACCAGCTGGG TCGTAGACCT GCCATGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAGAGGAAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCAC CCTACCCCGT TGTCCAGTTC AGTTCCAGTTC AGTTCCAGTTC AGTTCACGGG ACCCACCCCA TCGTCACCCGT TGTCCAGCTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG GCGAGGCCTG	120 180 240 300 360 420 540 600 600 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGCAAG CCAGAACCCT TGACAATGAC CACCACCACCACCACCACCACCACCACCACCACCACC	ATGCCTCACA GTGAATGGCA GGTGTAAGGC ATCCTTGGCA ACCTCGTGCA AACCTCCTA ACCTCACATG CCATCAATG TCCATCAATG AGGGGCAGC CTCTACCGG CCTCACTCAC CCTTCCTTCAC CCTTCACTGC AGCGGACAGG CTCACTCAC CCTTCACTGC AGCGGACAGG CTCACTCAC CTTCAGGGC AGCGGACAGG AGCGGACAGG AGCGGACAGG AGCGGACAGG ACTCACTCAC AGCGGACAGG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATACTCCC GCTCCTGGG ACTACCCAGA TGCCCTTGCT TCACTGCGG CCTTTCCCCA GAGAGATGGT GCAGTTCCCCATTCCCCA GAGAGATGGT GCTTTCCCCA TGCTGAGTTCC TGCTTAGCTC CCTTTCCCCA TGAGAGATGGT GCAGTTAGCT CCTTTCCCCA TGAGTTAGCT CCTTTCCCCA TGAGTTAGCT TGCTGAGTTC	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTCGGCGAG CCGGAGTCA CATCGCTCAG ACTAGCAT CATCGCTCAG ACTAGCAT CAACAGCACC CAACCTCTCG AAAGCAGCA CACCTCTCG CACCTCTCG CGGGCCCACG CTCCTCTGCC CACCTTTGCC CACCTTAGCCCCCCACG CTCCTCTGCC CACCCTTAGCC	GAGGGCTGA CGCCAGCGCA ATCCGGCTCA ATCCGGCTG AACATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG GACTCACAGA CACCACTCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGG GATTCACAGA CCCCCGAGG GATTCACAGA CCCCCGAGG CTGCCCGAGG ATCTCACAGA ACCCCCGAGG ATCTCACAGA ATCACCAGA ATCACCAGA ATCACCAGA ATCACAGA ATCACAGA ATCACAGA ATCACAGA ATCACAGA ATCACAGGCA ATCACAGGCA TACAGTTCCA	ACCAGCTGGG ACCAGCTGGGACCT GCCATGGTTG GAGTGATAGG ACTGCAAAGG ACGCGCACA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG GGAGCAGCAG ACACCAAAGG GGAAGGCAC ACTCCCCGT TGTCCAGTTC AAGTCGGCTCA ACTCCCCGT TGTCCAGTTC AGTTCGCCGA ACCCACCCCA TGTGGCAGC	120 180 240 360 420 480 660 720 780 900 960 1020 1020 1140 1200
50 55 60 65	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGCAAG GGTCAGCAAG GGAACCCT TGACAATGAC CACCTAGC AATGATGAC AATGATGAC CGACCCCAC CGACCCCAG CCTGACCCCTC CGAGCAGCCCCC CGGGGTCCCG CAGGCCCCTC CAGCCCCCTC CAGGCCCCTC CATCCCCACC AAGTGAATAC GCGCTTCCCCCCC GAGTGCACC CGAGCCCCTC CATCCCCACC AAGTGAATAC GCGCTTCCCCCCC GAGTGCACCC GAGTGCACCC CGGGTTCCCCC CATCCCCACC CAGCCCCTC CATCCCCACC CAGGCCCTCC CAGCCCCTC	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTAGTTG ACTGTGCCA AACCTCCTA ACTGATCATG TCCATCAATG TCCATCAATG CTCACCACGC CTCACCACCACCC CCTCACTCAC CCTTCACTCAC CCTTCACTCAC	ACTCCATCAG GACCTCTGCC CCTGGGACAT GGTACTACGA CCTCGGAGGAT GTGTCAGCTC TGGACAGCTG GGCTCCTGGG ATAGCTCC GGCTCCTGGG ATAGCTCCCAGA TGCCCTGCT CACTCGCCAT TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT GAGAGATGGT GCAGCTATGC CCTATGGCCA	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTCGGCGAG CCGGAGTCA CATCGCTCAG ACTAGCAT CATCGCTCAG ACTAGCAT CAACAGCACC CAACCTCTCG AAAGCAGCA CACCTCTCG CACCTCTCG CGGGCCCACG CTCCTCTGCC CACCTTTGCC CACCTTAGCCCCCCACG CTCCTCTGCC CACCCTTAGCC	GAGGGCTGA CGCCAGCGCA ATCCGGCTCA ATCCGGCTG ATCATCCGGA ATCATCCGGA AAGTTCCTGA AAGTCCCTGA CCCCAGCCG GACTCACAGA CACCACCTCG TCCCCCAGCC CTGGACGACG GATTCACAGA ACCCCCGAGC GTGTACCAGA ACCCCCGAGC GTGTACGGC CTGCCCGGAT ATCGCAGGAC ATCACCAGA ATCACCAGA ACCCCCGAGC ATCCCCAGCC ATCCCCCAGCC ATCCACACA ATCACAGA ATCACAGA ATCACAGACA ATCACAGACA ATCACAGCA ATCACAGCA ATCACAGCA ATCACAGCA ATCACAGCAC ATCACAGTTCCA	ACCAGCTGGG ACCAGCTGGGACCT GCCATGGTTG GAGTGATAGG ACTGCAAAGG ACGCGCACA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG GGAGCAGCAG ACACCAAAGG GGAAGGCAC ACTCCCCGT TGTCCAGTTC AAGTCGGCTCA ACTCCCCGT TGTCCAGTTC AGTTCGCCGA ACCCACCCCA TGTGGCAGC	120 180 240 300 360 420 540 600 600 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	GAATTCGGCG AGGGCCTTT GGCCCACCAG CGTCAGCAAG CCAGAACCCTT GGACAATGCA GCACACATTC CCACCTGATC CTCCACCTAC AATGGATGAC GGACCCGGA GTGCCCATTT CGAGCAGGGC CCTGACCCCTC GGTGGCAGAT TAGCTCCACC CAGGCCCCTC CATCCCCACC CAAGGGCCCTC CATCCCCACC AAGTGAATCACC GGGGTCCCG GCGCTTCCCC GCGCTTCCCC GAGTGCACCC Seq ID NO: Protein AC	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTAGTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG AGGCGGCAGC CTCACCAGC CCTCACTCAC CCTTCCTTCACTCC CCTTCACTCAC CCTTCACTCAC	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTC GGCTCCTGGG ATACTCCC GGCTCCTGGG ACTACCCCAA ACTGCGCTGC ACTACCCCAGA TGCCCTTGCCAT TATCTAGCTC CCTTTCCCAC GAGAGATGGT GCACTTCCCCAT GAGAGATGGT GCACTGGCT CCTTTCCCCAT GAGAGATGGT GCACTATGCC CCTATGCCCA SAGAGATGGT CCACGGCCTT Sequence NP_003457	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTCGGTGGAG CCTGAGCCGG CATTAATAGA ACTAGCATC CTCTCGCCAG GCCTATGCCCAG GCCTATGCC CAACACCACC CAACCTCTCG AAAGCACC CACCCTTCTG GGGCCCACG CTCCTCTGCCCCCCCCCC	GGAGGGCTGA GGCAGGCGCA CTCCGCGTCA ATCCGGCTG AACATTGGGG CTCCTGGCTG ATCATCCGGA AACATCCGTGA CCCCAGTCGG CCTGGCAGCG GACTCACCAGC TCCCCCAGCC TCGCAGCG GATCTACCAGA ACCCCCAGGG GATCTACCAGA ACCCCCGAGGG GATCTACCAGA TCCCCCGAGGC CTGCCCGGAT ATCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TCGCAGGCA TACAGTTCCA TAGTTGAAGC	ACCAGCTGGG ACCAGCTGGG ACCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCACAGA GCAGCACAGA GCACCACAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC AGTTCACGGG ACCCACCCCA TGGTGGCAGG CCACCCCA TGGTGGCAGG CCACCCCA TGGTGGCAGG TT	120 180 240 300 360 420 540 600 600 720 780 840 900 1020 1080 1140 1200 1260
50 55 60 65	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGCAAG CCAGAACCCT TGACAATGAC GCACCATTC CCACCTAC AATGACTAC AATGACTGATC CTGACCATT CGAGCCGGA GTGCCCATT CGAGCAGGGC CCTGACCCCT GGTGCCATT TAGCTCCAC CAGGCCCCT CATCCCCAC CAGGCCCTC CATCCCCAC CAGGCCCTC CATCCCCAC CAGGCCCTC CATCCCCAC Seq ID NO: Protein Ac 1	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTAGTTG ACTGTGCCA AACCTCCCTA ACCTCACATG TCCATCAATG AGGGGCACCTTC GAGCGGCAGC CTCACCACC CCTCACTCAC CCTCCATCAATG CCTCACTCAC CCTCCATCACT CCTCACTCAC CCTCCACTCAC TCCACCACCTG SO Protein CCGSSion #: 11	ACTCCATCAG GACCTCTGCG CCTGCGACAT GGTACTACGA CCTGCGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATACCCAGA TGCCCTTGCC ACTACCCAGA TGCCCTTGCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT GCAGTTCCCCA GAGAGATGGT GCAGTTAGCTC CCTTTCCCCA GAGAGATGGT GCAGTTAGCT CCTTTCCCCA GAGAGATGGT GCAGCTTATCCCCA TGCTGAGTTC CCACGGCCTT sequence NP_003457 21	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTGGTGGAG CCGAGACCGG CATTAATAGA ACTCGCTCAG ACTCGCTCAG ACTAGCAT CATCGCTCAG GGCCTATGCC CAACCTCTCG AAAGCAGGAC CGCCTTTTGC GGGGCCACG CTCCTCTGCC CACCCCTACT CACCCTACT GGGCCCACG CTCCTCTGCC CACCCCTACT CCACCCTACT TGACCATCTG	GGAGGGCTGA GGCAGGCGCA CTCCGCGTCA ATCCGGCTG ATCATCGGG ATCATCGGG ATCATCGGGA AAGTCCCTGA CCCCAGTCGG CCTGGCAGCG CTGGCAGCG TCCCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCGAGG GATTCACCAGA ACCCCCGAGG CTGTCACCAGA ACCCCCGAGG ATCTCACCAGA ACCCCCGAGG TCTGCCCGAGT ATCGCAGCA TAGCTTCACAGC TAGCTTCACAGCA TACAGTTCCACAGCA TACAGTTCCACAGCA TACAGTTCAAGCC	ACCAGCTGGG ACCAGCTGGGACCT GCCATGGTTG GAGTGATAGG ACTGCAAAGG ACGCGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG ACCCCACAAGGCAC ACTCCCCGT TGTCCAGTTC AAGTCGGCT AAGTCGCCT TGTCCAGTTC AAGTCGGCT TGTCCAGTTC AAGTCGGCT TGTCCAGTTC AAGTCGCCT TGTCACGCG TCGTTGCCAGT TGTCACGCG TCGTTGCCAGT TGTCACGCG TCGTTGCCAGT CATTCACGGG ACCCACCCCA TGTTGCCAGT CCATCAAGGCCT TT	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320
50 55 60 65 70	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGGCTCAGGAACCCTT TGACAATGAC CTCACCTAC CACCTAC CACCTAC CACCTAC CAGCCCGA GTGCCCATT CGAGCAGGC CCTGACCCT TGGTGGCAGAT TAGCTCACC CAGGCTCCCA CAGTCCCCC CATCCCACC CAGCCCTC CATCCCACC CAGTCCCC CATCCCCACC AAGTGAATAAC GGCTTCCCC GGGTCCCC GAGTGCACCT CATCCCCACC AAGTGAATAAC GGCTTCCCC GGTTCCCC GATTCCCCACC AAGTGAATAAC TACCCACC Seq ID NO: Protein AC MPHNSIRSGH	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTAGTTG ACTGTGCCA ACCTCCTA ACCTCACTA AGTGATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCATCAGG TCCACTCAGG TCCACTCAGG TCCACTCAGG TCCACTCAGG TCCACTCAGG TCCACTCAGG TCCACTCAGGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGGGACAGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGG TCTGAGGGGGACAGG TCTGGCAATG TCCCACCAGGT TCCAGGGGGACAGG TCTGGCAATG TCCCACCAGGGGGACAGG TCTGGCAATG TCCCACCAGGT TCCGGGAGGGGACAGG TCTGGCAGGGGACAGG TCTGGCAATG TCCCACCAGGT TCCGGCAGGGGACAGGGACAGGACAGAGAGAGAAGA	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT CTGGACAGCTC TGGACAGCTC GGCTCCTGGG ATACCTCC GGCTCCTGGG ACTACCCAA ACTGCGATGC ACTACCCAGA TGCCCTTGCT ACTACCCAGA TGCCTTGCT CACTGGGGGG CCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT TGAGCTG CCTATGGCCT CCACGGCCTT Sequence NP_003457 21	ATCTGGCCAT GGAAGTGGTC GGAGTGGAG GACTGGCAG CCGAGACCGG CATTAATAGA CCTCGCCAG CATCACCACC CAACACCACCA CAACACCACT CAACACCTCTG AAACCACTC GGGGCCACG CCCCTTTTTG GGGGCCCACG CTCCTCTGCC CACCCTCTGC CACCCCTAGC CCCATTATAT TGACCATCTGC CACCCCTAGC CCCCTTTTTGC CCCATTATAT TGACCATCTGC CACCCCTAGC CCCCTTTTTGC	GGAGGGCTGA GGCAGGCGCA CTCCGCGTCA ATCCGGCTG AACATTGGGG CTCCTGGCTG ATCATCCGGA AACTCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACCAGA ACCCCCAGCC CTGGACGAGCG ACTCACCAGA ACCCCCGAGCG GATCTGCAGCA TCACCAGA TCACCAGA TCACCAGA TCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTCCTCCTACAGCA TTACAGTTCCA	ACCAGCTGGG ACCAGCTGGG ACCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA GCAGCAGCAG AGCCGCTCGA ACACCAAAGG GGAAGGCCAC CCTACCCCGT TGTCCAGTTC AGTTCACGGG ACCCCCCCA TGGTGGCAGC TGTCACGCCT TT	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1320
50 55 60 65	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGCAG GGTCAGCAG GCAACCATTC CACGCTGATC CTCCACCTAC AATGATGAC GGACCCCG AGTGCCCAGT CGAGCAGCCCG CCGGGGTCCCG CCGGGGTCCCG CAGCCCCTC CAGCCCCTC CAGCCCCTC CAGCCCCTC CAGCCCCTC CATCCCCACC AAGTGAATAC GCGTTCCCC GAGTGCACC Seq ID NO: Protein Ac 1 MPHNSIRSGH ILGRYYETGS	ATGCCTCACA GTGAATGGCA GTGAATGGCA GTGAATGGCA GTGAATGGCA ACCTTGGCA ACCTATTTG ACTGTGCCA AACCTCCTTA AGTGATCAGG TCCATCAATG TCCATCACAGG CTCTACCGGC TCCACACAGG CCTTCACTCAC CCTTCACTCAC CCTTCACTGC AGCGGAATGG TCTGGCAATG TCTGGCAATG TCTGGCAATG CCACCACTG SO Protein Cession #: 11	ACTCCATCAG GACCTCTGGC CCTGGGACAT GGTACTACGA GTGTCAGCTC TGGACAGCTC GGCTCCTGGG ATAGCTCC GGCTCCTGGG ATAGCTCC GCTCCTGGG ATAGCTCC CACTGGGCATGC ACTACCCAGA TGCCCTGGT TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCTATGGCCAT GCAGCTATGC CCACGGCCTT SEQUENCE NP_003457 21 VNGRPLPEVVE PKVATPKVVE	ATCTGGCCAT GGAAGTGGTC GGAAGTGGAG CCTGGCCAG CCGAGACCAG CCTCGCCAG CATTAATAGA CCTCGCCCAG ACTAGCACC CAACAGCACC CAACACCTCTCG CAACACCTCTCG CAACACCTCTCG CCACCTCTTTT TGCTGCCTCC CACCCCCTAC CCACTCTTGCC CACCCCCTAC CCACTCTTGCC CACCCCCTAC CCACTCTTGCC CACCCCCTAC CCACTCTGCC CACCCCCTAC CCACTCTGCC CACCCCCTAC CCACTCTGCC CACCCCCTAC CCACTCTGCC CACCCCCTAC CCACTCTGCC CACCCCCTAC CCACTCTGCC CCACTCTCTGCC CCACTCTCTCC CCACTCTCTCC CCACTCTCTCC CCACTCTCTCC CCACTCTCTCCC CCACTCTCTCC CCCCCTCTCTCC CCACTCTCTCC CCACTCTCTCC CCACTCTCTCC CCACTCTCTCT	GGAGGGCTGA GGCAGGGCTGA CTCCGCGTCA ATCCGGCTG AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGATTCCTGGA CCCCAGTCGG CCTGGCAGCG GACTCACAGGA ACTCACCAGC CTGGACGACG GATCTACCAGGA ACTCCCGAGGG GATCTACCAGGA TCCCCGAGGC CTGCCGGAT ATCGCAGGCA TCCTCCTACA TACGTTCACAG TACGTTCACAG TACGTTCACAG TACGTTGAGGCA TTACGTTGAGGCA TTACGTTGAGAGCA TTACGTTGAGGCA TTACGTTGAGAGCA TTACGTTGAGGCA TTACGTTGAGGCA TTACGTTGAGGCA TTACGTTGAGAGCA TTACGTGAGAGAAA TTACGGCAGAGAAAAAAAAAA	ACCAGCTGGG ACCAGCTGGG ACCATGGTTG GAGTGATAGG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGTCAGCAAG GGGCTCCAAG GGGCTCCAAG GCAACCATT CACACTAC CACCTGATC CTCCACCTAC AATGCATGAC GGACCATT CGAGCAGGGC CCTGACCCCT GGTGGCAGAT TAGCTCCACC CAGCTCCCC CATCCCACC CAGCCCCT CATCCCACC CAGCCCTC CATCCCACC CAGCCCTC CATCCCACC AAGTGAACCCT CATCCCACC GAGTGCCCT CATCCCCACC AAGTGAATAC Seq ID NO: Protein AC 1 MPHNSIRSGH ILGRYYETGS TVPSVSSINR SINGLLGIAQ	ATGCCTCACA GTGAATGGCA GTGTAAGGC ATCCTTGGCA ACCTAGTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCATG GAGCGGCAGC CTTACCCGC CTTACCCGC CCTTACTCAC CCTTCCTTCATG CCTTCACTCAC CCTTCACTCAC CCTTCACTCAC CCTCCTTCACTCCCC AGCGGACAGG TCCACCACTC CCTCACTCAC CCTCACTCAC CCTCACTCA	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT GGTCAGCTC TGGACAGCTC GGCTCCTGGG ATACTCCC GGCTCCTGGG ACTACCCCAA ACTGCGCTGCT ACTACCCCAGA TGCCCTTGGC CCTTTCCCCA GAGAGATGGT GCACTGGTC CCTTTCCCCA GAGAGATGGT CCACTGGCT Sequence NP_003457 21 VNGRPLPEVV PKVATPKVVE PKVATPKVVE SDQDSCRLS1	ATCTGGCCAT GGAAGTGGTC GGAGTGGAG GACTGCAGC CATTAATAGA ACTAGCACC CCCGAGTCA ACTAGCATC CTACGCCAG GGCTATGCC CAACACCACC CAACACCACC CAACACTCTCG AAAGCACC CAACCTCTCG CACCTTTTTG GGGCCCACG CTCCTCTGCC CACCTTCTGCC CACCTTCTGCC CACCCTTCTGCC CACCCCTTACC CACCCTTACC CACCCTTA	GGAGGGCTGA GGCAGGCGCA CTCCGCGTCA ATCCGGCTG ATCCGGCTG ATCATCCGGA AAGATTGGGG CTCCTGGCTG ATCATCCGGA AAGTCCCTGA CCCCAGTCGG GACTCACAGC TCCCCCAGCC TCGCAGCGG ACCACCTCG GTGACGGGC CTGGACGGGC CTGCCGGAGG ATCTCACAGA ACCCCCGAGG TTCCCCAGAC TTGCAGGCC TTGCCGGAT ATCGCAGGAC TTGCAGGCC TTGCTGACAGCC TTGCTGACACATCCCACACCCC TTGCTGACAGCC TTGCTGACACCC TTGCTGACCC TTGCTGACACCC TTGCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACC TTGCTCTGACC TTGCTCTGACCC TTGCTCTGACCC TTGCTCTGACC TTGCTCTGACCC TTGCTCTGACC TTGCTCTCTTGACC TTGCTCTTGACC TTGCTCTCTTGACC TTGCTCTTGACCC TTGCTCTCTCTTCTCT	ACCAGCTGGG ACCAGCTGGG ACCATGGTTG GAGTGATAGG ACTACAAACG AGGGCGTCTG CCAAAGTGCA GTCCCGGACA ATTCCCTGGG ACAAGAGGAA ACACCAAAGG GGAAGGCAC ACACCACAAGG GGAAGGCCAC AGTCCCCGT TGTCCAGTTC AAGTCGGCTC AGTCACCGGT ACCACCCCA TGTTGCAGGCT TT LEVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF	120 180 240 300 360 420 640 720 780 960 1080 1140 1200 1320
50 55 60 65 70	GAATTCGGCG AGGGGCCTTT GGCCCACCAG GGGCTCAAG GGGCTCCAAG GGGCTCCAAG CCACGAACCCT TGACAATGAC CCACGCTAC AATGATGAC CGGACCCCGA GTGCCCATT CGAGCAGGCC CTGACCCCAC CAGGCTCCAC CAGGCTCCCG CAGGCCCCT CATCCCACC AAGTGAATAC GCGTTCCCCACC AAGTGAATAC GCGTTCCCG GAGTGCACCC Seq ID NO: Protein AC I MPHNSIRSGH ILGRYYETGS TVPSVSSINR SINGLLGIAR SERQHYPEAYA	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGAATGGCA ATCCTTGGCA ACCTAGTTGG ACCATGTTG ACTGTGCCA ACCTCCTA ACTGATCAGG AGGACTTCG GAGGGGCAGC CTCTACCGC CTCTACTCAC CCTTCACTGC AGCGGAATG AGCGAATG CTCTCACTGC CTCTCAGGC CTCTCACTGC CTCTCAGGC CTCTCACTGC CTCTCAGGC CTCTACCGC CTCTCACTGC CTCTCAGGC CTCTCACTGC CTCTCAGGC CTCAGGC CTCTCAGGC CTCAGGC CTCTCAGGC CTCAGGC CTCTCAGGC CTCTCAGGC CTCTCAGC CTCTCAGC CTCTCAGGC CTCTCAGC CTCAGC CTCTCAGC CTCAGGC CTCAGGC CTCAGGC CTCTCAGC CTCAGGC CTCAGGC CTCTCAGC CTCTCAGC CTCTCAGC CTCAGGC CTCAG	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT CTGGACAGCTC TGGACAGCTC GGCTCCTGGG ATACTCC GGCTCCTGGG ATACTCC GCTCTGCT CACTGCGCAT TATCTAGCTC CCTTTCCCCA TGCAGATGCT GCAGTAGTCC CCTTTCCCCA TGCAGATGCT TATCTAGCTC CCTTTGCCCAT TATCTAGCTC CCTTGGCCAT TATCTAGCTC CCTATGGCCAT TGCAGGCCTT SEQUENCE NP_003457 21 VNGRPLPEVVE NLPMSCVAT SDQDSCRLS1 LYPLPLLMST	ATCTGGCCAT GGAAGTGGTC GGAAGTGGAG CCTGGCCAG GACTGGCAGC CCCGGAGTCA CATCGCTCAG ACTAAGCAT CTCAGCCAG GCCTATAGCC CAACAGCACC CAACAGCACC CAACATCTTTG TGCTGCCTCAG ACTGCTCAG ACTATTTT TGCTGCCTCC CACCCCTAC CCCCTATTTT TGCTGCCTCC CACCCCTAC CCCATATTAT TGACCATCTGC CCCATATTAT TGACCATCTG KIGDYKRQNE KIGDYKRQNE KIGDYKRQNE LDDGKATLTF	GGAGGGCTGA GGCAGGGCA CTCCGCGTCA ATCCGGCTG ATCATCCGGCTG ATCATCCGGAA AAGATTCGTGA ATCATCCGGA AAGATCCCTGA CCCCAGTCGG CCTGGCAGCG GACTCACAGA ACCCCCAGCC CTGGACGAGCG GATCTACCAGA ACCCCCAGAGG GATCTACCAGA ACCCCCGGAGG GATCTGCAGCA TTCCTCCTACA TACGTTGCAGC TTGCAGGCC TTGCAGCC TTGCAGGCC TTGCAGGCC TTGCAGGCC TTGCAGGCC TTGCAGGCC TTGCAGCC TTGCAGGCC TTGCAGCC TTGCAGGCC TTGCAGCC	ACCAGCTGGG ACCAAGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCAG ACACCAAAGG GCAGCACCA ACACCAAAGG GGAAGGCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGCCT TGTCCAGTTC AAGTCGCTC TT 51 LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF THGTYPVVAD	120 180 240 360 480 540 660 720 780 900 900 1020 1140 1260 1320
50 55 60 65 70	GAATTCGGCG GAGGGCCCTACCACACACATTCCACCTAC CATCCCACACACACA	ATGCCTCACA GTGAATGGCA GTGTAAGGCA ATCCTTGGCA ACCTAGGTGG ACCATGTTGCA AACCTCCCTA ACCTCACATG TCCATCAATG AGTGATCAGG AGGCGCACCTCC CTCTACCCGC CCTCACTCAC CCTCCACTCAC CCTCCACTCACCC TCCCACCACTG ACCCGACCACTG LCGGACACGC TCCGCACCACTG II CCGGACCACTG III CGGGINQLGGAF IRPGVIGGSK IIRTKVQQPF PGSDKRNDDI SPSHTKGCQC TPEVSSSSTI	ACTCCATCAG ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT CTGGACAGCT TGGACAGCTC GGCTCCTGGG ACTACCCAGA TGCCCTTGCC ACTACCCCAG TGCCTTCCCCA TATCTACCTC GAGAGATGCT CCTTTCCCCA GAGAGATGGT CCTTTCCCCA TGCTGAGTTC CCATTGCT CCATTGCCCAT TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCTTTCCCCAT TATCTAGCTC CCATTGCCAT TGCTGAGTTC CCACGGCCTT SEQUENCE NP_003457 21 VNGRPLPEVV PKVATPKVVE NLPMDSCVAT SDQDSCRLSI LYPLPLLNST PSSLSSSAFI	ATCTGGCCAT GGAAGTGGTC CTCTCGCCAG GACTGGCAG CCGAGACCGG CATTAATAGA ACTAGCCAC CACCGGAGTCA CATCGCTCAG GGCCTATGCC CAACCTCTCG AAAGCACC CAACCTCTCG GGGGCCCACC CTCCTCTGCC CACCCCTAC CACCCCTAC CACCCCTAC CACCCCTAC CCCATATTAT TGACCATCTG KIGDYKRQNE KSLSPGHTLI DSQSSSSGPR LDDGKATLTT LDLQVGSCVF	GGAGGGCTGA GGCAGGCGCA CTCCGCCTCA ATCCGGCTCA ATCCGGCTG ATCATCCGGC ATCATCCGGCTG ATCATCCGGA ACCTCAGCTGG CCTGGCAGGCG GACTCACAGA ACCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC TACCAGACG ATCGCAGGC TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCGAT ATCGCAGGCC TTGCAGCGAT TACGTTCACA TACGTTCA	ACCAGCTGGG ACCAGCTGGG ACCAGCTGG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG ACTCCCTGGG ACAAGAGGAA ACTCCCTGGG ACAACAAGG AGCCGCTCGA ACACCAAAGG GGAAGGCAC AGTCCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGCAGGT CATCAAGGCC TT LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF TTQTYPVAD VYGQFTGQAL	120 180 240 300 360 420 640 720 780 960 1080 1140 1200 1320
50 55 60 65 70	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGTCAGCAAG CCAGAACCCT TGACAATGAC GCACCATT CCACCTAC AATGACAC GTGCCCATC GGTCCCACTAC AATGACACCT CGGACCCCT GGTGCCATT CGAGCAGGC CCTGACCCCC GGTGCCATT TAGCTCCAC CAGCCCTC CATCCCCAC AAGTGAATC CAGCCCTC CATCCCCAC AAGTGAATAC Seq ID NO: Protein Ac I MPHNSIRSGH ILGRYYETGS TVPSVSSINR SINGLLGIAQ ERQHYPEAYA PHSPFAIKQE LSGREMWGPT	ATGCCTCACA GTGAATGGCA GTGTAAGGCA ATCCTTGGCA ACCTAGGTGG ACCATGTTGCA AACCTCCCTA ACCTCACATG TCCATCAATG AGTGATCAGG AGGCGCACCTCC CTCTACCCGC CCTCACTCAC CCTCCACTCAC CCTCCACTCACCC TCCCACCACTG ACCCGACCACTG LCGGACACGC TCCGCACCACTG II CCGGACCACTG III CGGGINQLGGAF IRPGVIGGSK IIRTKVQQPF PGSDKRNDDI SPSHTKGCQC TPEVSSSSTI	ACTCCATCAG ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATACCTCCG GCTCCTGGG ATACCCCAA ACTACCCAGA TGCCCTTGCT ACTACCCAGA TGCCCTTGCT CCTTTCCCCA GAGAGATGGT GCATTCTCCCA GAGAGATGGT CCTTTCCCCA TGCTGAGTTC CCACGGCCTT Sequence NP_003457 21 VNGRPLPEVV PKVATPKVVAT SDQDSCRLS1 LYPLPLINST PSSLSSSAFI SGQGSYASSA	ATCTGGCCAT GGAASTGGTC GGAAGTGGTCA GACTGGCAG CCGAGACCGG CATTAATAGA ACTAGCATC CACCGTCAG GGCTTAGCC CAACCTCTCG AAAGCAGT CGACCTTTTTG GGGGCCACC CCACCTTTTTTG GCCATTTTTTG TCACCACG CTCCTCTGCC CACCTTTTTG CCACCCCTAC CACCTTTTTG TGACCATCTG CCCCTTAGCC CACCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCTAC CACCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCCTAC CACCCCCCTAC CACCCCCCTA	GGAGGGCTGA GGCAGGCGCA CTCCGCCTCA ATCCGGCTCA ATCCGGCTG ATCATCCGGC ATCATCCGGCTG ATCATCCGGA ACCTCAGCTGG CCTGGCAGGCG GACTCACAGA ACCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC TACCAGACG ATCGCAGGC TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCGAT ATCGCAGGCC TTGCAGCGAT TACGTTCACA TACGTTCA	ACCAGCTGGG ACCAAGTTG GAGTGATAGG ACTACAAACG AGGCGTCTG CCAAAGTGCA ATTCCCTGGG ACAGCAGCAG ACACCAAAGG GCAGCACCA ACACCAAAGG GGAAGGCAC CCTACCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGCCT TGTCCAGTTC AAGTCGCTC TT 51 LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF THGTYPVVAD	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 120 1320
50 55 60 65 70	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGGCTCAAG GGGCTCAAG GGGCTCAAG CTCACCTAC TGACAATGAC CTCACCTAC AATGATGAC CGGACCCCGA GTGCCCATT CGAGCAGGCC CTGACCCCT CGTGGCAGC CCTGACCCCT CATCCCACC AAGTGATAC CGGGTCCCG GCGGCTCCCG CATCCCCACC AAGTGAATAC GCGTTCCCC GAGTGCACCC Seq ID NO: Protein AC I MPHNSIRSGH ILGRYYETGS TVPSVSSINR SINGLLGIAG ERQHYPEAYA PHSPFAIKQE LSGREMYGPT NSSLLSSPYY	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGAATGGCA ATCCTTGGCA ACCTGTGCA ACCTCCTA ACCTCACTA ACTGATCAT AGTGATCAGG AGCACTTC GAGGGGCAGC CTCTACCGC TCCAACACGC CTCTACTCAC CCTTCACTGC AGCGGAAGG CTCTCACTGC CTCTCACTGC AGCGGAAGG TCTGACAGG ACCGCACACTG AGCGGACAGG TCTGCCATTGC TCTCACTGC AGCGGACAGG TCTGCCATTG AGCGACAGG TTTGGCAATG AACTCCAGCT SO Protein CGGBACAGG TITTGCCATGC TCCACCACTG SO POSTEIN CGGBACAGG TTTGGCAATG AACTCCAGCT SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGCC TCCACCACTG SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC TCCACCACTG TCCACCACCACTG TCCACCACTG TCCACCACCACTG TCCACCACCACCACCACCAC TCCACCACCACCACCACCACCACCACCACCACCACCACCA	ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT GGTACAGCT CTGGACAGCT GGCTCCTGGG ATACTCCC GGCTCCTGGG ATACTCC GCTCTGGC ACTCCCAGA TGCCCTGGT TATCTAGCTC CCTTTCCCCA TGCTGAGATGC GCAGATGC GCAGATGC TATCTAGCTC CCTTTCCCCA TGCTGAGTT CCACGGCCTT SEQUENCE NP_003457 21 VNGRPLPEVV PKVATPKVVE NLPMDSCVAT SDQDSCRLS1 LYPLPLLNST SGCGSYASSA PTTATAFPHI	ATCTGGCCAT GGAASTGGTC GGAAGTGGTCA GACTGGCAG CCGAGACCGG CATTAATAGA ACTAGCATC CACCGTCAG GGCTTAGCC CAACCTCTCG AAAGCAGT CGACCTTTTTG GGGGCCACC CCACCTTTTTTG GCCATTTTTTG TCACCACG CTCCTCTGCC CACCTTTTTG CCACCCCTAC CACCTTTTTG TGACCATCTG CCCCTTAGCC CACCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCTAC CACCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCTAC CACCCCCCCTAC CACCCCCCTAC CACCCCCCTA	GGAGGGCTGA GGCAGGCGCA CTCCGCCTCA ATCCGGCTCA ATCCGGCTG ATCATCCGGC ATCATCCGGCTG ATCATCCGGA ACCTCAGCTGG CCTGGCAGGCG GACTCACAGA ACCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC TACCAGACG ATCGCAGGC TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCGAT ATCGCAGGCC TTGCAGCGAT TACGTTCACA TACGTTCA	ACCAGCTGGG ACCAGCTGGG ACCAGCTGG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG ACTCCCTGGG ACAAGAGGAA ACTCCCTGGG ACAACAAGG AGCCGCTCGA ACACCAAAGG GGAAGGCAC AGTCCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGCAGGT CATCAAGGCC TT LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF TTQTYPVAD VYGQFTGQAL	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 120 1320
50 55 60 65 70 75	GAATTCGGCG AGGGCCTTT GGCCCACCAG GTCAGCAAG CCAGAACCCT TGACAATGAC GCACCATC CCACCTAC AATGACT CTCACCTAC AATGACT CGGACCCCT GGTGCCATT CGAGCAGGGC CCTGACCCCT GGTGCCATT CGAGCAGGGC CCTGACCCCT GGTGCCATT AGCTCCACC CAGGCCCTC CATCCCCAC CGGGGTCCG CAGGCCCTC CATCCCCAC Seq ID NO: Protein AC I MPHNSIRSGH ILGRYYETGS TVPSVSSINR SINGLIGIAC ERQHYPEATA PHSPFAIKQE LSGREMVGPT NSSLLSSPYY Seq ID NO:	ATGCCTCACA GTGAATGGCA GTGTAAGGCA ATCCTTGGCA ACCTAGGTGG ACCATGTTTG ACTGTGCCA AACCTCCCTA CCCAGCTCAG TCCATCAATG TCCATCAATG GAGCGCACCTTC GAGCGCACCC TCCAACACGC CCTCACTCAC CCTTCCTCTT CCCTTCAATG CTCCACCACC SO Protein CCGACCACTG 11 GGLNOLGGAE INTEVVQOPE PGSDKRKMDE SPSHTKCGC TPEVSSSST LPGYPPHIPT YSSTSRPSAE ST DNA BEG	ACTCCATCAG ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTGCGAGAT GTGTCAGCTC TGGACAGCTG GCTCCTGGG ATACCCAGA TGCCCTGCG ATACCCAGA TGCCCTTCGCCAT TATCTAGCTC CCTTTCCCCA GAGAGATGGT GCAGTATGCC CCTTTCCCCA GAGAGATGGT CCATTGCCCT Sequence NP_003457 21 VNGRPLPEVVE NLPMDSCVAT SDQDSCRLSI LYPLPLLNSI LYPLPLLNSI SGQGSYASSAP PTTATAFDHI TUENCE	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTGGTGGAG CCGAGACCGG CATTAATAGA ACTAGCCAG ACTAGCAG ACTAGCAG CCAACACCAC CAACCTCTCG AAAGCAGGAC CGGCCTATGC CAACCTCTCG CAACCTCTCG AAGCAGCAC CCCTATTAT TGACCATCT CCCCTACT CCACCCTACT CCACCCCTAC CCCATATTAT TGACCATCTG KIGDYKRQNE KSLSPGHTLI DLQVGSGYE LDDGKATLTT DLQVGSGYE LAGMVAGSEY	GGAGGGCTGA GGCAGGCGCA CTCCGCCTCA ATCCGGCTCA ATCCGGCTG ATCATCCGGC ATCATCCGGCTG ATCATCCGGA ACCTCAGCTGG CCTGGCAGGCG GACTCACAGA ACCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC TACCAGACG ATCGCAGGC TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCGAT ATCGCAGGCC TTGCAGCGAT TACGTTCACA TACGTTCA	ACCAGCTGGG ACCAGCTGGG ACCAGCTGG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG ACTCCCTGGG ACAAGAGGAA ACTCCCTGGG ACAACAAGG AGCCGCTCGA ACACCAAAGG GGAAGGCAC AGTCCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGCAGGT CATCAAGGCC TT LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF TTQTYPVAD VYGQFTGQAL	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 120 1320
50 55 60 65 70	GAATTCGGCG AGGGCCTTT GGCCCACCAG GGGCTCAGCAG GGGCTCAGCAG GGGCTCAGCAGC GCAACCATT CACACTAC AATGCATGAC CTCACCTAC AATGCATGAC CTCACCTAC CAGCCCGA GTGCCCATT CGAGCAGGGC CCTGACCCCT CATCCCACC CATCCCCC CATCCCCCC CATCCCCAC CAGGCCCTC CATCCCCAC AAGTGAATCAC GCGCTTCCCC GAGTGCACCT CATCCCACC AAGTGAATCAC GCGCTTCCC GAGTGCACC Seq ID NO: Probein AC 1 MPHNSIRSGH ILGRYYETGS: TVPSVSSINR SINGLLGIAQ ERQHYPEAYA PHSPFAIKG LSGREMVGPT NSSLLSSPYY Seq ID NO: Nucleic Ac	ATGCCTCACA ATGCCTCACA GTGAATGGCA GTGAATGGCA ATCCTTGGCA ACCTGTGCA ACCTCCTA ACCTCACTA ACTGATCAT AGTGATCAGG AGCACTTC GAGGGGCAGC CTCTACCGC TCCAACACGC CTCTACTCAC CCTTCACTGC AGCGGAAGG CTCTCACTGC CTCTCACTGC AGCGGAAGG TCTGACAGG ACCGCACACTG AGCGGACAGG TCTGCCATTGC TCTCACTGC AGCGGACAGG TCTGCCATTG AGCGACAGG TTTGGCAATG AACTCCAGCT SO Protein CGGBACAGG TITTGCCATGC TCCACCACTG SO POSTEIN CGGBACAGG TTTGGCAATG AACTCCAGCT SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGCC TCCACCACTG SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC SO POSTEIN CGGBACAGG TTTGGCAATG ACTCGAGC TCCACCACTG TCCACCACCACTG TCCACCACTG TCCACCACCACTG TCCACCACCACCACCACCAC TCCACCACCACCACCACCACCACCACCACCACCACCACCA	ACTCCATCAG ACTCCATCAG GACCTCTGCC CCTGCGACAT GGTACTACGA CCTCGGAGAT GTGTCAGCTC GGCTCCTGGG ATACTCCC GGCTCCTGGG ACTACCCAGA TGCCCTTGCT CACTGGGGCA CCTTCGCCAT TATCTAGCTGC CCTTTCCCA GAGAGATGGT GCACTGCT SEQUENCE NP_003457 21 VNGRPLPEVV PKVATPKVVE PKVATPKVVE PKVATPKVL SDQDSCRLSI LYPLPLINST PSSLSSSAFI SGQGSYASSS PTTATAFDHI LUENCE LUE	ATCTGGCCAT GGAAGTGGTC GGAAGTGGTC GGTGGTGGAG CCGAGACCGG CATTAATAGA ACTAGCCAG ACTAGCAG ACTAGCAG CCAACACCAC CAACCTCTCG AAAGCAGGAC CGGCCTATGC CAACCTCTCG CAACCTCTCG AAGCAGCAC CCCTATTAT TGACCATCT CCCCTACT CCACCCTACT CCACCCCTAC CCCATATTAT TGACCATCTG KIGDYKRQNE KSLSPGHTLI DLQVGSGYE LDDGKATLTT DLQVGSGYE LAGMVAGSEY	GGAGGGCTGA GGCAGGCGCA CTCCGCCTCA ATCCGGCTCA ATCCGGCTG ATCATCCGGC ATCATCCGGCTG ATCATCCGGA ACCTCAGCTGG CCTGGCAGGCG GACTCACAGA ACCCCAGCC CTGGACGACG ACTCACCAGA ACCCCCAGGC GTGTACGGGC GTGTACGGGC TACCAGACG ATCGCAGGC TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCG TTGCAGCGAT ATCGCAGGCC TTGCAGCGAT TACGTTCACA TACGTTCA	ACCAGCTGGG ACCAGCTGGG ACCAGCTGG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG AGGGCGTCTG ACTCCCTGGG ACAAGAGGAA ACTCCCTGGG ACAACAAGG AGCCGCTCGA ACACCAAAGG GGAAGGCAC AGTCCCCGT TGTCCAGTTC AAGTCGGCTC AGTTCACGGG ACCCACCCCA TGGTGCAGGT CATCAAGGCC TT LRVSHGCVSK LLAEGVCDND PQSDSLGSTY HHLEPLECPF TTQTYPVAD VYGQFTGQAL	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 120 1320

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	TTCAGAAGGA	 GGAGAGACAC	CGGGCCCAGG	GCACCCTCGC	 GGGCGGGCGG	ACCCAAGCAG	60
-	TGAGGGCCTG	CAGCCGGCCG	GCCAGGGCAG	CGGCAGGCGC	GGCCCGGACC	TACGGGAGGA	120
5			CTGCGAGCGA				180 240
	ATCTGGCCAT	CCCACCCCA	ACCAGCTGGG TCGTAGACCT	GGCCCACCAG	GTGAATGGCA	CCTGCGACAT	300
	CTCTCGCCAG	CTCCGCGTCA	GCCATGGCTG	CGTCAGCAAG	ATCCTTGGCA	GGTACTACGA	360
10	GACTGGCAGC	ATCCGGCCTG	GAGTGATAGG	GGGCTCCAAG	CCCAAGGTGG	CCACCCCAA	420
10			ACTACAAACG AGGGCGTCTG				480 540
			CCAAAGTGCA				600
	CGTGGCCACC	AAGTCCCTGA	GTCCCGGACA	CACGCTGATC	CCCAGCTCAG	CTGTAACTCC	660
15	CCCGGAGTCA	CCCCAGTCGG	ATTCCCTGGG ACAAGAGGAA	CTCCACCTAC	TCCATCAATG	ATACCTCCC	720 780
15	ACTAAGCATT	GACTCACAGA	GCAGCAGCAG	CGGACCCCGA	AAGCACCTTC	GCACGGATGC	840
	CTTCAGCCAG	CACCACCTCG	AGCCGCTCGA	GTGCCCATTT	GAGCGGCAGC	ACTACCCAGA	900
	GGCCTATGCC	TCCCCCAGCC	ACACCAAAGG GGAAGGCCAC	CGAGCAGGGC	CTCTACCCGC	CACTGGGGGG	960 1020
20	CAACAGCACC	ACTCACCAGA	CCTACCCCGT	GGTGGCAGCT	CCGCCCTTTT	GGATCTGCAG	1080
	CAAGTCGGCT	CCGGGGTCCC	GCCCTTCAAT	GCCTTTCCCC	ATGCTGCCTC	CGTGTACGGG	1140
	CAGTTCACGG	GCCAGGCCCT	CCTCTCAGGG	CGAGAGATGG	TGGGGCCCAC	GCTGCCCGGA	1200 1260
	ATGGTGGCAG	GAAGTGAATA	CAGCGGACAG CTCTGGCAAT	GCCTATGGCC	ACACCCCCTA	CTCCTCCTAC	1320
25	AGCGAGGCCT	GGGGCTTCCC	CAACTCCAGC	TTGCTGAGTT	CCCCATATTA	TTACAGTTCC	1380
			GCCCACCACT	GCCACGGCCT	TTGACCATCT	GTAGTTGCCA	1440
	TGGGGACAGT	G					
20		52 Protein					
30	Protein Acc	cession #: 1 11	NP_039246 21	31	41	51	
	Ī	1	1	1		i	
	MPHINSIRSGH	GGLNQLGGAF	VNGRPLPEVV	RORIVOLAHO	GVRPCDISRQ	LRVSHGCVSK	60
35	ILGRYYETGS	IRPGVIGGSK	PKVATPKVVE NLPMDSCVAT	KIGDYKRQNP	PSSAVTPPES	POSDSLGSTY	120 180
55	SINGLLGIAQ	PGSDKRKMDD	SDQDSCRLSI	DSQSSSSGPR	KHLRTDAFSQ	HHLEPLECPF	240
	ERQHYPEAYA	SPSHTKGEQG	LYPLPLLNST	LDDGKATLTP	SNTPLGRNLS	THQTYPVVAA	300
			MLPPCTGSSR TPPTPPTARP		WGPRCPDTHP	TSPPADRAAM	360
40	FEDEOGRAM	24412204101					
		53 DNA seq		400			
			n #: NM_012	421			
		uence: 43	924				
	1	uence: 43! 11	924 21	31	41	51	
45	1	11 	21 '	1	1	1	60
45	1 CTTGTGGTTC	11 CTCTCTACTT	21 GGGGAAATCA	 GGTGCAGCGG	CCATGGCTAC	 AGCAAGACCC	60 120
45	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC	120 180
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC	120 180 240
45 50	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA	120 180
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT	120 180 240 300 360 420
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAAGAAAGT GGCAGCAGAT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC GTTCCAGGGG	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTTGGTGCATC CGTCTCGGCC GTCAAATCCA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC	120 180 240 300 360 420 480
	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG GGCAGCAGGA GGCCAGCAGA ACTCTAACGA ACTCTAACGA GGCCCATCAA	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGTG TTTCAGGGTG GTTCCAGGGTG CCTCATGCTC CGTCTCCTCT	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GAGGCCGGGT ACCCAGCCGGT TTGGTGGATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCG CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAC CTGCTGGGAC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTTGCTA GCTCACCGGCC GTCACCAGTT TGGCTACTCC AGCTCCCACT AAAGTGCTTG	120 180 240 300 360 420
50	1 CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT GGCAGCAGAT ACTCTAACGA GACCCATCAA	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGTT TTCCAGGGG CCTCATGCTC CGTCTCCTCT CAAGAGCCCC	GTTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA ACATTGCCCT CAAGTGCACT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCTACAGCAGTT TGGCTACTCCACTCC	120 180 240 300 360 420 480 540 600
50	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GGGGGCACAC GGCAGCACAC GGCAGCACAC GGCGGCACAC GGCGGCACAC GGCGCACAC GGCGGCACAC GGCGGCACAC GGCGGCACAC GGCGGCACAC GCGTGCTAAG	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGCGCGGT TTTCAGAGT CGTCTCAGGG CCTCATGCTC CAGAGAGCCCC TCAGAAAAGG	GTTGCAGCGG ACAGCCTTGC CACCCCTTA GACGCCGGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TAGGTGCACT TAGGTGCACT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCGCC CACAGTGGCT TCCCCCACCC ACAGAAGAAT CTGCTGAGAC TCCCTAAGGT CTTACCCGAG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGGC CAGCAGCGGC GCTCACCAGTT TGGCTACTACT TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGTTACTACAGTTACACAGTT CAGCAGTTACTACAGTTACACAGTTACAGTTACAGTACAGTTACAGTAGTACAGTAGATACAT	120 180 240 300 360 420 480 540 600 660 720
50 55	1	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGCAGAT ACTCTAACGA GACCCATCAA GCCGGCACAAC GCGTGCTAAG TCTGCGCCGC TCTGCGCCGG TCTGCAATGG	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTGT GTTCCAGGGG CCTCATGCTC CAAGAACCC TCAGAAAAGG TGACAAAAGG CCTCCTGCAG	GTTGCAGCGG ACACCCTCTA ACACCCCTCTA GACGCCCGGT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT TGCGAGGATG GGTAGAGACT GGACTCGTGT	CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCCTAAGGT CTTACCCGAGG CCTGCCAGGG CCTGGGAGAGAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT	120 180 240 300 360 420 480 540 600
50	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGCCTGTGG GGCCTGTGG GGCCTGTGG GGCCTGTGG GCCCGGCCCA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA ACTCTAACGA GCGGGACAAC GCGTGCTAAG TCTGCGCCGG TCTGCAATGG ACAGACCGGGG ACAGACCGGGG ACAGACCGGGG ACAGACCGGGG ACAGACCGGGG ACAGACCGGGGACACC	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGCGGGTGT TTTCAGAGTC GTTCCAGGGG CCTCATGCTC CAACAGCCC TCAGAAAAGG TGACAAAAGG TGTCCCTGCAG TGTCCCTGCAG TGTCCCTGCAG TGTCCCTGCAG TGTCTACACG	GGTGCAGCGG ACAGCCTTA ACAGCCGGT TTGGTGCATC GTCAAATCCA ATCAAATCAC ATGAGCACT TGGTGCACT CAGTGCACT CAGTGCACT TGGAGATG AGATGCACT TGGAGATG AGATCGAGATG ACCTCTGCA	CCATGGCTAC TTCTGGGGT ACACCGTGCC GGATGACAG GGCAGGCGC CACAGTGGCT ACTACTCCCT TCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTTACCCGAG CCTGCCAGG CCTGCCAGGA AGTTCACCAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCC GCGACAGCT GCTCACCAGTT TGGCTACCACT TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGATCCAG	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCCGGCCCA GAAACCATCC	11 GGTGCTTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GGCGGCATCAA GGGGGCAACA TCTGCGCCGG TCTGCAATGG ACAGACCGG ACAGACCGG ACAGACCGG	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTG TTTCAGAGTC CGTCTCCTCT CAAGAGCCC TCAGAAAAGGA TGACAAAAGCA CTCCTTGCAG TGTCTCTCAGAG CTCCTTCAGAG CTCCTTCAGAG CTCCTTCAGAG CTCCTTCAGAG CTCCTTCACAG CTCCTTCACAG	GTTGCAGCGG ACAGCCTTTA ACACCCCTTA ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGC GTCAAATCGA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGTAGGACT GGTAGGACT ACCTCTGGT ACCTCTGT ACCCTCTGT ACCTCTGT ACCTCTGT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT TCCCCACCC TCCCCACCC TCCCTAAGGT CTTCCCTAAGGT CTTCCCTAGGC CCTGGGAC CCTGGGAC AGTTCACCAA GCACACCAG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG ATCCCACCT	120 180 240 360 420 480 540 660 720 780 840 900
50 55	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGGT TTGAATATCA GACACCATGT GGGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GACCCATCAA GCGGGACAAC GCGTGCTAAG TCTGCGCCGG ACACCGCGGAAGCCGGCCTACCC CGCCCATCCA CGCCCTACCA CCTCCAGCCCCC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGGTA TTTCAGAGTC GTTCCAGGGG CCTCATGCTC CAAGAGCCC TCAGAAAAGCA TGACAAAGCA TGTCTCCTCTCAGA TGTCTCACAG TGTCTCAGAG TGTCTACACG CTGAGTCATCA ACTCCTTCACAG TGTCTACACG	GGTGCAGCGG ACAGCCTTA ACAGCGGT TTGGTGCATC ATCAAACTGA ATCAAACTGA CATTGTCCCT TGGAGGAT GGATAGAGAT GGATAGAGAT ACCAGGAT TGCAGGAGAT TGCAGGAT TGCAGGAT TGCAGGAT TGCAGGAT ACCTCTGCA CCAGGACTCA GGACCTCAT TCTCCTGGAG	CCATGGCTAC CCATGGCTAC CGGATGACAG GGCAGGCCGC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTTCCCAGGG CCTGCCAGGG CCTGGCAGGG CCTGCCAGGG CCTCCCAGAG TCACCGAGAG TCACCGAGAGAGAA AGTTCACCAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTGCTACCACT TGGCTACCACT TAAGTGCTTAC CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG ATCCCCACCT GATGTTGACA CTTCCCCACC	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55 60	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACCG GCCCACTGCA ATAGGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGCCCTAGGC GCCGGCCCA GCACCACGCC GCTGCAGGGA ATGTTCATCT ATTGGGCTGA	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG ACTCTAACGA ACTCTAACGA CGCTGCAGAT ACTCTAACGA TCTGCACCGG TCTGCACCGG ACAACCGGG ACAACCGGG ACGACCCTGACC CCCGTGTCTCC	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTT TTTCAGAGTC CTCATGCTC CAGAGAGCCC TCAGAAAAGGA CTCCTCTACAC TGACTACACC ACTCCTTCACACC ACTCCTTCACACC ACTCCTTCACACC ACTCCTTTCACCC ACTCCTTCACACC ACTCCTTTCACCC	GGTGCAGCGG ACAGCCTTA ACAGCCGGT ACCCAGCGGT ACCCAGCGGT ACCCAGCGGT ACCCAGCGGT ACCAAATCCA ATCAAATCCA ATCAAATCGA CATTGTCCCT CAAGTGCACT GGACTCGGGT ACCTCTGGAC CCAGGACTCA GACCCTCATT TCTCCTGGAC CCTGGAC	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT TCCCCACCC ACAGAAGAAT CTGCTGGGAC TCTTACCCGAG CCTGGCGAGG CCTGGCGAGG AGGTACCCAAGGAGAAGAT AGTTCACCAAGA TCAGGGTCTG ATTTCCAAAA	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT TGGGTACTCC GTGACCCACCT AAATTCTGGG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGG CTTCCCCACCC CTGTCCCACGG	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080
50 55	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCAACC TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCTT ATTGGCTTGT	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGAAAGT GGCAGCAGAT ACTCTAACGA GCGGGACAAAC GCGTGCTAAG TCTGCGCCGG TCTGCACCGG ACAGACCGGG ACGCCCTGACC CCGGGCCCG CCGGTGCTCAC GCTGTCTCT GTCTCAATCT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGTCGGGGGGTGTG GTTCCAGGGG CCTCATGCTC CAAGAGCCCC TCAGAAAAGG TGTCTACACG TGTCTACACG GTGTCTACACG CCTCATGATCTCACCT ACTCCTTCAAGATCACCC ACTCCTTCAAGATCACCC TGAGACCACCCCTCACCCCCCCCCC	GTTGCAGCGG ACAGCCTTTA ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGGGAGGATG GGTAGGACT GGACTCGTGT AACCTCTGGC GACCTCGTGT ACCTCTGGC CAGTGCACA CCAGGGAACA CCAGGGAACA CCTGTGCAC CCTGGGGAACA CCTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC CCTCCTAAGGT CCTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTCACAGA AGTTCACCAA AGTTCACCAA CCAGGGTCTG TCAGGGTCTAGGT TCAGGGTTCAGGA ATTTCCAAGA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGARGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATACTCTG TGATCCTGT GTGATCCTGT GTGATCCACT GATGTTCCCCACC GATGTTGATCCCGACCT GATGTTCACGG CTTCCCCACC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 1020
50 55 60	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATTCA GACCCTGGCC AAAGATGTCA GTGTCTGGT TTGAATATCA GACACCATGT GGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGCTGA CGGGGGTTGC TCTCTGCAGC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT GGCAGCAGAT ACTCTAACGA GACCCATCAA GCGTGCTAACG TCTGCGACGG ACACCCGGG ACGCCCAACTC CAGCCCTGCA CTCCAGCCCC CCGTGTCTCT TCTGACCCAA	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGCGGGGGT TTTCAGAGTC GTTCCAGGGG CCTCATGCTC TCAGAAAGCA TGACAAAGCA TGACAAAGCA TGTCTCTCAGGAG TGTCTCCTCT TCAGAAAAGCA TGTCTTACACG CTGAGTCATC ACTCCTTTCA ACTCCTTTCA TGACCCCAGG CTAGGTCATC ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC	GTTGCAGCGG ACAGCCTTTA ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGGGAGGATG GGTAGGACT GGACTCGTGT AACCTCTGGC GACCTCGTGT ACCTCTGGC CAGTGCACA CCAGGGAACA CCAGGGAACA CCTGTGCAC CCTGGGGAACA CCTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC CCTCCTAAGGT CCTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTCACAGA AGTTCACCAA AGTTCACCAA CCAGGGTCTG TCAGGGTCTAGGT TCAGGGTTCAGGA ATTTCCAAGA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT TGGGTACTCC GTGACCCACCT AAATTCTGGG ATCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGG CTTCCCCACCC CTGTCCCACGG	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080
50 55 60	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCA ATATGAATGTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGCCCACGCCCA GCACCCATGT GGCCTGTGG GCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGCTGA CGGGGGTTGC TCTCTGCAGC Seq ID NO:	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG AGCTCTACTG ACTCTAACGA ACTCTAACGA TCTCAACGA TCTGCACCGG TCTGCAATGGA ACGCCTGACC CCGCTGTCTCT GTCTCAATCT TCTGACCCAA	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGGCGGTT TTTCAGAGTC CGTCTCCTCT CAAGAGCCC TCAGAAAAGCA CTCCTTGCAC TGACTACAC CTGAGTCACCC ACTCCTTCAC ACTCCTCAC ACTCCTTCAC ACTCCTTCA	GTTGCAGCGG ACAGCCTTTA ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGGGAGGATG GGTAGGACT GGACTCGTGT AACCTCTGGC GACCTCGTGT ACCTCTGGC CAGTGCACA CCAGGGAACA CCAGGGAACA CCTGTGCAC CCTGGGGAACA CCTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC CCTCCTAAGGT CCTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTCACAGA AGTTCACCAA AGTTCACCAA CCAGGGTCTG TCAGGGTCTAGGT TCAGGGTTCAGGA ATTTCCAAGA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGARGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATACTCTG TGATCCTGT GTGATCCTGT GTGATCCACT GATGTTCCCCACC GATGTTGATCCCGACCT GATGTTCACGG CTTCCCCACC	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080
50 55 60	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCAACC TATGAATCTG CACCTTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGCTGT ATTGGGCTGT TCTCTGCAGGC Seq ID NO: Protein AC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGCAGAT ACTCTAACGA GGCGGCACAAC GCGTGCTAAC TCTGCGCCCG TCTGCACCGG ACACACCCGCC CCGTGTCTCT TCTGACCCAA 54 Protein Cession #:	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGTCGGGGGGTAT GTTCCAGGGG CCTCATGCTC CAAGAAAGGA TGCTCCTCT CAAGAAAGGA TGCTCATCAGG TGTCTACACG TGTCTACACG CTGAGTCATC ACTCCTTCAG TGTCTACACG CTGAGTCATC ACTCCTTTCA CTGAGTCATC ACTCCTTTCA CTGGGGCA ATTTAGTCCC Sequence NP_036559	GTTGCAGCGG ACAGCCTTTA ACCCAGCCGT TTGGTGCATCC GTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGGGAGGATG GGTAGGACT GGACTCGTGT AACCTCTGGC GACCTCGTGT ACCTCTGGC CAGTGCACA CCAGGGAACA CCAGGGAACA CCTGTGCAC CCTGGGGAACA CCTTTCATCCT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT ACTACTCCT TCCCCCACCC ACAGAGAAT CTGCTGGGAC CCTCCTAAGGT CCTTACCGAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTCACAGA AGTTCACCAA AGTTCACCAA CCAGGGTCTG TCAGGGTCTAGGT TCAGGGTTCAGGA ATTTCCAAGA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGARGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATACTCTG TGATCCTGT GTGATCCTGT GTGATCCACT GATGTTCCCCACC GATGTTGATCCCGACCT GATGTTCACGG CTTCCCCACC	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080
50 55 60 65	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCACTGCA ATATGAATGTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGCCCTATGCA GACACCATGT ATTGGATATCA GCTGCAGGGA ATGTTCATCT ATTGGGCTGA CGGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGCAGCAGAT ACTCTAACGA GCCCATCAAA GCGGGACAAC GCGTGCTAAGG TCTGCAGCCGG ACAGCCCTGAC CCCCGTGTCTCT GTCTCAATCT TCTGACCCAA 54 Protein cession #: 11	21 GGGGAAATCA TECTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTGT CTTCAGAGTC CGTCTCCTCT CAAGAGCCC TCAGAAAAGCA CTCCTGCAG CTCACTACAC CTGAGTCACC ACTCCTTCAC ACTCCTTCAC CTGAGTCACC ACTCCTTCAC CTGAGTCACC ACTCCTTCAC CTGAGTCACC ACTCCTTCCA CCCGGGGCA ATTTAGTCCC Sequence NP_036559 21	GTTCAGCGG ACACCCTTA ACACCCGTT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGACTCGGT ACCTCTGGA CCAGGACTCA GACCCTCATT TCTCCTGGA CCTGGAACA CCTTCATCCT AGAAATAAAC	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC ACAGTGGCT TCCCCACCC ACAGAAGAAT CTGCTGGGAC TCTCCCTAAGG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAA AGTTCACCA TCAGGGTCTC ATTCCCAAA TCAGGGTCTG ATTTCCAAAA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTC AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG TTACCCTTGT GTGGATCCAG ATCCCACCT GATGTTGAGA CTTCCCCACC CTGTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 600 720 780 840 900 960 1020 1140 1200
50 55 60 65	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCGGCCCA GAAACCATCT GTTGAGTGA GCTGGAGGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC Seq ID NO: Protein Ac I MATARPPWMW	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGCAGAT ACTCTAACGA GACCATCAA GGGGGACAAC GCGTGCTAAG TCTGCGCCGG ACAGCCCATCAA CTCCAGCCCC CCGCTGTCTCT TCTGACCCAA 54 Protein cession #: 11 VUCALITALL	21 GGGGAAATCA TGCTCTGTAC TGCTCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGTGT TTTCCAGGGG CCTCATGCTC CAACAGACCC TCAGAAAAGG TGTCCATCAG TGTCTACACG TGTCTACACG CTGAGTCATC ACTCCTTCAG ACTCCTTTCA TGACCCCATG ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC Sequence NP_036559 21 LGVTEHVLAN	GTTGCAGCGG ACAGCCTTTA GACGCCGTT ACCCAGCCGT TTGGTGCATC CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT CAAGTGCACT GGACACTCGTGT AACCTCTGGC GGACACTCAT TCTCCTGGACA CCAGGACTCA CCTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTCCCAGAG CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCAGGTTTCACAGA TCAGGTTCAC TCAGGTTCAGGT TCAGGGTCAGG TCAGGGTCAGG TGAGAAGTGG TGAGAAGTGG	AGCAAGACCC CACAGAGCAT CTCTGGARGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATACTCT TGATCCTGT GTGATCCAC TGATCCTGT GTGATCCAG ATCCCCACCT GATGTTGATCAGA CTTCCCCACC GATGTTGAGA CTTCCCCACC TGTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 900 900 900 1020 1080 1140
5055606570	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATTARPPWMW DDSSSRIING	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA GCGGGACAAC GCGTGCTAAG TCTGCGACGG ACGCCCTACAC CCGCCTACC CCGTGTCTCT TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SDCDMHTOPW	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGTA TTTCAGAGTC GTTCCAGGGG CCTCATGCTC TCAGGAAAAGCA TGACAAAGCA TGTCTCTCT TCAGAATCAC TCAGAAAAGCA TGTCTACACG CTAGTTACACG CTCAGTTACACG CTCAGTTACACG CTCAGTTACACG CCCTGGGGCA ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC SEQUENCE NP_036559 21 GAALLLERNO COAALLLERNO OAALLLERNO OAALLLERNO OAALLLERNO OAALLLERNO OAALLLERNO OAALLLERNO OAALLERNO CGCGGGCAATCACCACGACGACGACGACGACGACGACGACGACGACGACG	GGTGCAGCGG ACAGCCTTA ACAGCCGGT ACCCGCTTA ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCAT CGTCTCGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGACTCGTGC ACCTCTTGGA CCAGGACTCAT TCTCCTGGAC CCTGGGAACA CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHE	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCGC CACAGTGGCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCTTACCCGAG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA AGTTCACCAA GCACACCGC CCTTCCCAGG TCAGGGTCTG TAGGTTCACCAAAA CAAGCTCAGG	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACCAGT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGG TTACCCTTGT GTGGATCCAG ATCCCCACCT GATGTTGAGA ATCCCCACCT GATGTTGAGA CTTCCCCCAC CTGTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 600 720 780 840 900 960 1020 1140 1200
50 55 60 65	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCGGCCCA GAAACCATC GCTGCAGGGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC Seq ID NO: Protein Ac I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGGTCTACTG GGGAGCAGAT ACTCTAACGA GCGGGACAAAC GCGTGCTAAC TCTGACCGA TCTCAACGA ACACCGGG ACACCACCAC CCGTGTCTCT TCTGACCCAA 54 Protein CCSSion #: 11 VLCALITALL SCOMMTOPW QQMFQGVKSI GTTKSPQVHS	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGCCGGGGTGTG TTTCAGGGG CCTCATGCTC CAAGAAAGGA CTCCCTCTAGAAAAGGA CTCCTCTCAGAAAAGGA CTCCTGCAG TGTCTACACG CTGATCATC ACTCCTTCA TGACCAATC CTAGTTGATC CCCTGGGGCA ATTTAGTCCC SeQUENCE NP_036559 21 GAALLLERPNC CPHPGYSHPGE PKVLQCLNIS	GTTCAGCGG ACACCCTTA ACACCCCTTA GACGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAAATCGA CATTGTCCCT CAAGTGCACT GGACTCGGT AACCTCTGG ACCTCTGGAC CCTGGGACA CCTGGGACA CCTGGGACA CCTTCATCCT AGAAATAAAC HILLIAM INDVSCDHPSM LYCGAVIVHE SNDLMLIKLM VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCACCCAA AGTTCACCAA AGTTCACCAA CAAGCTCAGG TTCACCAGG TTCACCAGA TCAGGGTCTG TTCACCAGA CATTCCCAAGA TCAGGTCTG TGAGAAGTGG TGAGAAGTGG TVPSGSNQDL QWLLTAAHCR RRIPPKDVR YPRQIDDTME	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCG GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC AAAGTGCTTG CCTCCAGTGC ACAGATACT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTCAGG CCTCCCACCT AAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200
5055606570	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCTGGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT GGGCCTGTGG GCCGGCCCA GAAACCATC GCTGCAGGGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC Seq ID NO: Protein Ac I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGGTCTACTG GGGAGCAGAT ACTCTAACGA GCGGGACAAAC GCGTGCTAACG TCTGCGCCCG TCTGCACCGG CCGCTCTCCT CTGCACCGC CCGTGTCTCT TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SCDCMHTOPW QQMFQGVKSI GTTKSPQVHS	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGGTA TTTCAGAGTC GTTCCAGGGG CCTCATGCTC TCAGGAAAGGA TGACAAAGCA TGTCTCTCT TCAGAATCAC CTCATGCAC TCAGAAAAGG TGTCTACACG CTGAGTCATC ACTCCTTCAG TGTCTCACGA CTCCTGCAG CTGAGTCATC CCTGGGGCA ATTTAGTCCC Sequence NP_036559 21 LGVTEHVLAN QAALLLRPNC PHPGYSRPGE	GTTCAGCGG ACACCCTTA ACACCCCTTA GACGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAAATCGA CATTGTCCCT CAAGTGCACT GGACTCGGT AACCTCTGG ACCTCTGGAC CCTGGGACA CCTGGGACA CCTGGGACA CCTTCATCCT AGAAATAAAC HILLIAM INDVSCDHPSM LYCGAVIVHE SNDLMLIKLM VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCACCCAA AGTTCACCAA AGTTCACCAA CAAGCTCAGG TTCACCAGG TTCACCAGA TCAGGGTCTG TTCACCAGA CATTCCCAAGA TCAGGTCTG TGAGAAGTGG TGAGAAGTGG TVPSGSNQDL QWLLTAAHCR RRIPPKDVR YPRQIDDTME	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCG GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC AAAGTGCTTG CCTCCAGTGC ACAGATACT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTCAGG CCTCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
5055606570	CTTGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCC AAAGATGTCA GTGTCTGGCT TTGAATATCA GACACCATGT TTGAATATCA GACACCATGT GGCCTGTGG GCCCGGCCCA GAAACCATCC GCTGCAGGGA ATGTTCAATC ATTGGGTTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG AGATCTACTG GGAAGAAAGT ACTCTAACGA GACCCATCAA GCGGGACAAC GCGTGCTAAG TCTGCGACGG ACACCACCAC CCGTGTCTCT GTCTCAACCA TCTGACCCAA CCGTGTCTCT TCTGACCCAA CCGTGTCTCT TCTGACCCAA CCGTGTCTCT TCTGACCCAA CCGTGTCTCT CCGTGTCTCT CCGTGTCTCT TCTGACCCAA CCGTGTCTCT CCGTGTCTCT TCTGACCCAA CCGTGTCTCT CCGTGTCT CCGTGTCTCT CCGTGTCTCT CCGTGTCTCT CCGTGTCTCT CCGTGTCT CCGTGTCTCT CCGTGTCT CCGTGTCT	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGCCGGGGAA CTTCAGAGTC GTTCCAGGGG CCTCATGCTC TCAGAAAGCA TGACAAAGCA TGTCTACACG CTAGATCACC CTAGATCACC CCCTGCGGC ACTCCTTCAC CCTAGGTCATC CCCTGCGGCA ATTAGTCCC LCCTGGGCCA ATTAGTCCC LGCTGGGCCA ATTAGTCCC LGCTGGCCA LGCTCGCCCC LGCTGGCCA LGCTCCCCCCC LGCTGGCCA ATTAGTCCC LGCTGGCCA LGCTCCCCCCC LGCTGCGCCA LGCTCCCCCCCC LGCTCCCCCCCCCCCCCCCCCCCCCC	GTTCAGCGG ACACCCTTA ACACCCCTTA GACGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAAATCGA CATTGTCCCT CAAGTGCACT GGACTCGGT AACCTCTGG ACCTCTGGAC CCTGGGACA CCTGGGACA CCTGGGACA CCTTCATCCT AGAAATAAAC HILLIAM INDVSCDHPSM LYCGAVIVHE SNDLMLIKLM VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCACCCAA AGTTCACCAA AGTTCACCAA CAAGCTCAGG TTCACCAGG TTCACCAGA TCAGGGTCTG TTCACCAGA CATTCCCAAGA TCAGGTCTG TGAGAAGTGG TGAGAAGTGG TVPSGSNQDL QWLLTAAHCR RRIPPKDVR YPRQIDDTME	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCG GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC AAAGTGCTTG CCTCCAGTGC ACAGATACT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTCAGG CCTCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50 55 60 65 70	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCTGGCC AAAGATGTCA GGGCCTGTGG GCCACTGGC GAAACCATGT GGGCCTGGG GCCGGCCCA GAAACCATCT ATTGGGTGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC Seq ID NO: Protein Ac I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGCAGAT ACTCTAACGA GGCGGCACAAC GCGTGCTAAG TCTGCACCGG ACAGCCATCAA CTCTAACGA CCGGTGCTAAG TCTCCAGCCCC CCGTGTCTCT TCTGACCCAA 54 Protein Cession #: 11 VUCCALITALL SDCDMHTQPW GQMFQGVKSI CTMSPQVHE CCMSLQGLVS 55 DNA sec cid Accessic	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGCCGGGGTA TTTCAGGGG CCTCATGCTC CAACAAAGGA TGCAAAAAGG TGTCCATCAG TGTCACAGAAAGGA CTCCCTGCAG TGTCTACACG ACTCCTTCA ACTCCTTTCA ACTCCTTTCA CACTCCTTCAG ATTTAGTCCC Sequence NP_036559 21 LGVTEHVLAN QAALLLRPNC PHPGYSHPGE PKVLQCINIS WGDYPCARPN QUENCE IN #: NM_002	GGTGCAGCGG ACACCCTTA ACACCCGTT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT CGTCAGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT GAGCTCGTGT GGACTCGTGT TCTCCTGGA CCAGGACTCAT CCTGGAACA CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHE SNDLMLIKLN VLSQKRCEDA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CCACAGTGGCT ACTACTCCCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA TCACCCAA AGTTCACCAA AGTTCACCAA CAAGCTCAGG TTCACCAGG TTCACCAGA TCAGGGTCTG TTCACCAGA CATTCCCAAGA TCAGGTCTG TGAGAAGTGG TGAGAAGTGG TVPSGSNQDL QWLLTAAHCR RRIPPKDVR YPRQIDDTME	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCG GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC AAAGTGCTTG CCTCCAGTGC ACAGATACT TGATTCTGGG TTACCCTTGT GTGATCCAG ATCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTGAGA CTTCCCCACCT GATGTTCAGG CCTCCCACCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
5055606570	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCA TATGAATCTG CACCCTGGCC AAAGATGTCA GTGTCTGGGCT TTGAATATCA GGGCCTATGG GCCCGGCCCA GAAACCATGT TTGATTCATTCA TTGGGTGA CGGGGTTGC GCTGCAGGGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPHMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac Coding seq	TI CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGGTCTACTG GGGAGCAGAT ACTCTAACGA GCGTGCTAACG GCGTGCTAAG TCTGCGCCGG ACGCCTGAAC CCGCCTGACCCC CCGTGTCTCT TCTGACCCAA S4 Protein Cession #: 11 VLCALITALL SDCDMHTOPW COMFQGVKSI GTTKSPQVHE CMGSLQGLVS 55 DNA sec cid Accessic uence: 681.	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGCGGGTA TTTCAGAGTC GTTCCAGGG CCTCATGCTC CAACAGCCCC TCAGAAAAGG TGTCTCCTTC AACACCCCTGCAG TGTCTCATC ACTCCTTCACAG ACTCCTTCACAG ACTCCTTCACAG CCCTGGGGCA ACTTCATTAGTCCC Sequence NP_036559 21 LGVTEHVLAN QAALLLEPNC PKVLQCLNIS WGDYPCARPN QUENCE UENCE	GGTGCAGCGG ACAGCCTTGC CACCCCTCTA GACGCCGGT TTGGTGCATC CGTCTCTGGCC GTCAAATCCA ATCAAACTGA CATTGTCCCT TGCGAGGATG GGTAGAGATG CCAGGACTCATT TACCTTCTGCA CCAGGACTCATT TTCTCTTGGAC CCTGGGAACA CTTTCATCCT ACACTCTTGCA CCTGGGAACA CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHE SNDLMLIKLN VLSQKRCEDA RPGVYTNLCK	CCATGGCTAC TTCTGGGGGT ACACCGTGCC GGATGACAG GGCAGGCCGC CACAGTGGCT TCCCCCACCC ACAGAAGAAT CTGCTGGGAC TCCTTACCCGAG CCTGCCAGGG CCTGCCAGGG AGTTCACCAA GCACACCGGC CCTTCCCAGA TCAGGTTCACCAA GCACACCGGC TTACCGAG TTACCGAG TTACCGAG TTACCGAG AGTTCACCAA TCAGGTTCACCAA TCAGGTTCACCAAA CAAGCTCAGG TTAGGAAGTGG TVPSGSNQDL TVPSGSNQDL QWLLTAAHCR RRIRPTKDVR TYPRQIDTME FTKWIQETIC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC GCTGTTGCTA GCTCACGGCC GTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CCTCCAGTGC ACAGATAGAT TGATTCTGGG ATCCCCACCT GATGTTGACA ATCCCCACCT GATGTTGACA CTTCCAGGG GCCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200
50 55 60 65 70	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCACTGCA TATGAATCTG CACCCTGGCC AAACATGTCA GACACCATGT TTGAATATCA GACACCATGT GGGCCTGGG GCCGGCCCA AATGTTCATCT ATTGGGTGA ATGTTCATCT ATTGGGTTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac I MATARPPHMW DDSSSRIING YSLSPYVESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac Coding seq I	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGGAGCAGAT ACTCTAACGA GGCGGCACAAC GCGTGCTAAG TCTGCACCGG ACAGCCCGTCACTG CCGCCCTGAC CTCCAGCCCTGAC CTCCAGCCCTGAC TCTGACCCAA 54 Protein Cession #: 11 VLCALITALL SDCDMHTQPW CQMFQGYKSI GTTKSPQVHE CNGSLCGLVS 55 DNA sec cid Accessic quence: 681. 11	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC GGCCGGGGGAA CTTCCAGGGG CTTCCAGGGG CTTCAGAAAAGG TGACAAAACA TGCTCCTCT CAAGAAAAGG TGTCTACTCAGA TGTCTACACG CTGAGTCATC ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC Sequence NP_036559 21 GVTEHVLAN QAALLLRPNC PHPGYSRPGB PKVLQCLNIS WGDYPCARPN QUENCE M#: NM_002 .2990 21	GGTGCAGCGG ACAGCCTGCA ACAGCCTGCA GACGCCGTT TGGTGCATC GTCTCTGGCC GTCAAATCCA ATCAAATCCA ATCAAATCCA TGCGAGGAT GGTAGAGAT GGACTCGTGT ACCTCTGCA CCAGGACTCA CCAGGACTCA CCAGGACTCA TTCTCCTGGAC CCTCATT TCTCCTGGAC CTTCATCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHF SNDLMLIKLN VLSQKCCDA RPGVYTNLCK 1214	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGCACACTGCCT ACTACTCCCT ACTACTCCCT ACTACTCCCT ACTACTCCCT ACTACTCCCT ACTACTCCCACC ACAGAAGAAT CTGCTGGGACA CCTTCCCAGAG CCTTCCCAGAG CCTTCCCAGAG TCAGCTAGGGTCTGCAGAGATCACCGGC TCAGAGATCACCGGC TCAGAGATCACGGCTCTGCCAGAACTACAGGTCTGC ATTTCCAAAACACTCAGG TGAGAAAGTGG TVPSGSNQDL VVPSGSNQDL QWLLTAAHCR TVPRQIDDTME TYPRQIDDTME TTKWIQETIC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCC CAGCAGCCGC CAGCAGCCGC CAGCAGCCGC CAGCAGCCC GTCACCAGTC TCGTCCCACT AAAGTGCTTG CCTCCAGTCC ACAGTTACCCTTGT GTGATCCCACT GATGTTCAGA ATCCCCACCT GATGTTCAGA CTTCCCCCAC CTGTCCAGGG GCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200
50 55 60 65 70	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCCAACC GCCCACTGCC AAAGATGTCT CACCCTGGCC AAAGATGTCA GGGCCTATCA GGGCCTGGC GAAACCATGT TTGAATATCA GGCCTGTGG GCCCGGCCCA GAAACCATGC ATTGGGCTGAGGG ATGTTCATCT ATTGGGCTGA CGGGGTTGC TCTCTGCAGC Seq ID NO: Protein Ac 1 MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac Coding seq 1 CCCAGAGCCGC	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGCTCTACTG GGAAGAAAGT GGCAGCAGAA ACTCTAACGA GACCATCAA GCGGGACAACA GCGTGCTAAG TCTGCGCCGG ACGCCTGCACCCC CCGTGTCTCT TCTGACCCAA 54 Protein Ccssion #: 11 VLCALITALL SDCDMHTQPW CNGSLQGLVS CTGCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC GGCCGGGGAA CGATATGCAC CGGGGGGAA CTTCAGAGTC GTTCCAGGG CCTCATGCTC TCAGAAAAGCA TGACAAAGCA TGACAAAGCA TGTCTCACGG CTGAGTCATC ACTCCTTCAGA TGTCTACACG CTGAGTCATC ACTCCTTTCA ACTCCTTTCA CCCTGGGGCA ATTTAGTCCC NP_036559 21 LGVTEHVLAN QAALLERNC PHPGYSHPGE PKVLQCLNIS WGDYPCARPN QUENCE N#: NM_002 .2990 21 LTTGCTGGCAT	GGTGCAGCGG ACAGCCTTCA ACAGCCGGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCAT ATCAAATCAA	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGGCCGC CACAGTGGCT TCCCCACCC ACAGAAGAAT CTGCTGGGAC CCTGCCAGGG CCTGCCAGGG CCTGCCAGGG CCTTCCCAGA AGTTCACCAA AGTTCACCAA CCACCCAGGGC CCTTCCCAGGA TCACGAGGTCTGCAGGGC TTACCCAGGA TCAGGGTCTG ATTTCCAAAA CAAGCTCAGG TGAGAAGTGG TVPSGSNQDL TCCCCTTGCC TCCCTTGCC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCCGC CAGCAGCCGC CAGCAGCCGC GCTGTTGGTA GCTCACCAGTT TGGCTACTCC TCGTCCCACT AAAGTGCTTG CTCCAGTGC ACAGATAGAT TGATTCTGGG ATCCCCACCT GATGTTGAGA ATCCCCACCT GATGTTGAGA CTTCCCCACCT AAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200
50 55 60 65 70	TITGTGGTTC CCCTGGATGT GTTCTCGCCA AACCAGGACC ATCATCAATG AGGCCAACC GCCACCTGCA TATGAATCTG CACCTTGGCT TTGAATATCA GACACATGT GGGCCTGCA GAAACCATCC GCTGCAGGGA ATGTTCATCT ATTGGGTTG TCTCTGCAGGA ATGTTCATCT ATTGGCTTGC Seq ID NO: Protein Ac I MATARPPWMW DDSSSRIING YSLSPVYESG AGTKCLVSGW CQGDSGGPVV Seq ID NO: Nucleic Ac Coding seq I CCCAGAGCCCT	11 CTCTCTACTT GGGTGCTCTG ACAATGATGT TGGGAGCTGG GATCCGACTG AGGTCTACTG GGGAGCAGAT ACTCTAACGA GGGGAGAAAG GCGTGCTAAG TCTGCGCCGG TCTGCACCGG ACAGACCGGG ACAGACCGGG ACGCCTGACC CTCCAGCCCC CGTGTCTCT TCTGACCAA 54 Protein Cession #: 11 VLCALITALL SCDCMHTQPW CQMPGGVKSI GTTKSPCVHF CNGSLQGLVS 11 CGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	21 GGGGAAATCA TGCTCTGATC TTCCTGTGAC TGCTCTGGGGAA CGATATGCAC CGGGGGGGTGT GTTCCAGGGG CCTCATGCTC CAAGAGCCCC TCAGAAAAGG TGTCTACACG TGTCTACTC ACTCCTTCAA CTCCTGCAG TGTCTACACG CCTGGGCAA ATTTAGTCCC ASEQUENCE NP_036559 21 LGVTEHVLAN CQAALLIRPNC CPHPGYSHPGE PKVLQCLNIS WGDYPCARPN TUENCE TTGCTGGCAA TTGCTGGAC TGTGACC TGGGCAAAAAGGAAATTAGTCCC TGACTCAAC TGACCCATGC TGCTCTCCTCTC	GGTGCAGCGG ACAGCCTTCA ACAGCCGTTA GACGCCGGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT ACCCAGCCGT CGTCAGATCCA CATTGTCCCT CAAGTGCACT GGACTCGTGT ACCTCTGGA CCAGGACTCA CCAGGACTCA CCTCGGAACA CTTTCATCCT AGAAATAAAC 31 NDVSCDHPSN LYCGAVLVHF SNDLMLIKLN CVLSQKRCEDA RPGVYTNLCK 2214 31 CCCCGAGCTTCC AGACGGGGCTCC AGACGGGGCTCC AGACGGGGCTCC AGACGGGGGCTCC AGACGGGGGCTCC AGACGGGGGCTCC ACACCCCCTCAT CCCCCAGCCTTCC AGACGGGGCTCC AGACGGGGCTCC AGACGGGGGCTCC ACACCCCCTCTTCATCCT AGACGGGGCTCC AGACGGGGCTCC AGACGGGGCTCC ACACCCCCTCTTCATCCT AGACGGGGCTCC AGACGGGGCTCC ACACCCCCTCTTCATCCT AGACGGGGCTCC AGACGGGGGCTCC ACACCCCCTCTTCATCCT AGACGGGGCTCC AGACGGGGGCTCC ACACCCCCTCTTCATCCT ACACCCCCTCTTCATCCT AGACGGGGCTCC AGACGGGGCTCC AGACGGGGCTCC ACACCCCCTCTCT ACACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCCTCTTCT ACCCCTCTTCT ACCCCCTCTTCT ACCCCTCTTCT ACCCCTCTTTCT ACCCCTCTTCT ACCCCTCTTTCT ACCCCTCTTTCT ACCCCTCTTTCT ACCCCTCTTTCT ACCCCTCTTTCT ACCCCTCTTTCT ACCCCTCTTTCTT	CCATGGCTAC TTCTGGGGGT ACACCGTGCC CGGATGACAG GGCAGCCCC CACAGTGGCT TCCCCACCC ACAGAAGAAT CTGCTGGGAC TCTCCCTAAGG CCTGCGGAG AGTCACCAA AGTTCACCAA AGTTCACCAA TCAGGGTTCACCAA TCAGGGTTCACCAA TCAGGGTTCCCAGG TTCACCAAA TCAGGGTCTG ATTTCCAAAA CAAGCTCAGG TGAGAAGTGG TGAGAAGTGG 41 TVPSGSNQDL QWLLTAAHCR RRIRPTKUVR YPRQIDDTME TTKWIQETIC TTKWIQETIC TTCCCTTGCC GCAAAGCTGC	AGCAAGACCC CACAGAGCAT CTCTGGGAGC CAGCAGCGCC CAGCAGCCGC CAGCAGCCGC CAGCAGCCGC CAGCAGCCC GTCACCAGTC TCGTCCCACT AAAGTGCTTG CCTCCAGTCC ACAGTTACCCTTGT GTGATCCCACT GATGTTCAGA ATCCCCACCT GATGTTCAGA CTTCCCCCAC CTGTCCAGGG GCCATCCCT AAAAAAAAAA	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1200

	TCCCCTCGAC	CTCGCCGGCG	TACCCTCCCA	CAGATCCAGC	АТСАСССАСТ	GAATGTACAT	240
		TCCCCCCAG					300
		TTATGCAGCA					360
_		CAGGCTGCGG					420
5	TGGCCGTCGA	AGGAGGTGCT	TCTCGCGGAG	ACCGCGGGAC	CCGCCGTGCC	GAGCCGGGAG	480
	GGCCGTAGGG	GCCCTGAGAT	GCCGAGCGGT	GCCCGGGCCC	GCTTACCTGC	ACCGCTTGCT	540
		GGGTCCGCCT					600
		TCGCCCGGGA					660
10		GTTTTGCATT					720
10	TCTGCCTGCA	AAACGACCGG	CGAGGTCCCG	CCTCGTTCCT	CTGGGCAGCC	TGGGTGTTTT	780
	CACTTGTTCT	TGGACTGGGC	CAAGGTGAAG	ACAATAGATG	TGCATCTTCA	AATGCAGCAT	840
		GTGCCTTGCG					900 960
	TTTCAGGTGG	ATCAAGAAGT TTCAATAGAA	GAACGITGIG	MIMITUTION TO THE TANK	AATITIAATA	CAAAAGGCI	1020
15	TTAATACCCA						1080
IJ		GAAAGTTCAT					1140
		ATCAATGCAC					1200
	CTAGAAAAAT	GGCATTTTTC	TCCCGTGACT	TTCGTCTTGG	ATTTGGCTCA	TACGTTGATA	1260
	AAACAGTTTC	ACCATACATT	AGCATCCACC	CCGAAAGGAT	TCATAATCAA	TGCAGTGACT	1320
20	ACAATTTAGA	CTGCATGCCT	CCCCATGGAT	ACATCCATGT	GCTGTCTTTG	ACAGAGAACA	1380
	TCACTGAGTT	TGAGAAAGCA	GTTCATAGAC	AGAAGATCTC	TGGAAACATA	GATACACCAG	1440
	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
0.5		AGGCATAGTG					1620
25		GACAACCATG					1680
		TAATGTCATC					1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACCTCA	1800
	ATAATTTGGT	AGTGGAAGCC	TATCAGAAGC	TCATTTCAGA	AGTGAAAGTT	CAGGIGGAAA	1860 1920
30		AGGCATCTAT AGGATGCAGA					1980
20	CAGGCATGGA	AAAATGTGAT	CECA CACCAC	CANADATOR	TOCANTARTO	AAIGIAACAG	2040
		AAAATGTGAT					2100
		TAAAGGAAAG					2160
	GTGATGAGAA	TAAATGTCAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
35	ACAAGGATCA	GCCTGTTTGC	AGTGGTCGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTCATGTC	2280
-		GCTTGGAAAA					2340
	CATATCACCA	TGGAAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
		CTGGGAAGGT					2460
40	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
40	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACCCTCA	CAATTTGTCT	CAGGCTATAC	2640 2700
		CAAAACCTCA					2760
	CAGAATGTTT	GTTGCTTAAA	GTCCTCATCA	TTAGACAGGT	CATCATTTC	TGGAATAGTA	2820
45		GTCCTCATCA					2880
10		TTGCACAAGA					2940
		CAAATTAAAT					3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
50	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACTTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACTGATTAC	ACTTTACAGG	3300
		CCCTACGCTT					3360
E E		GTACAGTAAT					3420
55		GGTTGCCAAA					3480
	ATGAATAAAT	GATTCGTGTT	TCACTCTTTC	AAGAGGTGAA	CAGATACAAC	CTTAATCTTA	3540 3600
	AAAGATTATT	GCTTTTTAAA	GTGTGTAGTT	TTATGCATGT	COCUMENTATION	TTTGTTTTCT	3660
						GCTAAGTTAC	3720
60						TTTAAAAGCT	3780
OO	GAATGTTAA	AMMACIAMI	MIMCAMIGI	CACITIATOR	GARIACIAGI		3.00
	GAALGIIAA						
	Seg ID NO:	56 Protein	sequence				
		cession #:					
65	1	11	21	31	41	51	
	1	1 '	1	1		1	
	MCGSALAFFT	AAFVCLQNDR	RGPASFLWAA	WVFSLVLGLG	QGEDNRCASS	NAASCARCLA	60
	LGPECGWCVQ	EDFISGGSRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENBINTQVTP	120
70						NDLSRKMAFF	180
70						TENITEFEKA	240
						ALDSKLAGIV	300
						YKDLLPLLPG	360 420
						SRKPGMEGCR CEDNRGPKGK	480
75	NALZUDEALL	NATALWEECH	AIGGWHAIT	VAIGUME IVE	CORCUCION	CSCHKIKLGK	540
, 5						QHCVNSKGQV	600
						QAILDQCKTS	660
						WNSNKIKSSS	720
		KLILQSVCTR					
80					-		
	Seq ID NO:	57 DNA seq	uence				
	Nucleic Ac	id Accessio	n #: NM_001	719			
		uence: 123.					
0.5	1	11	21	31	41	51	
85	1		1 .	1	1	1	
					20	93	
					23	, ,	

	GGGCGCAGCG						60
	CTGCCACCTG	GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT .	AGAGCCGGCG	120
					CTTCGTGGCG		180
_	CCCTGTTCCT	GCTGCGCTCC	GCCCTGGCCG	ACTTCAGCCT	GGACAACGAG	GTGCACTCGA	240
5	GCTTCATCCA	CCGGCGCCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
	CCATTTTGGG	CTTGCCCCAC	CGCCCGCGCC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
	CCATGTTCAT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCCCGGCG	420
	GCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA ·	480
					CATGAGCTTC		540
10					TCGAGAGTTC		600
					ATTCCGGATC		660
					CGTTTATCAG		720
	AGCACTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CCGTACCCTC	TGGGCCTCGG	780
	ACCACCCTC	CCTCCTCTTT	GACATCACAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
15					TGGGCAGAGC		900
10					GCAGCCCTTC		960
					CACGGGGAGC		1020
	TCTTCAMGGC	CTCCAAGACG	CCCDDGDACC	AGGAAGCCCT	GCGGATGGCC	AACGTGGCAG	1080
	BCRACACCAC	CICCANGACO	ACCCACCCCC	GTANGARGCA	CGAGCTGTAT	GTCAGCTTCC	1140
20					CTACGCCGCC		1200
20					CACCAACCAC		1260
							1320
	AGACGCTGGT	CCACTTCATC	AACCCGGAMA	CGGIGCCCAA	GCCCTGCTGT	CECCACGC	1380
	AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTCATC	CIGAAGAAAI	
25	ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	11CAGACCC1	1440 1500
23	TTGGGGCCAA	GTTTTTCTGG	ATCCTCCATT	GCTCGCCTTG	GCCAGGAACC	AGCAGACCAA	
					AAAGGTGTGA		1560
	AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620
	TCCTACAAGC	TGTGCAGGCA	AAACCTAGCA	GGAAAAAAA	ACAACGCATA	AAGAAAAATG	1680
20	GCCGGGCCAG	GTCATTGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
30	TTATGAGCGC	CTACCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGCGT	GGCAAGGGGT	1800
			GAAAGGAAAA	TTGACCCGGA	AGTTCCTGTA	ATAAATGTCA	1860
	CAATAAAACG	AATGAATG					
25		58 Protein					
35	Protein Acc	cession #: 1					
	1	11	21	31	41	51	
				j			
					FIHRRLRSQE		60
40	ILGLPHRPRP	HLQGKHNSAP	MFMLDLYNAM	AVEEGGGPGG	QGFSYPYKAV	FSTQGPPLAS	120
40	LQDSHFLTDA	DMVMSFVNLV	EHDKEFFHPR	YHHREFRFDL	SKIPEGEAVT	AAEFRIYKDY	180
	IRERFDNETF	RISVYQVLQE	HLGRESDLFL	LDSRTLWASE	EGWLVFDITA	TSNHWVVNPR	240
	HNLGLQLSVE	TLDGQSINPK	LAGLIGRHGP	QNKQPFMVAF	FKATEVHFRS	irstgskors	300
	HNLGLQLSVE ONRSKTPKNO	TLDGQSINPK EALRMANVAE	LAGLIGRHGP NSSSDQRQAC	QNKQPFMVAF	FKATEVHFRS DLGWQDWIIA	IRSTGSKQRS PEGYAAYYCE	300 360
Ω	QNRSKTPKNQ	EALRMANVAE	NSSSDQRQAC	QNKQPFMVAF KKHELYVSFR	FKATEVHFRS DLGWQDWIIA LNAISVLYFD	PEGYAAYYCE	
45	QNRSKTPKNQ	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC	QNKQPFMVAF KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC	QNKQPFMVAF KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC	EALRMANVAE MNATNHAIVQ	NSSSDQRQAC TLVHFINPET	QNKQPFMVAF KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
45	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO:	EALRMANVAE MNATNHAIVQ H	NSSSDQRQAC TLVHFINPET uence	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac	EALRMANVAE MNATNHAIVQ H 59 DNA seq	NSSSDQRQAC TLVHFINPET wence n #: NM_002	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
45 50	QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession	NSSSDQRQAC TLVHFINPET wence n #: NM_002	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ	DLGWQDWIIA	PEGYAAYYCE	360
	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequents	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession uence: 150. 11	NSSSDQRQAC TLVHFINPET uence a #: NM_0020 .3362 21	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 921	DLGWQDWIIA INAISVLYFD 41	PEGYAAYYCE DSSNVILKKY	360
	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC	NSSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 l TCGGGGTCGG	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 821 31 1 GCTCCGGCTG	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC	360
	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 1 AACTCCCGCC GCGCTCCGGT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accessio uence: 150. 11 TCGGGACGCC GCGTCCGCCT	NSSDQRQAC TLVHFINPET uence u#: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCCG	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGCGGAGCA	DLGWQDWIIA LNAISVLYFD 41 cGGCTGCTGC GTCTGCGGCC	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC	360 420
50	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 1 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accessic uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG	NSSDQRQAC TLVHFINPET uence a #: NM_002i .3362 21 TCGGGGTCGG CCTGTGCCGG CCCGCGGGA	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG GCTCCGGAGCA TGGGAGCTGC	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC CGCCGTGCGC CCGGCCAGAC	360 420 60
	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac Coding seq 1 AACTCCCGCC GCGCTCCGCT CCTCAGCTC CCCGCCGGTT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCGGCT TTTTCCTGAG GCCTCTGCTC	NSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCCGCGCA AGCGTCCTGC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGGAGCTGC TGCTGCCGCTT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGGATCC GCTGGGCGGT	PEGYAAYYCE DSSNVILKKY 51] TECGGCEGCCC CGCGTGCGC CGCGGCAGAC ACCCAGACAG	360 420 60 120
50	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCGCTT CCATTGTCTT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accessio uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG	NSSDQRQAC TLVHFINPET uence u#: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGGA AGCGTCCTGC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGGCGGT GCAGGGGGT	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC CGCCTGCGC CCGGCCAGACA ACCCAGACAG CGGGGCTGC	360 420 60 120 180
50	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCGCTT CCATTGTCTT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accessio uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG	NSSDQRQAC TLVHFINPET uence u#: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGGA AGCGTCCTGC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT	DLGWQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGGCGGT GCAGGGGGT	PEGYAAYYCE DSSNVILKKY 51] TGCGGCGCCC CGCCTGCGC CCGGCCAGACA ACCCAGACAG CGGGGCTGC	360 420 60 120 180 240
50	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT CCATGTCTT TTCGCTGTGA CTGTCCAGGA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GTTTGAGGCT CACGAGCGC CACCAAGCAG	MSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGGCGCGA AGCGTCCTGC CCGGCCCGC CCGGCCCGG	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGCGAGCA TGCGGAGCA TGCGGAGCTG TGCTGCCGCT AGGATGCACT TACATGTGTA AGGCCAGCAG	A1	PEGYAAYYCE DSSNVILKKY 51 1 TGCGGCGCCC CGCCGAGACAA ACCCAGACAA ACCCAGACAG GATGGGCCC GCAGCTGTGG	360 420 60 120 180 240 300
50 55	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding sequit AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT CCATTGTCTT TTCGCTGTGA CTGTCCAGGA ACCGGCTGCA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTTCGCTC CATCAAGCAG GGTTGATC CACGAGCGG GGACTCTGGC GGGACTCTGGC	NSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGGCCGGA AGCGTCCTCC CCGGGCCCGG CGTTCCTCC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGAGCA TCGCGAGCTG TGCTGCCGCTT AGGATGCACT AGGATGCACT AGGATGCACT AGGCAGCAG GTGTGGCTGC	A1 CGGCTGCTGC GCTGGCGGCC GCTGGCGGCT GCAGGCTC CCTGGCTGCTC CCTGAGCTT GGATGATGTC	PEGYAAYYCE DSSNVILKKY 51 1 TGCGGCGCCC CGGGCCAGA ACCCAGACAG CGGGCGCTGC GATGGGGCCG GATGGGGCCG GATGGGGCCG GATGGGAGAAG	60 120 180 240 300 420 480
50	QNRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq 1 1 AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCGGTT TCCACTGTCT TTCGCTGTGA ACCCGCCAGGA ACCCGCCAGGA	EALRMANVAE MNATNHAIVQ H 59 DNA sequid Accession 11 TCGGGACGCC TTTTCCTGAG GCCTCTCCTC CATCAAGCAG GGTTGAGGCT CACCGAGGGG GGACTCTGCC CACCAACGCC TGCCAACGCC TGCCAACGCC	NSSDQRQAC TLVHFINPET uence u#: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGGA AGCGTCCTGC CCGGGCCGG CGGTTCGCC CCGGGCCGG ACTTCCAGT TCCTTCAACA	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGGGAGCA TGGGAGCACT TGGGAGCACT AGGATGCACT AGGATGCACT TACATGTGA AGGGCAGCAG GTGTGGCTCG TCAAATGGAT	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGT GCAGGGGGTCCC CCTGAGCTTC TGAGGCTT TGAGGCAGGT TGAGGCAGGT	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CGGCCAGAC ACCCAGACAG CGGGCGCTGC GATGGGGCCC GCAGCTGTGG ACTGGAGAAG CCTGTGGAGAAG CCTGTGGTCC	60 120 180 240 360 420
50 55	QMESKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq AACTCCCGCC GCGCTCCGGT CCTAGCTCC CCCGCCGGTT TTCGCTGTGA CTGTCCAGGA ACCCGCAG AAGCCCCCAA TGAAGCATCC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACGAGCGG GGACTCTGCC TCACGAGCGG GGACTCTGCC TGCCAACGCC AGCCTTCGGAA	MSSDQRQAC TLVHFINPET Defice #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG AGGGTCCTGC CCGGGCCGGA AGGTTCTGCC CCGGGCCGG CCGTCTTCGCC ACCTTCAGT TCCTTCAACA GCTGAGATCC	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGCGAGCT TGCTGCCGCT TGCTGCCGCT AGGATGCACT TACATGTAT AGGCCAGCAG GTGTGGCTGC GTGTGGCTGA TCAATGGAT AGCCACAGAC	A1	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTCGCC CCGGCCAGAC ACCCAGACAG CGGGCGCTGC GATGGGGCC GCAGCTGTGGACAG CCTTGGTGGCC CTTCGTTGCC	60 120 180 240 300 420 480 540 600
50 55	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq i AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGGTT TCCATGTCT TTCGCTGTGA ACCGCTGCA AAGCCCGCAG TGAAGCATCG AAGTCGCAA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCT CACGGAGGGCT TGCCAACGCC AGCCTCGGG	MSSDQRQAC TLVHFINPET Mence # *: NM_0021 .3362 21 TCGGGGTCGG CCGCCGCG CCGCGCGCG CCGGCCCGG CCGGTCCTCC CCGGGCCCGG CGTTCGCC CGGTCCTCC CCGGGCCCGG ACCTTCACA GCTGAGATCC CCCACCTACC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT TACATGTTA AGGCCAGCAG GTGTGCTCG TCAAATGGAT AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AATGGTTCCG	A1 CGGCTGCTGC GCTGGCGGCT GCTGGCGGCT GCTGGCGGCT CCTGAGCTT GGATGATGT TGAGGCAGGT TCAGGTCACA AGATGGGACC	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCGGCCAGC ACCCAGACAG CGGGCGCCC GATGGGCCC GCAGCTGTG ACTGGAGAAG CCTTGGTTGC CCTTCGTTGCC	60 120 180 240 360 420 480 540 660
50 55	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq i AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGGTT TCCATGTCT TTCGCTGTGA ACCGCTGCA AAGCCCGCAG TGAAGCATCG AAGTCGCAA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCT CACGGAGGGCT TGCCAACGCC AGCCTCGGG	MSSDQRQAC TLVHFINPET Mence # *: NM_0021 .3362 21 TCGGGGTCGG CCGCCGCG CCGCGCGCG CCGGCCCGG CCGGTCCTCC CCGGGCCCGG CGTTCGCC CGGTCCTCC CCGGGCCCGG ACCTTCACA GCTGAGATCC CCCACCTACC	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 821 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTGC TGCTGCCGCT AGGATGCACT TACATGTTA AGGCCAGCAG GTGTGCTCG TCAAATGGAT AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AGCCACAGAC AATGGTTCCG	A1 CGGCTGCTGC GCTGGCGGCT GCTGGCGGCT GCTGGCGGCT CCTGAGCTT GGATGATGT TGAGGCAGGT TCAGGTCACA AGATGGGACC	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCGGCCAGC ACCCAGACAG CGGGCGCCC GATGGGCCC GCAGCTGTG ACTGGAGAAG CCTTGGTTGC CCTTCGTTGCC	60 120 180 240 300 420 480 540 600
50 55 60	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq AACTCCCGGC GCGCTCCGGT TCCAGGTCC CCGCCGGTTTTCCAGGA ACCCGCAGA ACCCGCAGGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAGA ACCCGCAG	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTTCCTGAG GCGTCTGCTC CATCAGCAG GGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCACCGC AGCCTCGGAA GCACCACAA GCACCACACA TAGTGGGCT TAGTGGGCT TAGTGGGCT	MSSDQRQAC TLVHFINPET Dence # * NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG AGCGTCCTGC CCGGGCCGGA AGCGTCCTGC CCGTCTTCAGT TCCTTCAGT TCCTTCAGT TCCTTCAGT TCCTTCAGAAAAC GCTAGAATCC CCCACCTACC GTAGCAGG TATTCCTGCT	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCAGCA TGGCAGCAC TGCTGCCGCT AGGATGCACT TACATGTA AGGCAGCAG GTGTGGCTG TCAAATGGTTA AGCCACAGAC AATGGTTCCG AGGACCGAA AGGACCGAA AGGCCCACAG	A1	51 TGCGGCGCCC CGCCGTCGCC ACCCAGACA ACCCAGACA ACCCAGACAG CGAGCTGTGG ACTGGAGAAG CCTGGGGCCC CCTTCGTTGCC CCCCTTTCTC CAGGCTTGCA	60 120 180 240 360 420 480 540 660
50 55	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq i AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCGCGGTT CCATTGTCTT TTCGCTGTGA ACCGCTGCA AAGCCTGCA AAGCCTGCA AAGCATCC ACATTGATGG ATGGTCAGAG ATGGTCAGAG ATGGTCAGAG AGCCCAGAG AGCACCAGAA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCGGCT TTTTCCTGA GCTTTGCTC CATCAGCAG GGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCAACGCC AGCCTCGGC AGCCTCGGC AGCCTCGGC AGCACCACAC TAGTGGGCTG CTTCACCTTG	MSSDQRQAC TLVHFINPET Mence # *: NM_0021 .3362 21 TCGGGGTCGG CCGCCGGA AGCGTCCTGC CCGGCCCGGA CGTTCCACA GCTTCAACA GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGAGCA TGGAGCTGC TGCTGCCGCT AGGATGCACT AGGATGCACT TACATGTGT AGGCACAGA AGGCCACAGA AATGGTTCCG AGGAGCGGAA ATGATCCG AGGACCGAAA ATGATCACACAGAC AATGATCACACACACACACACACACACACACACACACACA	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGTCC GCTGGCGGTTC GCAGGGGTTC CGTAGCTTT GGATGATT CCAGGTACC AGATGGACC CCTGACGCTC CCTGACGCTC TCACGCTGC TCACGCTGC TCACGCTGC TGCCACGGTGC TGCCACGGTGC TGCCACGGTGC TGCCAGGGTG TGCCAGGGTG TGCCAGGGTG	51 TGCGGCGCCC CGCGGCAGAC ACCCAGACAG ACCCAGACAG CGAGCTGTGG CCTTGGTCG CTTGGTGCC CTTCGTTGCC CCCTTTCTG CGGCAGCTGC CAGCTTGCA CTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTTGCACTGCA	60 120 180 240 360 420 540 600 720
50 55 60	QMRSKTPKNQ GECAFPLNSY RMMVVRACGC Seq ID NO: Nucleic Ac: Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCTGTT TTCGCTGTGA ACCCGCTGGA ACCCGCTGGA AGCCCGCAG ATGATGAGATCA ACTCCTGGAGA ACCGCTGAGA ACCGCTGAGA ACCGCAGA GCACCAGAA GCACCAGAA GCACCAGAA GCACGCAGA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCAACGCC AGCCTCGGA AGCACCACAC TAGTGGGCT GAACCACACAC TAGTGGGCT GCTACCTTG GGTAGTAGCGG	MSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCCTCC CCGGGCCGG ATTTCGCG TCCTTCAACA GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTCGGG AGGTATGAGG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTG TGCTGCCGCT TACATGTGTA AGGGCAGCAG AGGGCACAGAG ATGAATGGAT AGCCACAGAG AGGAGCGGAA AGGCCACAGA AGGCCCCACAG AGGAGCGGAA AGGCCCACAG ATGAAAGCTT AGGCCACTGTT AGGCCACTGTT AGGCCACTGTT	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGCT GCAGGCTGCT CCTGAGCTT GGATGATGTC TGAGCAGGT CCAGGTCACA AGATGGACC CCTGACCTC TGCTTTTGGC TGCCAGGTC TGCTTTTGGC CCAGTCACA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGGCCAGAC ACCCAGACAG CGGGCGCCC GCAGCTGCG GATGGGGCCC CTCGTTGCC CCCCTTTCTG CCGCCAGCTG CAGGCTTGCA CAGGCTTGCA CAGGCTTGCA CTCCTCAGCCC CTCCTTCCC CGCCAGCTG CAGGCTTCCA	60 120 180 240 420 420 480 600 600 720 780
50 55 60	QMRSKTPKNQ GECAFPLNSY RMMVVRACGC Seq ID NO: Nucleic Ac: Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCTGTT TTCGCTGTGA ACCCGCTGGA ACCCGCTGGA AGCCCGCAG ATGATGAGATCA ACTCCTGGAGA ACCGCTGAGA ACCGCTGAGA ACCGCAGA GCACCAGAA GCACCAGAA GCACCAGAA GCACGCAGA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACGAGCGG GGACTCTGGC TGCCAACGCC AGCCTCGGA AGCACCACAC TAGTGGGCT GAACCACACAC TAGTGGGCT GCTACCTTG GGTAGTAGCGG	MSSDQRQAC TLVHFINPET uence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGA AGCGTCCTCC CCGGGCCGG ATTTCGCG TCCTTCAACA GCTGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTCGGG AGGTATGAGG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCTG TGCTGCCGCT TACATGTGTA AGGGCAGCAG AGGGCACAGAG ATGAATGGAT AGCCACAGAG AGGAGCGGAA AGGCCACAGA AGGCCCCACAG AGGAGCGGAA AGGCCCACAG ATGAAAGCTT AGGCCACTGTT AGGCCACTGTT AGGCCACTGTT	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGCT GCAGGCTGCT CCTGAGCTT GGATGATGTC TGAGCAGGT CCAGGTCACA AGATGGACC CCTGACCTC TGCTTTTGGC TGCCAGGTC TGCTTTTGGC CCAGTCACA	PEGYAAYYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGGCCAGAC ACCCAGACAG CGGGCGCCC GCAGCTGCG GATGGGGCCC CTCGTTGCC CCCCTTTCTG CCGCCAGCTG CAGGCTTGCA CAGGCTTGCA CAGGCTTGCA CTCCTCAGCCC CTCCTTCCC CGCCAGCTG CAGGCTTCCA	60 120 180 300 360 480 540 660 720 780
50 55 60	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq: AACTCCCGCC GCGCTCCGGT TCCATGTCTT TTCGCTGTGA ACCCGCTGGA ACCCGCTGGA AAGCCCGCA AAGCCCGCA GTGAAACCATCC ACATTGATGA GTCATGAGA ACCCGCAGACT ACGCCAGAACT ACCCGCAGAACT ACCAGACGAGAA ACCAGGACGAGAA ACCAGGACGAGAA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAGCAG GGATCTGGCC TGCCAACGCC AGCCTCGGAA GCACCACAGA TAGTGGGCTG CTCACCTGGAA GCACCACCAC AGCTTCGGAA GCACCACCAC AGCTTCGGAA GCACCACCAC AGCTTCGGAA GCACCACCAC AGGTTCGGCT CATCACCTTGG CATCACCTTGG CATCACCAC AGGTTAGTAGCGCTG GGAGCTTGCAGG	MSSDQRQAC TLVHFINPET Gence # * NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG AGCGTCCTCCC CCGGGCCGGA AGCGTCCTCCC CCGGGCCGGG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCAGCAGCAGCAGCAGCAGACAGACCAGAC	A1 CGGCTGCTGC GCTGCGGGGGGCGC GCTGGGGGGGCGC CCTGGGGCTT CCTGAGGCTT TGAGGCAGG CCAGGTCAAA AGATGGAC TCCCAGAGGT TGCTTTTGGC TGCTTTTGGC TGCTTTTTGGC TGCCAGGTCAAG TGCCAGGTCAAG TGCCAGGTCAAG TGCCAGGTCAAG TGCCAGGTCAAG TGCCAGGTCAAG	51 TGCGGCGCCC CGCCGTCGCC GCCAGACA ACCCAGACA ACCCAGACA ACCCAGACA ACCTGGGGCC GCAGCTGTGG ACTGGAGAAG ACTGGAGAAG ACTGGTGTC CCTTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGCCTTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTC	60 120 180 240 360 420 540 660 660 720 780 840 996
50 55 60 65	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq i hACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGGT TCCATGTCT TTCGTTGTA ACCGCGCA AGCCCGCA AGCCCGCA AGCCCGCA AGCCCCCAA AGCACCCCC ACATTGATGA ACCGCAGAA CCCAGGACGT AGCCACCACA TCCGGCACA TCCGGCACA TCCGCCCCACA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCT CACGAGCGG GGACTCTGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC CAACCACAC ATAGTGGGCT CTTCACCTTG CGTAGTAGCG GGACTCCGAG CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCCTCCGCAGA CCCTCCGCAGA CCCTCCGCAGA CCATCCCGCAGA CCATCCCGCAGA CCATCCAGGG CCTCCACAGAG CCTCACAGAG CCTCCACAGAG CCTCACAGAG CCTCCACAGAG CCT	MSSDQRQAC TLVHFINPET MENCE A #: NM_0021 .3362 21 TCGGGGTCGG CCGCCGCG CCGG CCGGCCCGG CCGTCTCCC CCGGGCCCGG ACCTTCACA GCTTCACA GCTAGAGATC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGCATGT ATCACAGTGT	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGAGCA TGGAGCTGC TGCTGCCGCT AGGATGCACT AGGATGCACT TACATGTGT AGGCACAGA GTGTGCTCG GTGTGCTCG TCAAATGGAT AGCCACAGA GCGCCACAG ATGATAGAT AGGACCAGA TTGAAATGTT AGGACCAGA TTGCCAACG TTGCCACGC TTGCCACGC TTGCCACGC TTGCCACCC	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGCTGCTGC GCTGGCGGCTGCTGC CCTGAGGTTC CCAGGTCACA AGATGGACC TCCTGAGGCTC TGCTTTTTGGC TGCTGCTGC TGCTCTTCTGGC TGCCTGAGGTGC TGCCTCTGCTGC TGCTTTTTGGC TGCCTGAGGTGC TGCCTTTTTGGC TGCCTGAGGTGC CCATTGCCAGGTGC CCATTGCCAGGTGC CCATTGCCAGGTGC GCGCCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGCAGAGGGGGAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGCAGAGGAG	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCC CGCGTGCGC CCGGCCAGACAG CGGGCGCAGC GATGGGGCCC CTTCGTTGGC CCTTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA CTTCTGCAGCTC ATCTCGCAGCTG CAGGCTTGCA CTCCCCCTTCCAGCCC CTCCCCCCCCCC	60 120 180 240 360 420 540 660 660 720 780 840 996
50 55 60 65	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq i hACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCCCCGGT TCCATGTCT TTCGTTGTA ACCGCGCA AGCCCGCA AGCCCGCA AGCCCGCA AGCCCCCAA AGCACCCCC ACATTGATGA ACCGCAGAA CCCAGGACGT AGCCACCACA TCCGGCACA TCCGGCACA TCCGCCCCACA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGCT CACGAGCGG GGACTCTGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC CAACCACAC ATAGTGGGCT CTTCACCTTG CGTAGTAGCG GGACTCCGAG CCTCCGCAGA CCTCCGCAGA CCTCCGCAGA CCCTCCGCAGA CCCTCCGCAGA CCCTCCGCAGA CCATCCCGCAGA CCATCCCGCAGA CCATCCAGGG CCTCCACAGAG CCTCACAGAG CCTCCACAGAG CCTCACAGAG CCTCCACAGAG CCT	MSSDQRQAC TLVHFINPET MENCE A #: NM_0021 .3362 21 TCGGGGTCGG CCGCCGCG CCGG CCGGCCCGG CCGTCTCCC CCGGGCCCGG ACCTTCACA GCTTCACA GCTAGAGATC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGGTATGAGG TGGCTCTTTG AGCATGT ATCACAGTGT	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGAGCA TGGAGCTGC TGCTGCCGCT AGGATGCACT AGGATGCACT TACATGTGT AGGCACAGA GTGTGCTCG GTGTGCTCG TCAAATGGAT AGCCACAGA GCGCCACAG ATGATAGAT AGGACCAGA TTGAAATGTT AGGACCAGA TTGCCAACG TTGCCACGC TTGCCACGC TTGCCACGC TTGCCACCC	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGCTGCTGC GCTGGCGGCTGCTGC CCTGAGGTTC CCAGGTCACA AGATGGACC TCCTGAGGCTC TGCTTTTTGGC TGCTGCTGC TGCTCTTCTGGC TGCCTGAGGTGC TGCCTCTGCTGC TGCTTTTTGGC TGCCTGAGGTGC TGCCTTTTTGGC TGCCTGAGGTGC CCATTGCCAGGTGC CCATTGCCAGGTGC CCATTGCCAGGTGC GCGCCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGCAGAGGGGGAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGGCAGAGGGGCAGAGGGGCAGAGGGGCAGAGGGGGCAGAGGGGGCAGAGGGCAGAGGCAGAGGAG	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCC CGCGTGCGC CCGGCCAGACAG CGGGCGCAGC GATGGGGCCC CTTCGTTGGC CCTTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGGCTTGCA CTTCTGCAGCTC ATCTCGCAGCTG CAGGCTTGCA CTCCCCCTTCCAGCCC CTCCCCCCCCCC	60 120 180 300 360 480 540 660 720 840 900 900
50 55 60	QMRSKTPKNQ GECAFPLNSY RMMVVRACGC Seq ID NO: Nucleic Ac: Coding sequity AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TCGCTGTGA ACCCGCTGCA AAGCCCGCAG TGAAGCATCC ACATTGATGG GTCCTGAGCA GCAGCCAGAA GCCACCACA GCCCCCCCACA TCCGCCACG TCCGCCACG TCCGCCACG TCATCCTGGA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCCC CATCAAGCAG GGATCAGCC CACCAAGCAG GGACTCTGGC TGCCAACCACA TAGTGGGCT GGTACTGG CATCACCTG GGTACTGGC CACCCTCGGCAG CACCCTCGGCAGA CATCACCACACAC TAGTGGCTGGCTCCCCCCCGGAGCCCCTCGCCAGAC AGCCTCGAGAGCCCCCCCCCC	MSSDQRQAC TLVHFINPET dence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGCGG AGGTCCTCC CCGGGCCGG TCCTTCCAGT TCCTTCAACA GCTGAGATCC GCACAGTGT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGCT AGCATTGTTG GCCACAGTGT ATCTACCGCT ATTACCGCT CACCTAGCAG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGGGAGCA TGGGAGCA TGGGAGCACA TGGGAGCACT AGGATGCACT AGGATGCACT AGGCAGAGCA ATGGTACCAC AATGGTT AGCCACAGAC AATGGTT AGCCACAGAC ATGAAAGCTT AGGCCACAG TGAAAGCTT AGGCACTGTT AGGATGAAC ATTGCCAACGG GCATTGCAACGA AGATTGAAAGAC ATTGCCAACGA AGATTGAAAGAC AATTGCAACGA	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGGTCC GCTGGCGGCT GCAGGCTGCT CCTGAGCTT GGATGATGTC TGAGCAGGT CCAGGTCACA ACATGGACC CCTGACCTC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC GCTCTTTGCTG GCAGGAGG CCATCACAC	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGGCCAGCA ACTGGAGAAG CCTGTGGTCC CCCCTTTCTG CCGCCAGCTG CAGCTTGCA CCCCCTTTCCA CCCCCTTCCA CCCCCACCCA CTTCTCAGCCCC AACCGCAGTC CTGACCCAGC TTTGAGCCAC TTTGAGCCAC	60 120 180 240 360 420 540 660 720 780 840 960 1020 1080
50 55 60 65	QMRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq AACTCCCGCC GCGCTCCGGT CCATGGTT TCCATGTGT TTCCTGTGA ACCGCTGGA ACCGCTGGA ACCGCTGGA ACCGCTGGA ACCGCTGGA ACCGCTGGA ACCCCCGAGA CCCAGGACGT AGCACCCC GCCCCCACA TCCGGCCACG TCATCCTGGC TCATCCTGGC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT CACCAACCA AGCCTCGGAA GCACCACCA TAGTGAG GCACCTCGG CAACCACCA CATGCAGGC GGACCTCGGA CCTCGCAGA CCTCGCAGA CACCACCA CAATGCAGAG AGCCACACT AGCTGCAGA CACCACCAGA CAATGCAGAG CAGCCACACT AGCTGCAGA	MSSDQRQAC TLVHFINPET Defice ##: NM_0020 .3362 21 TCGGGGTCGG CCTGTGCCGG AGGGTCGTGCCGC CCGTCCTCCC CCGTCCTCCC CCGTCCTCAGATCC CCTACAGATCC CCCACCTACC GTCAGATCC GTCAGCAGCA AGGTATAGAGG AGGTATAGAGG TGGCTCTTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCACTTGCG TGCCCCTACCG GTCACCAGTGT ATCTACCGCT CACCTAGCAGC GGAGAGCGTGG GAGGAGCGTG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG GCTCCGGCTG CCGCAGAC TGCTGCCGCT AGGATGCACT AGGCAGCCAA ATGGTTCCA ATGGTTCCA AGGCCACAGAC ATGAAAGGTT AGCCCACAGAC ATGAAAGCT AGGCATGTT AGGATGAAC TTGCCAACGG AGATTGAACA TGCCTGCCT	A1 CGGCTGCTGC GTCTGCGGGATCC GCTGGGGGTC CCTGAGCTTT GGATGATGT CCAGGTGCAC AGATGGGAC TGCTGACGT TGCTGACGT TGCTACGT TGCTACGT TGCTACGT TGCTACGT TGCTTTTGGC TGCTTCTCGC TGCTTCTCC TGCTGACGT TGCTTTTTGC TGCTTCTCCG TGCTTTTGC TGCTTTTGCC TGCTTTTGCC TGCTTTTGCC TGCTTTTGCC TGCTTTTGCC TGCTTTTGCC TTCCAGGTC TCCATGCCGTA TCCCCCAAG	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CGCGCAGAC ACCCAGACAG ACCCAGACAG CGAGCGTGG CGAGCTGTGG CCTTGGTGGC CCTTGTTGCC CCCCTTTCTG CGGCAGCTG CAGGCTGCAG CTGCTGCAG CTGCAGCCAG CTGCAGCCAG CTGCCAGG CGCCACCCA TTTGAGCCAC GGCCCACCA CGTCTGCCAG	60 120 180 240 360 420 540 660 720 780 840 960 1020 1080
50 55 60 65	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq: AACTCCCGCC GCGCTCCGGT CCTCAGCTC CCCGCCGGT TTCGCTGTGA ACCGCTGCA AGCCCGCGA TGAAGCATCC ACATTGATGG ATGGTCAGAG GCCCCCACA CCCGCCACA TCCGGCCACG TCATCCTGA GGGTGTTAA	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCGCCT TTTTCCTGG GCCTCTGCTC CATCAAGCAG GGTTGAGGCT TCACGGAGGGG GGACTCTGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC CAACCACACA TAGTGGGCT CTTCACCTTG GGTAGTAGCG GAGCCTGCAG CATCACGCG AGCCTGCAG CATCGCAGAG CATCGCAGAG CATCGCAGAG CATCGCAGAG CATGGCAGAG CATGCAGAG CATGCAGAG CATGCAGAG CATGCAGAG CATGCAGAG CATGCAGAG CATGCAGAG AGCCACACTT AGCTGCAGAG GAGCACACTT AGCTGCAGAG GAGCACACTT AGCTGCAGAG	MSSDQRQAC TLVHFINPET MENCE A #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCCGGA AGCGTCTGC CCGTCTTGCC CGGGCCGGA AGCTTCTACACA GCTTCAACA GCTAGAGATCC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTTG AGCATTGCTG AGGTATGAGG TGGCTCTTTG AGCATTGCTG AGGATAGAGG GCCACAGTGT ATCTACCGCT CACCTAGCAG CGAGGAGGGT CACCCTAGCAG CGAGGAGGGT CACCCGGGAGGGGGAGGGGGAGGGGGAGGGGGGAGGGGGG	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGAGCA TGCTGCCGCT TACATGTGTA AGGCCACAGA ATGGTGCCGA ATGGTGCCGAA ATGGTTCCG AGGAGCGAA ATGGTTCCG AGGACCAAG ATGATTT AGCACAGAC ATGATGAAGA TTGCCAACGG TTGCCACGCT TCCGGCTGCC	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGTCC GCTGGCGGTCC GCTGGCGGTCC GCTGGCTG	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCGTGCGC CGCGCAGAC ACCCAGACAG CGGGCAGTGGGC CTTGGTGG CCTTGGTGG CCTTGTGGGCCC CTTCGTGGGCC CTTCGTGGCC CTTCTTGG CAGCCTTGCA GTGCTGGCAC TTCTCAGCCC AACCGCAGTC TGCACCCAG GGCCCACCCA TTTGAGCCAC AGGGTCTGCA GGTCTGCAC AGGGTCTACC	60 120 180 300 360 420 480 540 660 720 780 900 900 91080 1140 1260
50 55 60 65 70	QMRSKTPKNQ GECAFPLNSY RMMVVRACGC Seq ID NO: Nucleic Ac. Coding sequity AACTCCCGCC GCGCTCCGGT CCATCGCTCC CCCCCCGGT TCCATGTCT TTCCCTGGAC ACCGCTGCA ACCCGCAG ACCGCAGA ACCCGCAG ACCCCCCC GCCCCCCCC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTTCAGCT CATCAAGCAG GGTTGAGCT CACCACACAC AGCCTCGGAG CCACCACACAC TAGTGGGCT GCTACCTGG CATCACCTGG CATCACCTGG CATCACCTGG CATCACCTGG CATCACCTGG CATCACCTGG CATCACCTT GGTAGTAGCG GGTACTACCT GGTAGTAGCG CATCCGCAGA CCTCCGCAGA CCACCACTT AGCTGCAGGG GCCTCGCAGA CCACCACTT CAGTGGTGGGG CCTCGCCAGA CCACCACTT CAGTGGCGGGG CCTCGCCAGA CCACCACTT CAGTGGCGGGG CCTCGCCAGA CCACCACTT CAGTGGCGGGGGGGGGG	MSSDQRQAC TLVHFINPET dence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGGCCGGA AGCGTCTGCC CCGGCCCGG AGCTTCGCC ACCTTCAACA GCTGAGATCC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGAGG TGGCTCTTGG TGGCTCTTGG TGCACAGTGT AGCATTGCTG AGGTATGAGG TGGCTCTTGG GCACAGTGT ACCTTACCGGT CACCTACCGGT TATCCTGCT TACCTGCT TACCTGCT TACCTGCT TACCTTCAACA TATTCCTGCT AGCATTGCTG CACCTAGCAG TATCACCGGT CACCTAGCAG TATCACCGGT CACCTAGCAG TATCACCGGT TATCACCGGT TACCTACCAG TATCACCGGGAG TTGGCCAATA	ONKOPFMVAF KHELYVSFR VPKPCCAPTO 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCA TGGGAGCA TGGGAGCACA ATGGATCACT AGGCACAGAC AATGGATCA AGGCACAGAC AATGGATCA AGGCCACAGA TGAAAGCT AGGCCACAGA TGGAAGCT AGGATGAGAC TTGCCAACG ATGCAAGAC TTGCCAACG TTGCCACG TTGCCACG TTGCCACG TTGCCACG TTGCCACG TTCCGCTGCC TTCCTGAAAG	A1 CGGCTGCTGC GTCTGCGGCC GCGGGGATCC GCTGGCGGCT GCAGGCTGCTC CCTGAGCTTT GGATGATGTC TGAGGCAGT CCAGGTCAC AGATGGGAC CCTGACGCTC TGCTTTTGGC TGCCTTTTGGC TGCCTCTCTGCTG TGCTCTCTGCTG GCGCAGGGAGG CCATCACT GCCCCCAGG CATCCCCAGG CATCCCCAAG TCCCCAAGGC TCCCCAAGGC TCCCCAAGG CACCCATGGC TGCATGCCGCTA	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCCC CGCGTGCGC CCGGCCAGACAG CGGGCCAGCAGCTGCGCCAGCCGCCTTCCTGCCCCCCTTTCTGCCCCCCTTCCTGCAGCCAGC	60 120 180 300 360 420 480 540 660 720 780 900 900 91080 1140 1260
50 55 60 65 70	QMESKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq AACTCCCGGC GCGCTCCGGT TCCATGTCT TTCGCTGTGA ACTCCCGGCT GCATGTCT AAGCCCGCA AAGCCCGCA GCCCCAGACA GCCACCAG GCCCCACA TCCGGCCACA TCCGGCCACA TCCGGCCACA AGGCTCCACA AGGCTCCACA AGGCCCACA AGCACCCCC ACAGACGT AGCACCCCC ACAGACGT AGCACCCCC ACAGACGT AGCACCCCC ACAGACGT AGCACCCCC AGGCCCACA AGCCCCCACA AGCCCCCACA AGCCCCCACA AGCACCGCC AGACGGT AGAACGCCCA AGCACGCGC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCGTCCGCCT CATCAAGCAG GGTTCAGCTC CATCAAGCAG GGATCTGGGC TGCCACCTCGG AGCCTCGGAA GCACCACCAC CAACCACACA CCACCACCAC CAATGCAGGA CAATGCAGGA AGCACACTT AGCTGGCAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGAG CGAGCTGGGAG CGAGCTGGGAG CGAGCTGGGAG CGAGCTGGGAG CGAGCTGGGAG CGAGCTGGGGAG CGAGCTGGGGAG CCACCTTG	MSSDQRQAC TLVHFINPET Defice ##: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG AGCGTCCTGC CCGGGCCGGA AGCGTCTCGC CCGTCCTCCC CCGGGCCGG AGCGTCTCGC ACCTTCAGT TCCTTCAACA GCTAAGATCC CCACCTACC GTAGCAGC AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATCAGTT CACCTACCGGT ATCTACCGCT CACCTACCGGGAGG GAGGAGCGTG CACCCGGGAGG TTGGCCAATA	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 GCTCCGGCTG CCGCGGAGCA TGGAGCTGC TGCTGCGCTG AGGATGCACT AGGATGCACT AGGATGCACT AGGATGCAC ATGGTAGCAGAC ATGATAGAT AGCCCACAGAC ATGAAAGCT TTGCCAACAG TTGCCAACAG AGATTAGACA TTGCCAACAG TTGCTGAAAG TGACTGCCT TCCGGCTGCC TTGCTGAAAAG GACAGGATGT	A1 CGGCTGCTGC GCTGCTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTCGCC CGCGCAGAC ACCCAGACAG CGGGCAGAC ACCCAGACAG CGGGCGCTGC GCAGCTGTGG ACTGGAGAAG CCTGGTGGCC CCTTCTGTGCC CCCTTTCTG CAGCCTTCCAG GTGCTGCAG TTCTAGACCAG GGCCACCA TTTGAGCAC GGCCACCA TTTGAGCCAC GGCCACCCA GGTCTGCCAG GGCCACCCA GGTCTGCCAG GGCCACCCA GGTCTACACCT GTGGCCACTG GTGGCCACTG	60 120 180 240 300 480 540 660 720 1020 1020 1140 1200 1260 1380
50 55 60 65	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seqi AACTCCCGCC GCGCTCCGGT CCTCAGCTC CCCGCCGGTT TTCGCTGGA ACGCCTGGT ACGCCCGGT TGAGCATCC ACATTGATGA ACGCCCGGGT AGGCCAGGA ACCGCCGCGGT AGCACCCC ACATTGATGG ATGGTCAGAG ACCCCCCACA TCCGGCCACG TCATCCTGGA AGCCACCCG TCATCCTGGA AGCCCCCCACA TCCGGCCACG TCATCCTGGA AGCCCACGGT AGAAGGGCCA AGCCCACGT AGAAGGGCCA AGCCCACGT AGAAGGGCCA TCCCCCCCCTCT AGAAGGGCCA TGCCCCCCCTCT TGCCCTCCTGT	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCTTCTGCTC CATCAAGCAG GGTTCAGCTG CACCACCACACA AGCACCACCACACACACACACACAC	MSSDQRQAC TLVHFINPET dence a #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGGCGCA AGCGTCCTCC CCGGGCCGCA AGCGTCTCACA ACCTTCCACT GCTAGCAGCA ACCTACCGGTCACCTACC GTCAGCAGCA AGCTATGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG CACCTACAGCAG GCCACAGTGT CACCTAGCAG GCACAGTGT CACCTAGCAG CACCTAGCAG CACCTAGCAG CACCTAGCAG CACCTAGCAG CACCTAGCAG CACGCGGAG CTTGGCCAACACA	QNKQPFMVAF KRHELYVSFR VPKPCCAPTQ 31 31 GCTCCGGCTG CCGCGAGCG TGCTGCGCT AGGATGCACT TACATGTGA AGGCCACAGAC AATGGTTCCG AGGAGCCACAG ATGAAAGCT AGGCCACAGAC ATGAAAGCT AGGCCACAGAC ATGAAAGCT TCCCACAGG TTGCCACAGG TTGCCACAGG TTGCCACAGG CATTGACAG TTGCCACAGG TGCCACAGAC AGATTGAAGG TTGCCACAGG TGCCACAGG TCCACAGG	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGTCC GCTGGCGGTTC CCTGAGCTTT GGATGATGCC CCTGAGCTTT CCAGGTCC CCTGAGCTTT GGATGAGCAGG TCCACTACAC AGATGGGAC TGCCTGCT TGCTTTGGC TGCTTTGGC TGCTTTGGC TGCTTTGGC TGCTTTGGCAGGT CCATGCCGTC GTCTCTGCTG GGGGCAGAGG CACCATGCCGT TGCTTTGCAGGTC CACATGCCGCTA TCCCCCAAG CACCATGCC TGCTTTGCTG GGGGCAAA	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CGGCCAGAC ACCCAGACAG ACTGGGGCCC GAGCTGTGGC CTTCGTTGCC CCCTTTCTG CGGCAGCTG GTGCTGCA CTGCTGGCA CTTCTCAGCCC ACCGCAGCT ACCGCAGCT ACCGCAGCT ACCGCACCA ACGGCACCA ACGGCACCA CTTTGAGCCAC GGTCTGCCAG AGGGTCTACC GTCTACACCT CCCGGCCACT CCCGGCTACT CCCGGCTACT CCCGGCTACT CCCGGCTACT CCCGGCTACT	60 120 180 360 360 360 480 540 660 720 840 900 900 1020 1140 1260 1320 1380
50 55 60 65 70	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq: AACTCCCGCC GCGCTCCGGT CCTCAGCTCC CCCGCCGGTT TTCGCTGGA ACCGCGGT AGCCCCCAA AGCCCGCAA AGCCCGCAA GCCACCAGA CCCAGCAGA CCCAGCACAC TCAGCACAC TCACCCCCCAC TCACCACGCT TCACCCCCCCAC TCACCCCCCCAC TCACCCCCCCAC TCACCCCCCCC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCC CATCAAGCAG GGTTCAGCGC GGACTCTGGC TGCCAACGCC AGCCTCGGC CACCACACA AGCACCCTCGG CAACCACACA TAGTGGGCT GCTCACCTTG GGTAGTAGCG AGCCTCGAG CCTCCGCAGA CCATCCGCAGA CCATCCGCAGA CCATCCGCAGA CCACCACTC GGGGCTGCAG CCTCCGCAGA CCACCACT CGTGGTGGGGG CCTCCGCAGA CCACTGCTG CGTGGTGGGGGG CCTCAGCAGA CCACTGCTG CGTGGTGGGAGA CCACCTGGCG CCACCACTGCTG CGTGGTGGGAGA CCACCTGGCGGGGGGGGGG	MSSDQRQAC TLVHFINPET MENCE A #: NM_0021 .3362 21 TCGGGGTCGG CCGCGCGGA CCGTCCTCCC CCGGGCCCGG ACCTTCACA ACCTTCACA GCTAGAGATC CCCACCTACC GTCAGCAGCA TATTCCTGCT AGCATTGCTG AGGTATGCG AGGTATGCG AGGTATGCG GCACAGGGAG TTTCCTTTTG AGGTATTGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCTG AGGTATGCGG AGGTACCGTAGCAG CCCCACGGAGA CCCCAAGAA	ONKOPFMVAF KHELYVSFR VPKPCCAPTO 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCA TGGGAGCA TGGGAGCA TGGGAGCA TGCTGCCGCT TACATGTGTA AGGGCAGCAG AGGAGCAGAGA AGGATGAGC AGGAGCGGAA TGGAAGCT AGGATGAGC TTGCCAACGG ATGCAAGCT TGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTGCCACGG TTCCTGAAAG TCACGGTTGC TCCGGCTGCC TTGCTGAAAG GACAGGATGT GCCAGCTGGA CTACAGTTGT	LIGMQDWIIA LNAISVLYFD 41 CGGCTGCTGC GTCTGCGGCC GCTGGCGGCTGCTGC GCTGGCGGCTGCTCC CCTGAGGTTCT GGATGATGT TGAGGCAGGT TCCAGGTCACA AGATGGGACC TGCTTTTTGGC TGCCTGATGGC TGCCTGAGGT TGCCAGGTG CCATTGCCAG TCCCATAGC TGCTCTGCTG GGGGCAGAGG CACCCATGGC TGCCCATAGC TGCCATAGC TGCCATAGC TGCCATAGC TGCCATAGC TGCCATAGC TGCCATAGC TGCCATAGC TGGAGGGCAAA	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCC CGCGTGCGC CCGGCCAGACAG CGGGCGCAGC GATGGGCCC CTTCGTTGCC CCTTCTTCTG CGGCAGCTGC CAGCTTGCAC CTTCAGCCC ATTCAGCCC ATTCAGCCC ATTTGAGCCAC GTTTGACCAC GTTTGACCAC GTTTGACCAC GTTTGACCAC GTTTGACCAC GTTTGACCAC GTTTGACCAC GTTTACACCT GTGGCCACT ACCAGATGC CCCGGCTACT AACCAGATGC	60 120 180 360 420 480 540 660 720 780 960 1080 1140 1260 1380 1450
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50 55 60 65 70	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCCTCTGCTC CATCAAGCAG GGATCTGGCT GGACCCTCGG AGCCTCGGCAG AGCCTCGGA GCACCACCA CAGCCTGGAA GCACCACCT CTTCACCTG GGTAGTAGCG CAGCCTGCAG CAGCTGGAG CAGCTGGAG CAGCTGGAG CAGCTGGAG CAGCTGGAG CAGCTGGGAG CAGCTGGGAG CAGCTGGGAG CAGCTGGCAG CAGCTGGAG CAGCTGGCAG CAGCTGGTC CAGCTGGCAG CAGCTGGTC CAGCTGGCAG CAGGCC CAGCTGGCAG CAGCTGCAG CAGCTGGCAG CAGCTGCAG CAGCTGGCAG CAGCTGGCAG CAGCTGGCAG CAGCTGCAG CAGCTCAG CAGCTGCAG CAG	MSSDQRQAC TLVHFINPET UEENCE 1 #: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG CCGTCCTCCC CCGGCCGG	QNKQPFMVAF KHELYVSFR VPKPCCAPTQ 31 31 GCTCCGGCTG CCGCGGAGCA TGGCAGCAGCA TGGCAGCAGCA TACATGGTTA AGGCAGCAGA ATGGTTCCG AGGACCCACAGA ATGATAGCT AGGCATGCT TGCCACAGAC ATGAAAGCT TTGCCAACAG TTGCCAACAGAC TTGCCAACAGAC TTGCTGAACAG TTGCTGAACAG TTGCTGAACAG TTACATGTTA AGGTTGCCA TTGCTGAACAG TTACATGTT TCACAGATGC TTCACAGAGAC TTGCTAAAGAT TCACAGATTGC TCACAGTTGC TTCACAGTGCA AGGTTACAGTT TCACAGATTGC GACAGGTTCACAGTTCC GGTACAGTTCC GGTACAGTTCC GGTACAGTTCC GGTACAGTTCC GGTACAGTTCC GGTACAGTTCC GGTACAGCCC GGAGCCCCCC GGAGCAGCCCC GGAGCAGCCCC	A1 CGGCTGCTGC GTCTGCGGCC GCTGGGATCC GCTGGGGCGC CTGGCTGCTC CCTGAGCTTT GGATGATGTC CCTGAGCTTT GGATGATGTC TGAGCAGGT CCAGTCACA AGATGGGAC TGCTTTGGC TGCTTTGGC TGCTTTGGC TGCTTTGGC TGCTTTGGC TGCTTAGCAG TCCAATGCCGT CCAATGCCGTA CTCCCCAAG CCACCCAAG CACCCAAGG CACCCAAGG CACCCAAGG CACCCAAGG CACCCAAGG CACCCACACA CACCCACACA CACCCACACA CACCCACACA CCACACCAC	PEGYAATYCE DSSNVILKKY 51 TGCGGCGCCC CGCCGTGCGC CGCCAGAC ACCCAGACAG ACCCAGACAG ACCCAGACAG ACCCAGACAG ACCCAGACAG CGGGCGTGCG CTTGGTGGC CCTTGGTGCC CCCTTTCTG CGGCCAGCCA ACCGCAGCCA ACCGCAGCCA TTTGAGCCC GTCTACACCT GTGCCACCA AGGGTCTACC GTCTACACCT GTGGCCACT CCCGGCTACT ACCGGATAC ACCGGATAC CCCCGGCTACT ACCCAGATGC GCCAGCAGC GCCAGCAG GCCAGCAGC GCCCAGCAC GGCCAGCAG GGCAGCAC GGCCGAGAGA GTGACAGACA	60 120 180 300 360 480 540 660 720 1080 1120 1260 1380 1500 1500 1680 1740 1680 1740
50 55 60 65 70	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seqi AACTCCCGCC GCGCTCCGGT CCTCAGCTC CCCGCCGGTT TTCGCTGGA ACCGCCGGT TTCGCTGGA ACCGCCGGGT AGCCCCCGA AGCCCGGGA TGAAGCATCC ACATTGATGG ATGGTCAGAG GCCCCCCACA TCCGGCAGGA GCCCCCCCACA TCCGGCCACG TCATCCTGGA AGCCACGGGC TGATCTCAGA AGCCAGGGA AGCACCCCC TGATCTCAGA AGCCCACGGGC TGCCTCCTGA AGGCCACGGGC AGAGGGCAAGA AGCCACGGGC AGAGGGCAAGA AGCCCACTA AGCCCACGAGA AGCCCACTA AGCCCTGGGAC AGCCCACTA AGCCCTGGGAC ACCCTGCGGAC ACCCTGCGGAC ACCCTGCGGAC ACCCTGCGGAC ACCCTGCGCAC ACCCTGCGCAC ACCCCCCCTC ACCCTGCCT ACCCTCCT ACCCTGCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCTCCT ACCCT ACCT ACCCT AC	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TOGGGACGCC GCGTCGGCCT TTTTCCTGG GCTCTGCTC CATCAGGAGGC CATCAGGCG GGACTCTGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC AGCCTCGGC CATCACCCC GGTAGTAGCG CATCACCC GGTAGTAGCG CATCACCC GGTAGTAGCG CATCACCC GGTAGTAGCG CATCACCC CACCCC CACCC CACCCC CACCC CACCCC CACCC CACC CACCC CACC CACCC CACC CACC CACCC CACC	MSSDQRQAC TLVHFINPET WEENCE ##: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCG CCGCGCGGA AGCGTCCTCC CCGGGCCGGA AGCGTCTCACA ACCTTCCAGT TCCTCAACA TATTCCTGCT AGCATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGGATTGCTG AGCATTGCAGAAA CCCCAACAAA CCCCAACAAA CCCCAACAAA CCCCAACAA	ONKOPFMVAF KHELYVSFR VPKPCCAPTO 31 GCTCCGGCTG CCGGCAGGCA TGGGAGCA TGGGAGCAC TGGGAGCAC TGGGAGCAC TGGGAGCAC AGGCCACAGAC ATGGATCCG TCAAATGGAT AGCCACAGAC ATGGATCCG ATGCACAGAC TTGCCAACAG TTGCCACAG ATGAAAGCT AGGATGAGAC TTGCCAACAG CGACTGCCC TTCCTGAAAG TTACAGCTGCC TTCCTGAAAG CGACAGCTGC CTACAGTTGC CGGTGCCCACAGG GGACAGCTGCACAGC CTACAGTTGC CGCAGCTGGAC CTACAGTTGC CGGTGCCCC CTCGAGATGC CGGAGCAGCCC CTCGAGATGC CCTCGAGATGC CCTCGAGATGC	A1 CGGCTGCTGC GTCTGCGGCC GCTGGCGGGATCC GCTGGGGGATCC GCTGGGGGGTTC GCAGGGGGTGT CCAGGGTGT CCAGGGTGT CCAGGTGTC TGCCAGGGTG TGCCAGGGTG CCATTGCCAG TGCCATCACT GGTCTCTGCGG CATGCCGCT GGCAGGTG CAACATCACT GGAGGGCAAA CTGGTACAGA CTGGTACAGA CTGGTACAGA CTGGTACAGA CTGGCACAG CCACCAGGC CACCCAGGC CACCCCAGGC CACCCAGGC CACCCCAGGC CACCCAGGC CACCCCAGGC CACCCCAGC CACCCCAGGC CACCCCCAGGC CACCCCAGGC CACCCCAGC CACCCAGC CACCCCAGC CACCCCCAGC CACCCCCAGC CACCCCAGC CACCCCCAGC CACCCCCCAGC CACCCCCCAGC CACCCCCCAGC CACCCCAGC CACCCCAGC CACCCCAGC CACCCCCCAGC CACCCCCAGC CACCCCCCAGC CACCCCCAGC CACCCCAGC CACCCCAGC CACCCCAGC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCCACAC CACCAC	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG ACTGGGGCCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCAC TTCTCAGCCC ACCGCAGCCA AGGGTTGCA GGCCACCCA ACGGCAGCC GGCTACCC GTCTACACCT CCCGGCTACC ACCAGATGC ACCAGACAC GGCCGAGACA GGCCGAGCAC GGCCGAGCAC TTACACAGC GCCCAGCCAC TCCAGCCAC TCCAGCCAC TCCAGCCAC TCCAGCCAC TTACACAGCAC TCCAGCCAC TTACACAGCAC TCCAGCCAC TTACACAGCAC TTACACATGCA TTACACTTGCA	60 120 180 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1500 1500 1680 1740 1860
50 55 60 65 70	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac: Coding seq: AACTCCCGCC GCGCTCCGGT CCATGGTC CCGCTGGT TTCCCTGTGA ACCCGCTGGA ACCCGCTGGA ACCCGCTGGA ACCCGCTGGA ACCCGCTGGA ACCCGCCAGG GTGAAGCATCC ACATTGATGG GTCATGAGG GTCCTGAGCA GCACCCCC GCCCCACA TCCGGCCACG TCCGGCCACG TCATCCTGGA GGGTGTTAC AGCCCACGGCT TCATCTGGA GGGTGTTAC AGAGGGCA AGAGGGCA AGAGGGCA AGAGGGCA AGAGGGCA AGAGGGCA AGAGGGCA AGCAGTGCAT AGCCCACTAT AGCCCACTAT AGCCCACTAT AGCCCACCAC ATTGCCTCCAP TTGCTCCACT TTGCTCCACT TTGCTCCACT TTGCTCCCATTTCCACT TTGCTCCCATTTCCCTCCATTTCCTCATTTCCCTCCATTTCCCTCCATTTCCCTCCATTTCCCTCCATTTCCTCC	EALRMANVAE MNATNHAIVO H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC GCGTCCGCCT TTTTCCTGAG GCCTCTGCTC CATCAGCAG GGATCTGGCC AGCCTCGGCA TAGTGGGCT CACCACAC TAGTGGGCT GGAGCTCGGGA GCACCCCGG GAGCCTCGGA CATCAGCAG CATCAGCC GAGCTGGAG CATCAGCC GGAGCTGGAG CACCACAC TAGTGGGCT CGACCAGAG CATCAGCC GGAGCTGGAG CCTCGGCAGA CAGCTGGAG CCGCTGCAGAG CCGCTGCAGAG CCGCTGCAGAG CGACTGGTG CGACTGGCAG CGACTGGCAG CGACTGGCAG CCACTGGATTTT CGGGCCCAG CCTGCATTTT CGGGCCCAG	MSSDQRQAC TLVHFINPET Gence ##: NM_0021 .3362 21 TCGGGGTCGG CCTGTGCCGG ACGTCCTCCC CCGGGGCAGA AGCGTCCTCCC CCGGGCCGG AGCTTCGCCG ACCTTCAGT TCCTTCAGT TCCTTCAGT AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCTGC AGCATTCCTG AGGATTCCTGC AGCATTCCTG AGGATTCCTGC AGCATAGAGA TATTCCTGCT AGCATAGAGG TGGCTCATAGAGA AGGTCAACAAAA CCCAAAAAA TTCGAGGTCT TGGTACCGTA ACGACAAAAA ACGACAAAAA CGTCAAGACAA ACGACAAAAA CGTCAAGACAAAA CGCCAAGACAA ACGACAAAAA CGTCAAGACAAAAAAAAAA	ONKOPFMVAF KHELYVSFR VPKPCCAPTO 31 CTCCGCTG CCGCGGAGCA TGGGAGCA TGGGAGCA TGGGAGCA TGGGAGCA TGGTGCCGCT AGGATGCACT AGGCACAGAC AGATGTTCA AGGCACAGAC AATGGTTCA AGGCACAGAC ATGAAAGCTT AGGCCACAGAC ATGAAAGCTT AGGCCACTGTA AGGATGAGAC TTCCCGCTGCC TCCGGCTGCC TCCGGCTGCC TCCGGCTGCC TCCGGCTGCC TCCGGCTGCC TCCGGCTGCC TCCGGCTGCC TCCTGAAAGC TCCAGGATGT CTCAAGATGC GGAGCCCTCGAGATGC GGAGCAGCCTC GGAGCCCCTC GGAGCACCCTC GGACCCCCTC GGAGCCCCTC GGGACCCCTC GGGACCCCTC GGGACCCCTC GGGCCCCACT GTGCCCCATCT GTGCCCCATCT CTCCACATCT CTCCACTC CTCCACATCT CTCCACATCT CTCCACATCT CTCCACATCT CTCCACATCT CTCCACTC CTCCACATCT CTCCACATCT CTCCACATCT CTCCACTC CTCCACTC CTCCACTC CTCCACTC CTCCACT CTCCAC	A1 CGGCTGCTGC GTCTGCGGGGGGGGGGGGGGGGGGGGGG	PEGYAATYCE DSSNVILKKY 51 TGGGGCGCCC CGCCGTCGCC CCGCCTGCGC ACCCAGACAG ACCCAGACAG ACCCAGACAG ACCCAGACAG CCTGGGGCCC CTTCGTTGCC CCCCTTTCTG CGGCCAGCTG CAGCCTTCCAGCCAGCTG CAGCCTTCCAGCCAGCTG CAGCCTACCAGCTG CTCACCCAGCTG GGCCACCCA TTTCAGCCCAGCTG GGCCACCCA CGCCAGCAGCTG CCCCAGCCAGCTG CCCCAGCCAGCTG ACCAGCAGTG ACCAGCAGTG ACCAGCAGTG ACCAGCAGTG ACCAGCAGTG ACCAGCAGTACC ACCAGCCAGCAGCAGAGAGAGAGACATCAACACTGCAGCCAGC	60 120 180 360 420 360 480 540 660 720 780 960 1080 1140 1260 1380 1440 1560 1560 1620 1740 1800 1800 1920
50 55 60 65 70	QMRSKTPKNQ GECAPPLNSY RNMVVRACGC Seq ID NO: Nucleic Ac. Coding seq	EALRMANVAE MNATNHAIVQ H 59 DNA seq id Accession uence: 150. 11 TCGGGACGCC TTTTCCTGAG GCGTCTGCTC CATCAAGCAG GGTTCAGCTG CACCACCA GGACTCTGGC AGCCTCGGA GCACCTCGG AGCCTCGGA GCACCTCGG CAACCACCA CAATGCAGGAG CACCACCACA CACCACCA CACCACCA CACCACCA CACCAC	MSSDQRQAC TLVHFINPET Defice ##: NM_0021 .3362 21 TCGGGGTCGG CCGGCGGGA AGCGTCCTGC CCGGCCGGG AGCGTCCTGC CCGTCCTCCC CCGGGCCGG AGCGTCCTGC CCGGTCCTCAGATC CCCACCTACC GTCAGATCC GTCAGATCG CCACCTACCGGT AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCATTGCTG AGCACTAGCAG CACCAGGGGAG TTGGCCAATAAAC CACCAAAAAC CCCAAGAACA ACGCGGGAG TTCGAGGTCT TGGTCATAAACA CCCAAGACA CCCCAAGACA CCCAAGACC CCAAGACC CCCAAGACC CCAAGACC CCCAAGACC CCCAAGAC CCCAAGC CCCAACAC CCCAAGC CCCCAAC CCCCCAAC CCCCCC CCCC CCCCC CCCCC CCCCC CCCCC CCCC	QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ 31 31 GCTCCGGCTG CCGCGGAGCA TGGGAGCAGCA TGGCAGCAGA ATGGTTCCG TACATGTTA AGGCACAGAC AATGGTTCCG AGGACCAGAC ATGAAAGCT TGCCAACAG TTGCCAACAG TTGCCAACAG TTGCCAACAG TTGCCAACAG TTGCCAACAG TTGCCAACAG TTGCCAACAG TTGCTGAACAG TTCTGAAGA TGAACAGATC TCCGGCTGCC TCCAGGTAGC TCCAGGATGT CCGGTGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCAGCCCT CCGCACCT CCGCCCCT CCGCACCT CCGCCCTCT CCGCCTCT CCGCCCTCT CCGCCCTCT CCGCCCTCT CCGCCCTCT CCGCCCTCT CCGCCCTCT CCCCCTCT CCGCCTCT CCCCCTCT CCCCCTCT CCCCTCT CCCTCT C	A1 CGGCTGCTGC GTCTGCGGGCC GCTGGGGCTC CCTGAGCTTT GGATGATGCT CCAGGTCACA AGATGGGAC TGCTGCGGGC TGCTGCGGGGCG CCATTGCGG TGCTGCCGC TGCTGCCC TGACGTT TGCAGGGTG CCATTGCGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCTTTTGGC TGCAGGTG CCATGCGGTA TCCCCAAG CCACCACACA CAGGGCAAA CTGGTACAGT CAACACCACA CCAGAGTGG CCCAGAGTGG CCCAGAGTGG CCCAGAGTGG CCCAGAGTGG CCCAGAGTGG CCCAGAGTGG CCCAGGCCAC CCAGGGCCAC CCAGGCCAC CCAGGGCCAC CCAGGCCAC CCAGGGCCAC CCAGGGCCAC CCAGGCCAC CCAGCCAC CCACCAC CCAGCCAC CCAGCCAC CCAGCCAC CCAGCCAC CCAGCCAC CCAGCCAC CCAGCCAC CCAGCCAC CCACCAC CCACCAC CCACCAC CCACCAC CCACCA	PEGYAATYCE DSSNVILKKY 51 1 TGCGGCGCCCC CGCCGTGCGC CGCGGCAGAC ACCCAGACAG ACTGGGGCCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCC CTTCGTGGCAC TTCTCAGCCC ACCGCAGCCA AGGGTTGCA GGCCACCCA ACGGCAGCC GGCTACCC GTCTACACCT CCCGGCTACC ACCAGATGC ACCAGACAC GGCCGAGACA GGCCGAGCAC GGCCGAGCAC TTACACAGC GCCCAGCCAC TCCAGCCAC TCCAGCCAC TCCAGCCAC TCCAGCCAC TTACACAGCAC TCCAGCCAC TTACACAGCAC TCCAGCCAC TTACACAGCAC TTACACATGCA TTACACTTGCA	60 120 180 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1500 1500 1680 1740 1860

	TCCTGGACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAATGGC	TCCCTGGTGA	2100
	TOTATES COT	GGCCCCTGAG	CACTCACCCC	CCTA CA CCTC	CATTCCAGGC	AACAGCTGCA	2160
		CACGGAGGCC					2220
-		CAGCCCTCCC					2280
5	CCGCTGTGGC	CTACATCATT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
_	A A CCCCA A CCC	GCTGCAGAAG	CACCCCCACC	CCCACCACCC	DOMONTOGAN.	TOCCTCAACG	2400
		GCAGAACGGG					2460
	GCTTGGGCTC	CGGCCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
		TAGCCTGCAG					2580
10							2640
10	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCUIGGIA	CIIGIGAAGA	
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	CCANCCTCAN	CCACGCCAAC	GTGGTGCGGC	TOTTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
		GCTGGAATAT					2820
		TGAAAAATTG					2880
15	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	acrece area	TAACTGCCTG	CTCACTCCCC	ACACACAACT	CAACCTCTCT	CCCCTCCCCC	3000
	TGGCTGCGCG	TAACTGCCTG	GICAGIGCCC	MOMONCAMOI	GAMGGIGICI	GCCC1GGGCC	
		TGTGTACAAC					3060
	CCTCCATCTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	0010011010	GCTGATGTGG	CAACECEEE	CACAMOCACA	CATCCCCCAT	CCTCCCCACC	3180
20							
20	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	COTCOCOTTO	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	0010000110	CAGTGAGATT	COCTOCOCC	TOCCO A CACACAC	CACCCTCCAC	ACCAACCCCT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CACCATGATG	GGCAAGATCC	CTGTCCTCCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25		CTGAGCAGGG					3540
25	TIGCIGAGGI	CIGAGCAGGG	CCIGGCCIII	CCICCICIIC	CICACCCICA	TCCTTTGGGA	
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTTCCTCT	ATCAGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTCT	GGCCTTCAAC	3660
		GACCGGGTCC					3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
•		TGAGTCCTCC					3900
	CCCCACCCTT	CTCTCCTTTC	CTCATCCTAA	GTGCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GCCCTTTTTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
		GGTGGGTGGG					4080
25							
35		CCCCACACTT				TTTTTGTTTT	4140
	TOTTOTTOTT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTA		
		60 Protein					
	Protein Acc	cession #: 1	NP 002812				
40	1	11	21	31	41	51 '	
	-						
		1	1	11	1	1	
	1	1	1	1	1	1	
		 PRRLPLLSVL		AIVFIKQPSS			60
				AIVFIKQPSS			60 120
	VHVYWLLDGA	PVQDTERRFA	QGSSLSFAAV	AIVFIKQPSS DRLQDSGTFQ	CVARDDVTGE	EARSANASFN	120
A.E.	VHVYWLLDGA IKWIEAGPVV	PVQDTERRFA LKHPASEAEI	QGSSLSFAAV QPQTQVTLRC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY	CVARDDVTGE QWFRDGTPLS	earsanasfn DGQSNHTVSS	120 180
45	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA	CVARDDVTGE QWFRDGTPLS DESPARVVLA	EARSANASFN DGQSNHTVSS PQDVVVARYE	120 180 240
45	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA	CVARDDVTGE QWFRDGTPLS DESPARVVLA	EARSANASFN DGQSNHTVSS PQDVVVARYE	120 180
45	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR	120 180 240 300
45	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGPP	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG	120 180 240 300 360
45	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGPP VRLPTHGRVY	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD	120 180 240 300 360 420
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGPP VRLPTHGRVY	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD	120 180 240 300 360
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VRLPTHGRVY SQLEEGKPGY	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR	120 180 240 300 360 420 480
45 50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI	PVQDTERFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETP ITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQMFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QCMEFDKEA	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD	120 180 240 300 360 420 480 540
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA LASNGPQGQI	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER	120 180 240 300 360 420 480 540
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA LASNGPQGQI	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER	120 180 240 300 360 420 480 540
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGQQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQM TRDDAGNYTC PLIQWKGKDR	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG	120 180 240 300 360 420 480 540 600 660
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VULPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF I ILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGGGSPPPYK	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP TCLPPKGLP TCLPTCLTPKGLT TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVI	120 180 240 300 360 420 480 540 600 660 720
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VWLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT FTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEBGS AAVAYIIAVL SLGSGPAATN	120 180 240 300 360 420 480 540 600 650 720 780
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGQGQRGFP VWLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT FTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS	CVARDDVTGE QWFRDGTPLS DESFARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEBGS AAVAYIIAVL SLGSGPAATN	120 180 240 300 360 420 480 540 600 660 720
	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMPYCKRC KRHSTSDKMH	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVETAGSEER CHAANLAGQR LISEDSRFEV QCCMEFDKEA IAENGPQGQI ILDPTKLGPR EGGCSPPPYK GGPLQNGQPS FLAKAQGLEE	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MCQTIGLSVG AEIQEEVALT GVAETLVLVK	EARSANASFN DCQSMHTVSS PCDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPOD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVI, SLGSGPAATN SLQTKDEQQQ	120 180 240 300 360 420 480 540 600 650 720 780
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVVQGHTAL RYTCIAGNSC GLMPYCKKRC KRHSTSDKMH LDFRRELEMF	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAGGDPK NIKHTEAPLY KARRLOKOPE PPRSSLQPIT GKLMHANVVR	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLIN TLGKSEFGEV LIGLCREAEP	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHIRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IAENGPQGQI ILDPTKLGPR EGPESPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS	EARSANASFN DCQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ	120 180 240 300 360 420 480 540 660 720 780 840 900
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VBLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLIAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT TYVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LENNRFVHKD	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA	CVARDDVTGE CWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VBLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLIAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT TYVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LENNRFVHKD	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA	CVARDDVTGE CWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGQGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMPYCKRC KRHSTSDKMH LDFRELEMF PLSTKQKVAL YHFRQAWVPL	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA CKGHELVLAN LDCLTQATPK EAQARVQVLE EAQARVQVLE KAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPESS GEFEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGQGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMPYCKRC KRHSTSDKMH LDFRELEMF PLSTKQKVAL YHFRQAWVPL	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLIAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPESS GEFEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVVQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV NICHTEAPLY KAKRLQKQPE PPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLIN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VBLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE SEQ ID NO:	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPEPSLQWLF IILEATLHLA QKGHELVLLA LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYTT PTVWWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGQGQRGPP VBLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE SEQ ID NO:	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV NICHTEAPLY KAKRLQKQPE PPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGYTT PTVWWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 900 960
50 55	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKRC KRHSTSDKMH LDFRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE EAQARVQVLE HAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LLGILCREAEP LSNNRFVHKD QRCWALSPKD WENCE #: NM_006	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 900 960
50 55	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVID TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE GFRSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29.	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVM QRCWALSPKD uence #: NM_006	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGG LGDSTVDSKP	EARSANASFN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ	120 180 240 300 360 420 480 540 660 720 780 900 960
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKRC KRHSTSDKMH LDFRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE EAQARVQVLE HAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LLGILCREAEP LSNNRFVHKD QRCWALSPKD WENCE #: NM_006	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLT FROGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MYQTIGLSVG AETQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ	EARSANASFN DGQSHITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY	120 180 240 300 360 420 480 540 660 720 780 900 960
50 55	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVID TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE GFRSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29.	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVM QRCWALSPKD uence #: NM_006	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA	CVARDOVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGG LGDSTVDSKP	EARSANASFN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ	120 180 240 300 360 420 480 540 660 720 780 900 960
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTVYQGHTAL RYTCIAGNSC GLMFYCKKG KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE EAQARVQVLE HAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECIN TLGKSEFGEV LLGLCREAEP LESNRFVHKD QRCWALSPKD uence n #: NM_006 406 21	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA LASINGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLRQFLRIS QRQVKVSALG LGDSTVDSKP	EARSANASFIN DGQSMITVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ	120 180 240 360 420 480 540 660 720 780 900 960 1020
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGYV CMSSTPAGSI GSSLPEWVID TTVVQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV NIKHTEAPLY KARRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDW QRCWALSPKD LSL NM_006 406 21 ATAGCACCAT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLARAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG AEIQEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGG LGDSTVDSKP	EARSANASFN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ	120 180 240 360 420 540 660 720 780 960 1020
50 55 60	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGGGGRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCLAGNSC GLMPYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: NUCleic Ac Codding seq 1	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDF5TKSDVW QRCWALSPKD uence 1 #: NM_006 21 ATAGCACCAT TGCTGTTCGG	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGULMWEVF RPSFSEIASA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG ABIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA	120 180 240 300 360 420 540 600 720 780 840 960 1020
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMPYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCCTC CGAGACTGGCC GAGAGACTGGCC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPESS GEEPEMECIN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD uence n #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGTT CTTCACCCTA TGACCAGAAC	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVOLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC TGCACGCAAG	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMPYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCCTC CGAGACTGGCC GAGAGACTGGCC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPESS GEEPEMECIN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD uence n #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGTT CTTCACCCTA TGACCAGAAC	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVOLTVAV MHIFQNGSLV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC TGCACGCAAG	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC	120 180 240 300 360 420 540 600 720 780 840 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVID TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGAAGACTGGC	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFAR NAGTLHFAR KARLQKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA BEQ id Accessio uence: 29 11 CCGCCCGGGC CTCAGCCTGGC TGCGCCCGG TGCGCCGGCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT FTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD uence n #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGTG ACCTCAAGTG	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGPGSPPPYK GGPLQNGQPS FLARAQGLEE HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT GTTCACCCTAG TGACCAGAAC CTGCAGCAGCGCG	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE TVPCSATGRE GVAETLVLVK MIQTIGLSVG ABIQEEVALI GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA GGCTGTGCCA	EARSANASFN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VFSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT	120 180 240 300 360 480 540 660 720 780 960 1020
50 55 60	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMPHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVVQGHTAL RYTCLAGNSC GLMPYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGCGAA TCTCTGCCCA	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKOPE PPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessic uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEFFEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDF5TKSDVW QRCWALSPKD uence #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGG ACCTCAAGTG AGGGTTCCTG	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RPVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGULMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT CTTCACCCTA TGACCAGACG CCCCCAGGTG	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLPP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAA ACATTAACT	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER INDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC TTCCCCAGCT	120 180 240 300 360 420 600 720 780 840 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCTC GAAGACTGGC GGACAGCGAA TCTCTGCCAA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE NAGTLHFARV NIKHTEAPLLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH GCPSKLYRLM 61 DNA Beq id Accessic uence: 29 11 CCGCCCGGGGC CTCGCCCGGGC GTGTGCCCCG TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC CGGCCCGGCC CGGCCCGGCC CGGCCCGGCC CGCCCCGGCC CGCCCCGGCC CCCCCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPESS GEEPEMECIN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD UENCE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGC ACCTCAAGTG AGGGTTCCTG GCCAGGTGGA	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFDKA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGTT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCCAGGTG CCGCCCAGGTG	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCDTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCC TGCACGCAAG GGCTTGCCA AACATTAACT CCTGGCCAGAA	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEEMS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQO KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCAGCT TGAAATGCTG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCTC GAAGACTGGC GGACAGCGAA TCTCTGCCAA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE NAGTLHFARV NIKHTEAPLLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH GCPSKLYRLM 61 DNA Beq id Accessic uence: 29 11 CCGCCCGGGGC CTCGCCCGGGC GTGTGCCCCG TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC CGGCCCGGCC CGGCCCGGCC CGGCCCGGCC CGCCCCGGCC CGCCCCGGCC CCCCCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPESS GEEPEMECIN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD UENCE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGCTCCAGGC ACCTCAAGTG AGGGTTCCTG GCCAGGTGGA	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFDKA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGTT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCCAGGTG CCGCCCAGGTG	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCDTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCC TGCACGCAAG GGCTTGCCA AACATTAACT CCTGGCCAGAA	EARSANASFN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER INDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC TTCCCCAGCT	120 180 240 300 360 420 600 720 780 840 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGPP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVID TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGCGAA TCTCTGCCCA CGGCCTCTCT CCGCAATGGC	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KARRLQKQPE GRENGARVER GRENGARVER 61 DNA seq id Accessio uence: 29 11 CCGCCCGGGC CTGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGCACA AATGATAAGG CCGGGACCAGT TGTGGGAAGG	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IASSDAGVYT FTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPEES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD UEENCE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG ACCTCAGGC ACCTCAGGT AGGGTTCCTGGT GGCAGGTGGA	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR EGPCSPPPYK GGPLQNGQPS FLAKAQGLES HYMVLEYVDL LAARNCLVSA AFGYLMWEVF RPSFSEIASA 31 GCCTGCTTGT CTTCACCCTA TGCCCCAGGTG CCGCCAGGTG CAGCCAGGTG CAGCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCCAGTTG CAGCCCCAGTTG CAGCCCAGTTG CCACCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCAGTTG CAGCCCCAGTTG CAGCCCAGTTG CAGCCCCAGTTG CAGCCCCAGTTG CAGCCCCAGTTG CAGCCCCCAGTTG CAGCCCCCAGTTG CAGCCCCCCAGTTG CAGCCCCCCAGTTG CAGCCCCCCCAGTTG CAGCCCCCCAGTTG CAGCCCCCCAGTTG CAGCCCCCCCAGTTG CAGCCCCCCCCAGTTG CAGCCCCCCCAGTTG CAGCCCCCCCAGTTG CAGCCCCCCCCAGTTG CAGCCCCCCCCAGTTG CAGCCCCCCCCCAGTTG CAGCCCCCCCCAGTTG CAGCCCCCCCCCC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MITGUSSLV MIQTIGLSVG GELGEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGQ LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGAG GGCTGTGCCA AACATTAACT CCTGGCCAGG TTCTGAGGTC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCCACCAC	120 180 240 300 360 420 480 540 660 720 780 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVVQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGCACGCACC CGCCTCTCT CGCAACTGCCC CGCCATGGCC CAGGCTCAGC CAGCCTCAGC CAGCTCAGC CAGCCTCAGC CACCTCAGC CAGCCTCAGC CACCTCAGC CACCTCAG	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV NAGTLHFARV KARRLQKOPE PPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVYT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTT PLLQWKGKDR VVDKPVPES GEEFEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD LEGLCREAEP LSNRFVHKD GDFSTKSDVW QRCWALSPKD LGLCREAEP AGGCACCAT AGGCACCAT AGGCACCAT AGGCTCCAGGC ACCTCAAGGC ACCTCAAGGC ACGCTAAGTG ACGCTAGTGG ACGCTAGTGGA AGGGTTCCTGGTGT GGAAGGTTCCT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA SSQNFTLSIA RUFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMULEYVDL LARNCLVSA AFGULMWEVF RPSFSEIASA 103 31 GGCTGCTTGT CTTCACCTA TGACCAGACG CCCCCAGTG CAGCCAGTGT CACTCCCAAT GCCTGGCCCT	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MIQTIGLSVG AEIQEEVALT GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAGG AGCATGACCAGA ACATTAACT CCTGGCCAGGT TCTGAGGTC GCATTGAGGTC GCATTGAGGTC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCCTC GAAGACTGGC GGACAGCGAAA TCTCTGCCCA CGGCCTCTGT CCGCAATGGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGCCTCCCC CGCACTCCCCC CAGCCTCCCCC CAGCTCCCCC CAGCCTCCCCC CACCCCCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCCCCCCC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE NAGTLHFARV NIKHTEAPLLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTCGCCGGGC GTGTGCCCCG GTGTGCCCCG TGCGCCAGAC AATGATAAGG CAGGACAGT TGTGGGAAGA TTTTTTCGGGA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LLGICREAEP LSNNRFVHKD QRCWALSPKD UENCE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGGTTCCTG GCCAGGTGGA TGTCCTGTGTT GAAGTTTCT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTTG CAGCCACT CCTCTGGGCCT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCCACCAC	120 180 240 300 360 420 480 540 660 720 780 960 1020
50556065	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCCTC GAAGACTGGC GGACAGCGAAA TCTCTGCCCA CGGCCTCTGT CCGCAATGGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGCCTCCCC CGCACTCCCCC CAGCCTCCCCC CAGCTCCCCC CAGCCTCCCCC CACCCCCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCCCCCCC	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV NAGTLHFARV KARRLQKOPE PPRSSLQPIT GKLMHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LLGICREAEP LSNNRFVHKD QRCWALSPKD UENCE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGGTTCCTG GCCAGGTGGA TGTCCTGTGTT GAAGTTTCT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTTG CAGCCACT CCTCTGGGCCT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCCTCCTC GAAGACTGGC GGACAGCGAAA TCTCTGCCCA CGGCCTCTGT CCGCAATGGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGGCTGAGC CAGCCTCCCC CGCAATGGC CAGCCTCCCC CGCACTCCCCC CAGCCTCCCCC CAGCTCCCCC CAGCCTCCCCC CACCCCCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCC CAGCCTCCCCCCCCCC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE NAGTLHFARV NIKHTEAPLLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTCGCCGGGC GTGTGCCCCG GTGTGCCCCG TGCGCCAGAC AATGATAAGG CAGGACAGT TGTGGGAAGA TTTTTTCGGGA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LLGICREAEP LSNNRFVHKD QRCWALSPKD UENCE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGGTTCCTG GCCAGGTGGA TGTCCTGTGTT GAAGTTTCT	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTTG CAGCCACT CCTCTGGGCCT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHVYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY VRLSTAGNSC GLMFYCKKRC GLMFYCKKRC KRHSTSDKMH LDFRELEMF PLSTKQKVAL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGGGAA TCTCTGCCCA CGGCTCTGC CGCGCTCCTC CGCGCTCCTG CAGGCTCAGC CGCCTCCTC CCCCAACCAAT	PVQDTERRFA LKHPASEAEI LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFAR NAGTLHFAR KARLQKOPE PRESSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA BEQ id Accessio uence: 29 11 CCGCCCGGGC CTGCGCCCGG TGCGCCCGG TGCGCCCGG TGCGCCGGACA AATGATAAGG CGGAACAGT TTTTTCGGGA AATGATAACCA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IASSDAGVYT FTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VVDKPVPES GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD GDFSTKSDVW QRCWALSPKD UENCE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCGG AGGCTCCAGGCG ACCTCAAGTG AGGGTTCCTG GCCAGGTGGG GCAGGTGGG GAAAGTTTCT CTCTGTATTC CTCTGTATTC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTTG CAGCCACT CCTCTGGGCCT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFY VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGGGAA TCTCTGCCCA CGGCTCTGT CCGCAATGGC CAGGCTAGGC CAGGCTGAGC CAGGCTGAGC CAGGCTCCCC CCCAACCAAT Seq ID NO:	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA CKGHELVLAN LDCLTQATPK EAQARVQVLE EAQARVQVLE EAGARGEP KAKKLOKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTGCCCGGGC CTGCCCCGGGC TGCGCCGGCC TGTGCCCCGGCC TGTGGCCACA AATGATAAGG AGTGAGGAGA TTTTTCGGGAAGG TGTGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TAGTGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TAGTGGGAAGA TTTTTCGGGA TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTAGCACAC TTTTTCGGGAAGG TAGTGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGACAC TTTTTCGGAAGACAC TTTTTCGGCACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACACAC TTTTTCGGCACACACACACACACACACACACACACACACA	QGSSLSFANV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPESS GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD UNDERSTRESDVW QRCWALS	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTTG CAGCCACT CCTCTGGGCCT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFY VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGGGAA TCTCTGCCCA CGGCTCTGT CCGCAATGGC CAGGCTAGGC CAGGCTGAGC CAGGCTGAGC CAGGCTCCCC CCCAACCAAT Seq ID NO:	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LKDLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTCCCGCCGGCC GTGTGCCCCG TGCCTGC TGCGCCACA AATGATAAGG CGGGACCAGT TGTGGGAAGG TTGTGGGAAGG TTGTGGGAAGG TTGTGGGAAGG AGTGAGGAGA TTTTTCGGGA TTGTGGGAACG TTGTGGGAAGG AAAGTAAACCA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IASSDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIM GEEPEMECIM GEKSEFGEV LIGLCREAEP LESNRFVHKD QRCWALSPKD UERICE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTGG AGGGTTCCTG GCCAGGTGAA TGTCCTGTGTI GCAAAGTTCTI CTCTGTATTC CTCTGTATTC CTCTTGTATTC CTCTGTATTC CTCTGTATTC CTCTGTATTC Sequence NP_006094	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACGCGC CCCCCAGGTG CCCCCAGGTG CAGCCAGTGT CAGCCAGTAG CAGCCAGTGT CCCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTGTGCCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC TTCTGAGGTC GCATCTGGTT TGACCACAGGC AAAA	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGGTAGCCGC CGAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCCACC CCAGCCCACC TTCTCCCTTT	120 180 240 300 360 480 540 600 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFY VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGGGAA TCTCTGCCCA CGGCTCTGT CCGCAATGGC CAGGCTAGGC CAGGCTGAGC CAGGCTGAGC CAGGCTCCCC CCCAACCAAT Seq ID NO:	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA CKGHELVLAN LDCLTQATPK EAQARVQVLE EAQARVQVLE EAGARGEP KAKKLOKQPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTGCCCGGGC CTGCCCCGGGC TGCGCCGGCC TGTGCCCCGGCC TGTGGCCACA AATGATAAGG AGTGAGGAGA TTTTTCGGGAAGG TGTGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TAGTGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TTTTTCGGGAAGG TAGTGGGAAGA TTTTTCGGGA TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTAGCACAC TTTTTCGGGAAGG TAGTGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGG TAGTGGAAGACAC TTTTTCGGGAAGACAC TTTTTCGGAAGACAC TTTTTCGGCACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACAC TTTTTCGGCACACACAC TTTTTCGGCACACACACACACACACACACACACACACACA	QGSSLSFANV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KLKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPESS GEEPEMECLN TLGKSEFGEV LLGLCREAEP LSNNRFVHKD QRCWALSPKD UNDERSTRESDVW QRCWALS	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA SSQNFTLSIA RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTTCACCCTA TGACCAGAGC CTGCACGGGG CCCCCAGGTG CAGCCAGTGT CACTCGCACT CCTCTTGGGC	CVARDDVTGE CWARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MCTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTTGCCA ACCATTAACT CCTGCAGGTT TCTGAGGTC TGCACGCATTCCAGGTT TCTGAGGTC GCATCTGGTT TGACCACAGC	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAG VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSGPAATM SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCACCAC CCAGCCACC	120 180 240 300 360 480 540 600 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVADL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGCGAA TCTCTGCCA CGGCCTTCTT CCGCAATGGC CAGGCTGATC CCCCAACCAAT Seq ID NO: Protein Ac	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LKDLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLY KAKRLQKQPE PPRSSLQPIT GKLNHANVVR CTQVALGMEH RWMSPEAILE GCPSKLYRLM 61 DNA Beq id Accessio uence: 29 11 CCGCCCGGGC CTCCCGCCGGCC GTGTGCCCCG TGCCTGC TGCGCCACA AATGATAAGG CGGGACCAGT TGTGGGAAGG TTGTGGGAAGG TTGTGGGAAGG TTGTGGGAAGG AGTGAGGAGA TTTTTCGGGA TTGTGGGAACG TTGTGGGAAGG AAAGTAAACCA	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IASSDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIM GEEPEMECIM GEKSEFGEV LIGLCREAEP LESNRFVHKD QRCWALSPKD UERICE 1 #: NM_006 406 21 ATAGCACCAT TGCTGTTGG AGGGTTCCTG GCCAGGTGAA TGTCCTGTGTI GCAAAGTTCTI CTCTGTATTC CTCTGTATTC CTCTTGTATTC CTCTGTATTC CTCTGTATTC CTCTGTATTC Sequence NP_006094	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACGCGC CCCCCAGGTG CCCCCAGGTG CAGCCAGTGT CAGCCAGTAG CAGCCAGTGT CCCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCA TGCACGCAAG GGCTGTGCCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC TTCTGAGGTC GCATCTGGTT TGACCACAGGC AAAA	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SLGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGGTAGCCGC CGAGGAGCAGA AGTGCGTCTC CCTTCTGCCT TTCCCCAGCT TGAAATGCTG CAGCCCACC CCAGCCCACC TTCTCCCTTT	120 180 240 300 360 480 540 600 780 960 1020
5055606570	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC GGAGACTGGC GGACAGGGAA TCTCTGCCA CGGCCTCTGT CCGCAATGGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGGCTGAGC CAGCCTCCCC CCCAACCAAT Seq ID NO: Protein Ac 1	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA LDCLTQATPK EAQARVQVLE EAQARVQVLE EAQARVQVLE KAKRLQKQPE FPRSSLQPIT GKLHHANVVR CTQVALGMEH GCPSKLYRLM 61 DNA seq id Accessio uence: 29 11 CCGCCCGGGC CTCAGCCTGC GTGTGCCCCGG TGCGCCGACA AATGATAAGG CAGGACCAGT TGTGGGAAGG TTTTTTCGGGA TTTTTTCGGGA AAAGTAACCA 62 Protein cession #: 11	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LIGICREAEP LSNNRFVHKD QRCWALSPKD UERICE 1 #: NM_006 406 406 406 ACCTCAAGTG AGCTCCAGGC ACCTCAAGTG AGGTTCCTG GCCAGGTGGA TGTCCTGTATTC CTCTGTATTC CTCTTCAGCAA Sequence NP_006094 21	AIVFIKQPSS DRIQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEFDKEA IASNGPQGQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GGCCTGCTTGT GCTCACCCTA CTGCACCGC CCCCCAGGTG CACCCCAGTGT CACTCCCAAT GCCTGCCCTC CCTCTTGGGCC CCCCTGTGGCCCT CCTCTTGGGCCCT CCTCTTGGGCCCT CCTCTTTGGGCCCT CCTCTTTGGGCCCT CCTCTTTGGGCCCT CCTCTTTGGGCCCT CCTCTTTGGGCCCT CCTCTTTGGGCCCT	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGHP RQDVNITVAT FKNGTLRINS TVPCSATGRE RABVQLTVAV MHIFQNGSLV MQTIGLSVG GVAETLVLVK GDLKQFLRIS QRQVKVSALG THGEMPHGGQ LGDSTVDSKP 41 CGCCTAGGCC GCTCTCAGGCA TGCACGCAAG GGCTTTGCCA AACAATTAACT CCTGCCAGGA TTCTCAAGGTC CGCATCTGGTT TGACCACAGC	EARSANASFIN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAE VPSWWEHAE PSTWWEHAE FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSEPAATN SLQTKDEQQO KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGGAGGA AGTGCGTCTC CCTTCTGCCT TTCCCAGCT TGAAATGCTG CAGCCAACCAC CCAGCCCACC TTCTCCCTTT	120 180 240 300 360 480 540 600 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKG KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTG CGAAGACTGGC GGAAGACTGGC GGAAGACTGGC CAGCCTCTGT CCGCAATGGC CAGCCTCTGT CCGCAATGGC CAGCCTCCTG CCCCACCTCGCT CCCCAACCAAT Seq ID NO: Protein Ac 1 MPACRLGPLA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH ACCESSIO UCCCCCGGGC CCTCAGCCTGC GTGTGCCCCGG TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKKPTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPEES GEEPEMECIN TIGKSEFGEV LIGLCREAEP LESNRFVKBUW QRCWALSPKD UERICE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCG AGGGTTCCTA GGCAGGTGGA TGTCCTGGGT CGCAGGTGGA TGTCCTGGGT CTCTGTATTC CTTTCAGCAA SeQUENCE NP_006094 21 GGFTLVSGTGF	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQQQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCAGGTG CCCCCAGGTG CCCCCCAGGTG CCCCCCAGTGT CCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAG GGCTGTGCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC AACATTACT TGACCACAGGC AAAA 41 ADQNCTQECV	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SIGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVINSEY ADDEVLADLQ 51 CGGTAGCCGC CCAGGAGCAGA AGTGCGTCTC CCTTCTGCCTT TTCCCCAGCT TCCCCAGCT TCCCAGCT TGAAATGCTG CAGCCACCC CTTCTCCCTTT 51 SDSECADNLK	120 180 240 300 360 480 540 660 720 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKG KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTG CGAAGACTGGC GGAAGACTGGC GGAAGACTGGC CAGCCTCTGT CCGCAATGGC CAGCCTCTGT CCGCAATGGC CAGCCTCCTG CCCCACCTCGCT CCCCAACCAAT Seq ID NO: Protein Ac 1 MPACRLGPLA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH ACCESSIO UCCCCCGGGC CCTCAGCCTGC GTGTGCCCCGG TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKKPTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPEES GEEPEMECIN TIGKSEFGEV LIGLCREAEP LESNRFVKBUW QRCWALSPKD UERICE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCG AGGGTTCCTA GGCAGGTGGA TGTCCTGGGT CGCAGGTGGA TGTCCTGGGT CTCTGTATTC CTTTCAGCAA SeQUENCE NP_006094 21 GGFTLVSGTGF	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQQQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCAGGTG CCCCCAGGTG CCCCCCAGGTG CCCCCCAGTGT CCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAG GGCTGTGCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC AACATTACT TGACCACAGGC AAAA 41 ADQNCTQECV	EARSANASFIN DGQSNHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAE VPSWWEHAE PSTWWEHAE FITFKVEPER IHDVAPEDSG AAVAYIIAVL SLGSEPAATN SLQTKDEQQO KSKDEKLKSQ LSKDVYNSEY ADDEVLADLQ 51 CGCTAGCCGC CAGGGAGGA AGTGCGTCTC CCTTCTGCCT TTCCCAGCT TGAAATGCTG CAGCCAACCAC CCAGCCCACC TTCTCCCTTT	120 180 240 300 360 480 540 600 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGQGGPPP VRLPTHGRVY SQLEEGKPGY SQLEEGKPGY CMSSTPAGSI GSSLPEWVID TTVYQGHTAL RYTCIAGNSC GLMFYCKKRC KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWVPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCTCT CGCAACCACC GGACGACTGCACC CGCCTCTGC CCCCACCTGCACC CGCCTCTGC CCCCAACCAAT Seq ID NO: Protein Ac 1 MPACRLGPLA CCSAGCATFC	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH ACCESSIO UCCCCCGGGC CCTCAGCCTGC GTGTGCCCCGG TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCCGC TGCGCCCGGCC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGCC	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKKPTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPEES GEEPEMECIN TIGKSEFGEV LIGLCREAEP LESNRFVKBUW QRCWALSPKD UERICE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCG AGGGTTCCTA GGCAGGTGGA TGTCCTGGGT CGCAGGTGGA TGTCCTGGGT CTCTGTATTC CTTTCAGCAA SeQUENCE NP_006094 21 GGFTLVSGTGF	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQQQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCAGGTG CCCCCAGGTG CCCCCCAGGTG CCCCCCAGTGT CCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAG GGCTGTGCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC AACATTACT TGACCACAGGC AAAA 41 ADQNCTQECV	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SIGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVINSEY ADDEVLADLQ 51 CGGTAGCCGC CCAGGAGCAGA AGTGCGTCTC CCTTCTGCCTT TTCCCCAGCT TCCCCAGCT TCCCAGCT TGAAATGCTG CAGCCACCC CTTCTCCCTTT 51 SDSECADNLK	120 180 240 300 360 480 540 660 720 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGQRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTVYQGHTAL RYTCIAGNSC GLMFYCKKG KRHSTSDKMH LDFRRELEMF PLSTKQKVAL YHFRQAWPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTG CGAAGACTGGC GGAAGACTGGC GGAAGACTGGC CAGCCTCTGT CCGCAATGGC CAGCCTCTGT CCGCAATGGC CAGCCTCCTG CCCCACCTCGCT CCCCAACCAAT Seq ID NO: Protein Ac 1 MPACRLGPLA	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH 61 DNA seq id Accessio uence: 29 11 CCGCCCGGGC CTCAGCCTGC GTGTGCCCCG GTGTGCCCCG TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCCCCGGCC TGCGCCCGGCC TGCGCCGCGC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGGCC TGCGCCGCGC TGCGCCGCGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCCCGC TGCCCCGC TGCCCCGCCGCC TGCCCCGCCGCC TGCCCCGCCCG	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGNYT PTVVWYRNQM KIKKPTPPPQP TRDDAGNYTC FLIQWKGKDR VUDKPVPEES GEEPEMECIN TIGKSEFGEV LIGLCREAEP LESNRFVKBUW QRCWALSPKD UERICE n #: NM_006 406 21 ATAGCACCAT TGCTGTTCG AGGGTTCCTA GGCAGGTGGA TGTCCTGGGT CGCAGGTGGA TGTCCTGGGT CTCTGTATTC CTTTCAGCAA SeQUENCE NP_006094 21 GGFTLVSGTGF	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQQQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCAGGTG CCCCCAGGTG CCCCCCAGGTG CCCCCCAGTGT CCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAG GGCTGTGCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC AACATTACT TGACCACAGGC AAAA 41 ADQNCTQECV	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SIGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVINSEY ADDEVLADLQ 51 CGGTAGCCGC CCAGGAGCAGA AGTGCGTCTC CCTTCTGCCTT TTCCCCAGCT TCCCCAGCT TCCCAGCT TGAAATGCTG CAGCCACCC CTTCTCCCTTT 51 SDSECADNLK	120 180 240 360 480 540 660 720 780 960 1020
505560657075	VHYWLLDGA IKWIEAGPVV KERNLTLRPA EAMFHCQFSA CIGGGGRGFP VRLPTHGRVY SQLEEGKPGY CMSSTPAGSI GSSLPEWVTD TTYYQGHTAL RYTCIAGNSC GLMFYCKKC KRHSTSDKMH LDFRRELEMF PLSTKQKVAPL AGKARLPQPE Seq ID NO: Nucleic Ac Coding seq 1 CACCTGCACC CGCCTCCTC GAAGACTGGC GGACAGGGAA TCTCTGCCA CGGCTTGTT CCGCAATGGC CAGGCTGGC CAGGCTGGC CAGGCTGGC CCCAACCAAT Seq ID NO: Protein Ac 1 MPACRLGPLA CCSAGCATFC VTPNF	PVQDTERRFA LKHPASEAEI GPEHSGLYSC QPPPSLQWLF IILEATLHLA QKGHELVLAN LDCLTQATPK EAQARVQVLE NAGTLHFARV LQCEAQGDPK NIKHTEAPLLY KAKRLQKOPE FPRSSLQPIT GKLNHANVVR CTQVALGMEH 61 DNA seq id Accessio uence: 29 11 CCGCCCGGGC CTCAGCCTGC GTGTGCCCCG GTGTGCCCCG TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCCCCGGCC TGCGCCCGGCC TGCGCCGCGC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGGCC TGCGCCGCGC TGCGCCGCGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCCGGCC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCGCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCGCCCGC TGCCCGC TGCCCCGC TGCCCCGCCGCC TGCCCCGCCGCC TGCCCCGCCCG	QGSSLSFAAV QPQTQVTLRC CAHSAFGQAC EDETPITNRS EIEDMPLFEP IAESDAGVT PTVVWYRNQM KIKFTPPPQP TRDDAGNYTC PLIQWKGKDR VUDKPVPEES GEEPEMECIN TLGKSEFGEV LIGICREAEP LSNNRFVHKD QRCWALSPKD UNICLE ATAGCACCAT TGCTGTTCGG AGCTCCAGGC ACCTCAAGTG AGCTCCTGGTT GCAGGTTCCTG GCAGGTTCGG AGGTTCCTG GCAGGTTCGG AGGTTCCTG GCAGGTTGGA TGTCCTGTATTC CTTTCAGCAA Sequence NP_006094 21 CGFTLVSGTGF CCPQVNINFPC	AIVFIKQPSS DRLQDSGTFQ HIDGHPRPTY SSQNFTLSIA RPPHLRRATV RVFTAGSEER CHAANLAGQR LISEDSRFEV QQCMEPDKEA IASNGPQQQI ILDPTKLGPR GGPLQNGQPS FLAKAQGLEE HYMVLEYVDL LAARNCLVSA AFGVLMWEVF RPSFSEIASA 103 31 GCCTGCTTGT CTTCACCCTA TGACCAGAAC CTGCACCGCG CCCCCAGGTG CCCCCAGGTG CCCCCCAGGTG CCCCCCAGTGT CCTCTTTGGGC AAAAAAAAAA	CVARDDVTGE QWFRDGTPLS DESPARVVLA FANGSLLLTQ VTCLPPKGLP RQDVNITVAT FKNGTLRINS TVPCSATGRE RAHVQLTVAV MHIFQNGSLV MIQTIGLSVG GUEVALT GUAETLVLVK GDLKQFLRIS QRQVKVSALG LGDSTVDSKP 41 CGCCTAGGCC GTCTCAGGCA TGCACGCAAG GGCTGTGCA AACATTAACT CCTGGCCAAG TCCTGGCCAGGC AACATTACT TGACCACAGGC AAAA 41 ADQNCTQECV	EARSANASFIN DGQSMHTVSS PQDVVVARYE VRPRNAGIYR EPSVWWEHAS VPSWLKKPQD VEVYDGTWYR KPTIKWERAD FITFKVEPER IHDVAPEDSG AAVAYIIAVIL SIGSGPAATN SLQTKDEQQQ KSKDEKLKSQ LSKDVINSEY ADDEVLADLQ 51 CGGTAGCCGC CCAGGAGCAGA AGTGCGTCTC CCTTCTGCCTT TTCCCCAGCT TCCCCAGCT TCCCAGCT TGAAATGCTG CAGCCACCC CTTCTCCCTTT 51 SDSECADNLK	120 180 240 300 360 480 540 660 720 780 960 1020

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20		GTCGCTATGG					960
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		GCACCAAACG AGTCTTACAT					1440 1500
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		GCTGGGCTCA AAATGTCAGA					1800
35		GAAAGCCAAC					1860
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45	DSGLPVVTSG	CLGLEGSDFQ	CRDTPIPHQR	RSIECCTERN	ECNKDLHPTL	PPLKNRDFVD	120
		SVTVCSLLLV					180
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05	ACAACGCAGC	TTGCACCGAG	TANTGAGGCT	TCCCACACACT	TGGATTCTGA	AAAGGGATCC TATCCGTAGA	420 480
	GGTTTGGAGA	GCAACGTGAA	TGTTGAATTA	CTGAATGCTT	TACATAGTCA	CATGATTAAT	540
	AAGAGAATGT	TGACCAAGGA	CTTAAAAAAT	GGCATGATTA	TTCCTTCAAT	GTATAACAAT	600
70						TGCTCGAATC	
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	TTTGCTCCCA	CCAATGAGGC	TTTTGAGAAA	CTTCCACGAG	GTGTCCTAGA	AAGGTTCATG	900
75	GGAGACAAAG	TGGCTTCCGA	AGCTCTTATG	AAGTACCACA	TCTTAAATAC	TCTCCAGTGT	960
13.						AATTGAGATA AAAGGATATT	
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	CAAGTTATTG	AGCTGGCTGG	AAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
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	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGTCTGCAT	TGAAAATTCA	1440
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	GACACACCTG	TTGGAAATGA	TCAACTGCTG	GAAATACTTA	TAATTAATA	CAAATACATC	1980
			TAGCACCTTC				2040
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	ACAGAAGAAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTCAC	CAAATTCATT	2400
1.5	GAAGGTGGTG	ATGGTCATTT	ATTTGAAGAT	GAAGAAATTA	AAAGACTGCT	TCAGGGAGAC	2460
15	ACACCCGTGA	GGAAGTTGCA	AGCCAACAAA	AAAGTTCAAG	GTTCTAGAAG	ACGATTAAGG	2520 2580
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	GAAACATGAG	GGAAATTGTG	GAGTTAGCCT	CCTGTGGTAA	AGGAATTGAA	GAAAATATAA	2760
20	CACCTTACAC	CCTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
						AACTGTTATC	2880
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25	CAACTAATTT	TGTACTCTCA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTTAA	3120
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35	KLREEIEGKG	SFTYFAPSNE	AWDNLDSDIR	RGLESNVNVE	LLNALHSHMI	NKRMLTKDLK	180 240
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR EALGRDGHFT	INGNOTATI	GAAHAIDKAR	MCDKVASEAL	300
	MKYHILNTLO	CSESIMGGAV	FETLEGNTIE	IGCDGDSITV	NGIKMVNKKD	IVTNNGVIHL	360
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40	VORLLKLILQ	NHILKVKVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKGSKQG	480
	RNGAIHIFRE	IIKPAEKSLH	EKLKQDKRFS	TFLSLLEAAD	LKELLTQPGD	WTLFVPTNDA	540
	FKGMTSEEKE	ILIRDKNALQ	NIILYHLTPG IHVVDKLLYP	VFIGKGFEPG	VINILKTIQG	SKIFLKEVND	600 660
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45	TEVINGEPII	KKYTKIIDGV	PVEITEKETR	EERIITGPEI	KYTRISTGGG	ETEETLKKLL	780
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55	Nucleic Ac Coding sequil 1 ATGCCTGGGG TTCTCCTCT CAGTGCCCG AATCTAACGG AACCAGCTGG AGCCTCAGGC	id Accession uence: 1-92' 11	n #: EOS se 7 21 GGGCCCGCC CTGGGTTCC CTGGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT	31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGGA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA	GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA	GCTGGCGCGA GCCATCCTCC GCTGCCGGAC CGTTAACCGC CCTAACCGC CCAACTGCCC CGTGTCCTTC	120 180 240 300 360 420
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55	Nucleic Ac Coding sequil 1 ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGCCGTT CGCTGTGCGA ACGTGCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA	n #: EOS se 7 21 GGGCCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTAA	31 GCCGGGGACG TCGTCTTCTC GCCGTGTCCG GCACGCGGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA	GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT	GCTGGCGCGA GCATCCTCC GCTGCCGGAC CCTTAACCGC CCTACCGCC CCACTGCCTC CGGTCCTTCAC GGACAACAAC	120 180 240 300 360 420 480 540
55	Nucleic Ac Coding sequilary and a control of the co	id Accession uence: 1-92' 11	m #: EOS section #: E	31 GCCGGGGACG TCGTCTTCC GCCGTGTCCG GCAGCGCGCA CTGCCGCGGG TCGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACCT	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA	GCTGGCGCGA GCCATCCTCC GCTGCCGGAC CCTTACCGGC CCTACCGGC CCAACTGCCC CGTGTCCTTCAC GGGACAACAAT AACAGAGGTA	120 180 240 300 360 420 480 540 600
55 60	Nucleic Ac Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTC CTGGGTCT GTGCAGGGCA	id Accession uence: 1-92' 11	m #: EOS sec 7 21 GGGCCCGCC CTGGGTTCC CTGGCTTCC GTGCTCCAG GGACCTGCCAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA	31 GCCGCGGACG TCGTCTTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC TCGCTGGTGA CTGGAGGACA CCCCACATTA ATGGTGACCT	GGCGTCTGCG CCACCTCCTC CCCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTCTGGC GCCTCACCTA ATGCCTCAA GGGTTTTCCT GGCTCAACGA AAATGAGGAA	CTGGCGCGA GCATCCTCC GCTGCCGGAC CGTTAACCGC CCTACCGGC CCAACTGCCC CGTGCCTTCAC GGACAACAAC AACAGAGGTA TCGGGTCCTC	120 180 240 300 360 420 480 540
55	Nucleic Ac Coding sequil 1 ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCGG AACTGACCGG AGCCTCAGGC CGCAACCTGG AGTGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGCGCCGTT CGCTGTGCGA ACGTGCCAC ACCTGGACTT CACATCTAGA TGCGTAGTT GGGACTAGCA ACGTGTAGTA ACAGTGCTGA ACAGTGCTGA ACAGTGCTGA	m #: EOS se 7 21 GGGCCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CCTGGACTGT TGTTTTAGCC	31 GCCGCGGACG TCGTCTTCTC GCCGTGTCCG GCACCGCGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTCCTGGC GCCTGACCTA ATGCCCTAA ATGCCTCAA AAATCAAGAA AAATCAAGAA TTCCCCCATC	GCTGGCGCGA GCTGCCGGAC CCTTACCGGC CCTACCGGC CCACTGCCCC GGTGTCCTTC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCTTTTG	120 180 240 300 360 420 480 540 660 720 780
55 60	Nucleic Ac Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC GTGCAGGGCA TTGGAACTCA TCTTATGTCT	id Accession uence: 1-92' 11	m #: EOS sec 7 21 GGGCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTATAAAA AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG	31 GCCGGGGACG TCGTCTTCTC GCAGTGCC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCAATTC CTGATAGGC ATGCATAACA	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTTGC GCCTGACCTA ATGCCCTCAA GGGTTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCCT TCAGGAGATGC	CCTGGCGCGA GCTGCCGGAC GCTAACCGC CCTTACCGG CCTACCGGC CCGTCCTTC GGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCATTC CCTGCAAACC CCTGGTTTTTC CTGCAGGGAT	120 180 240 300 360 420 480 540 600 660 720 780 840
55 60	Nucleic Ac Coding sequil ATGCCTGGGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTC TGTGAGGGCA TTGGAACTCA TCTTATTGTCT TATTTGAACC CACATGGAAG	id Accession uence: 1-92' 11	m #: EOS sec 7 7 21 GGGCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTATATAT AAGCCTCAC GCAAGGAC CACCTGTGCA CTGGCAGCC CACCTGGCACTGT TGTTTTAGC CAGATATAAA	31 GCCGGGGACG TCGTCTTCTC GCAGTGCC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCAATTC CTGATAGGC ATGCATAACA	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTTGC GCCTGACCTA ATGCCCTCAA GGGTTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCCT TCAGGAGATGC	GCTGGCGCGA GCTGCCGGAC CCTTACCGGC CCTACCGGC CCACTGCCCC GGTGTCCTTC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCAAACC CCTGCTTTTG	120 180 240 300 360 420 480 540 660 720 780
55 60	Nucleic Ac Coding sequil ATGCCTGGGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTC TGTGAGGGCA TTGGAACTCA TCTTATTGTCT TATTTGAACC CACATGGAAG	id Accession uence: 1-92' 11	m #: EOS sec 7 7 21 GGGCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTATATAT AAGCCTCAC GCAAGGAC CACCTGTGCA CTGGCAGCC CACCTGGCACTGT TGTTTTAGC CAGATATAAA	31 GCCGGGGACG TCGTCTTCTC GCAGTGCC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCAATTC CTGATAGGC ATGCATAACA	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTTGC GCCTGACCTA ATGCCCTCAA GGGTTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCCT TCAGGAGATGC	CCTGGCGCGA GCTGCCGGAC GCTAACCGC CCTTACCGG CCTACCGGC CCGTCCTTC GGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCATTC CCTGCAAACC CCTGGTTTTTC CTGCAGGGAT	120 180 240 300 360 420 480 540 600 660 720 780 840
556065	Nucleic Ac Coding sequil 1 ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCG ACCACCTGG AGCCTCAGGC CGCAACCTGG AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATTGTCT TATTTGAACC CACATGGAAG AGTTCTAACT	id Accession uence: 1-92' 11	m #: EOS Sec. 7 21 GGGCCCCGCC CTGGGTTCC GTGGTTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CTTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGAGTGA	31 GCCGGGGACG TCGTCTTCTC GCAGTGCC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCAATTC CTGATAGGC ATGCATAACA	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTTGC GCCTGACCTA ATGCCCTCAA GGGTTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCCT TCAGGAGATGC	CCTGGCGCGA GCTGCCGGAC GCTAACCGC CCTTACCGG CCTACCGGC CCGTCCTTC GGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCATTC CCTGCAAACC CCTGGTTTTTC CTGCAGGGAT	120 180 240 300 360 420 480 540 600 660 720 780 840
55 60	Nucleic Ac Coding sequilar ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGTCT GTGCAGGGCA TTGGAACTCA TCTTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT	id Accession uence: 1-92' 11	m #: EOS Sec. 7 21 GGGCCCCGCC CTGGGTTCC GTGGTTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CTTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGAGTGA	GCCGGGGACG GCGTGTCTCTC GCGGTGTCCG GCAGCGCGC CTGCCGCGGG CCTGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGATAGCA ATCATGCGG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA AGGGTTTTCCT GGCTCAAGGA AAATGAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT	GCTGGCGCGA GCTGCCGGAC CCTTACCGGC CCTACCGGC CCAACTGCCT CGGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCTCCTCGCTCGGTCCTTCAC CCTGCAAACAC CCTGGAAACAC CCTGGAAACC	120 180 240 300 360 420 480 540 600 660 720 780 840
556065	Nucleic According sequilar attentions of the control of the contro	id Accession uence: 1-92' 11	m #: EOS sec 7 21 GGGCCCCGCC CTGGGTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CCTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGAGTGA Sequence	GCCGGGGACG GCGTGTCTCTC GCGGTGTCCG GCAGCGCGC CTGCCGCGGG CCTGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGGCG ATGATAGCA ATCATGCGG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTTGC GCCTGACCTA ATGCCCTCAA GGGTTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC CTATTTTCCT TCAGGAGATGC	CCTGGCGCGA GCTGCCGGAC GCTAACCGC CCTTACCGG CCTACCGGC CCGTCCTTC GGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGCATTC CCTGCAAACC CCTGGTTTTTC CTGCAGGGAT	120 180 240 300 360 420 480 540 600 660 720 780 840
556065	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCGC TGGACGCTC TTATTGAACCT TATTTGAACCT CACATGGAACT Seq ID No: Protein Ac 1	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA ACGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA ACGCGGT ACAGTGCTGA TCCTGGGTAT CGCATCTAGA TGCTGATGT CGGATTCCTG 68 Protein CGGSIOn #: 11	m #: EOS sec 7 7 21 GGGCCCCGCC CTGGCTTCC GTGCTCCGAG GGACCTGCCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA AAAAAAGTC CACCTGTGCA CAGATATGAA CGAGTATGA GAGTATGAA CGAGTGA GAGATATGAA CGAGTGA CAGATATGAA CGAGTGA CAGATATGAA CGAGTGA Sequence EOS sequence 21	GCCGGGGACG GCGTGTTCTC GCGTGTCCG GCAGCGCGC GCCTACGTGC CTGCCGCGGG TCGCTGGTGA ATGGTGACATTA ATGGTGACCT TATCCGGAAA GACCCATTA GACCCACTATA ATGATAGCG ATGCATACA ATCAATGCGG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA TTCCCCCATC TCAGAGATGC ACCCCAGATT	GCTGGCGCGA GCTGCCGGAC CGTTAACCGC CCTTACCGG CCTACCGGC CGTGCCTTC GGTCCTTCA GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTG CTGCAGGGAT AACAAGAGGTA AACAAACCTC	120 180 240 360 420 480 540 660 720 780 900
55606570	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AACTGACCC CCCTGGGTCT GTGCAGCGCA TCTTATGTCT TATTTGAACC CACATGGAC AGGTTCTAACT Seq ID NO: Protein Ac MPGGCSRGPA	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CGCTGTGCGA AGGTGCCCAC ACCTGGACTT CACATCTAGG TGGCTGAGTT GCGACTGCGA TCGTGAGTT GCGACTGCGA TCCTGGGTAT TCCTGGGTAT CGGATGCTGA TCCTGGGTAT CGGATGCTGA TCCTGGGTAT CGGATGCTCT 68 Protein CGGSIOn #: 11 AGDGRLRLAR	m #: EOS section #: E	31 GCCGGGGACG GCCTACTGC GCAGTGTCCG GCAGCGCGCA CCTGCCGGGG TCGCTGGTGA ATGGTGACCT TATCCGGAAA ATCCAGAAC ATCATACGCG ATGCATAACA ATCATGCGG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATGAGGAA ATTACCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCT CGGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCTTC CCTGCAAACC CCTGGTTTTG CTGCAAACC CCTGGTTTTTG CTGCAGACC CCTGGTTTTT AACAACCTC	120 180 240 360 420 540 660 720 780 840 900
556065	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AACTGACCTGG AGCCTCAGGC CGCAACCTGG AGTGCACCC CTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA MPGGCSRGPA	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGCGCGTT CGCTGTGCGA ACGTGCCAC ACCTGGACTT CACATCTAGA TGCTCAGTT GCACTGACTT GCACTGGTAT GCACTGCGT ACAGTGCTGA TCCTGGGTAT GCAAGGGGAT GGATGCCT 68 Protein cession #: 11 AGDGRLRLAR	m #: EOS Sec. 7 21	GCCGGGGACG GCCTACTGC GCAGTCCG GCAGTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC CTGATAGCG ATGCATAACA ATCAATGCGG	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTCCTGGC GCCTGACCTA ATGCCCTAA ATGCCCTAAGGA AAATCAGGAA ATTCCCCCATC TCAGAGATGC ACCCCAGATT 41	GCTGGCGCGA GCTGCCGGAC CGTTAACCGC CCTTACCGGC CCAACTGCCC CGTGTCCTTC GGACAACAA AACAGAGGTA TCGGGTCCTC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CTGCAGGGAT AACAAACCTC	120 180 240 300 360 420 540 600 660 720 780 840 900
55606570	Nucleic Ac Coding sequitary ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCG AACCAGCTGG AACCAGCTGG AACCAGCTGG AATGGCACCC GTGCAGCCTCAGGC CCCTGGGTCT GTGCAGGGCA TTGGAACTCA TCTTATTGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac MPGGCSRGPA MPGGCSRGPA SCHLDLSNN	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CGCTGTGCGA ACGTGCCCAC ACCTGGACTT CACATCTAGA TGCTGAGTT GCGACTGCCA AGGACGGCT ACAGTGCCA AGGACGGCT ACAGTGCTGA TCCTGAGTT GCAAGTGCTGA TCCTGAGTT GCAAGTGCTA AGGACGGCT ACAGTGCTGA TCCTGGATT CGAAGTGCTGA TCCTGGATT TCGGATTCATTA CGATGTCCT 68 Protein CGGATGTCCT 11 AGGGTATCATTA CGGATGTCCT 11 AGGGTATCATTA CGGATGTCCT SGATGTCCT SGATGTCT SGATGTCCT SGATGTCT SGATGT	m #: EOS sec 7 7 21 GGGCCCCGCC CTGGGTCTCC GTGCTCCCGGGCTCCC GTGCTCCAAGTATAAT AAGCCTCCAC GCAAGGTCTA CATGGCAGAC CACCTGTGCA CACCTGGACTGT TGTTTTAGCC AAAAAAGTGG CAGATATGAA CGGTGA Sequence EOS sequence 21 LALVLLGWVS NLTEVPTDLE RNLTHESLH	GCCGGGGACG GCCTGCTGCC GCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGCGGG TCGCTGGTGA CCCCACTATA ATGGTGACT TATCCGGAAA GACCCAATTC CTGATAGCG ATGATAGCG ATGATAGCG ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTAA ATGCCCTAA ATGCCCTAA ATTCCCCATC TCAGGA AAATCAGGA ATTCCCCATC TCAGAGATGC ACCCCAGATT 41 FSSSAPFLAS NQLASNHFLY NGTLAELQGL	GCTGGCGCGA GCTGCCGGAC CGTTAACCGC CCTTACCGGC CCTACCGGC CCTACCTCC CGTCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTTC CTGCAAACC CCTGCAAACC CCTGGTTTTG CTGCAGGGAT AACAAACCTC 51 AVSAQPPLPD LPRDVLAQLP PHIRVFLDINN	120 180 240 360 420 540 660 720 780 840 900
55606570	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG ATCTCCTCCT CAGTGCCCCG AATCTGACCG AACCTGGACCTGG ACCTCAGGC CGCAACCTGG ACTGGAACCTG TGGAGCGCA TCTTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA TCCTGGGTAT GCGACTGCGA TCCTGGGTAT GCAAGCGGGAT TCCTGGGTAT GCGATCTCTTA GGTATCATA GGTATCATA GGTATCATA CGGATGTCCT 11 AGDGRLRLAR AARTVKCVMR SLVSLTYVSF MYTWLKETEV	n #: EOS Sei 7 21	GCCGGGGACG GCGTGTTCTC GCGTGTTCGG GCAGCGCGCA GCCTACGTGC CTGCGGGGA CTGGAGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC ATCAATGCGG ATGATAACA ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKULH TYPEKMENRVL	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CGTTAACCGC CCTTACCGGC CCAACTGCCC CGTGTCCTTC GGACAACAA AACAGAGGTA TCGGGTCCTC CCTGCAACC CCTGCAACC CCTGCAACC CCTGCAACC CTGCAGGGAT AACAAACCTC	120 180 240 360 420 480 540 660 720 780 900
5560657075	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG ATCTCCTCCT CAGTGCCCCG AATCTGACCG AACCTGGACCTGG ACCTCAGGC CGCAACCTGG ACTGGAACCTG TGGAGCGCA TCTTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGCGA AGGTGCCCAC ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA TCCTGGGTAT GCGACTGCGA TCCTGGGTAT GCAAGCGGGAT TCCTGGGTAT GCGATCTCTTA GGTATCATA GGTATCATA GGTATCATA CGGATGTCCT 11 AGDGRLRLAR AARTVKCVMR SLVSLTYVSF MYTWLKETEV	n #: EOS Sei 7 21	GCCGGGGACG GCGTGTTCTC GCGTGTTCGG GCAGCGCGCA GCCTACGTGC CTGCGGGGA CTGGAGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC ATCAATGCGG ATGATAACA ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKULH TYPEKMENRVL	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCC CGTGCCTTAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGACC CCTGGTTTTTG CTGCAGACC CTGCAAACC CTGGTTTTTG CTGCAGACC CTGGTTTTG CTGCAGACC CTGCACACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCACACC CTGCACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTGCAC	120 180 240 360 420 540 660 720 780 840 900
55606570	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AATCTAACCG AATCTAACCG AACCTGAGCC CCCTGGGTCT GTGCAGGGC TTGTATGTCT TATTTGAACCT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDISNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCCGTT CGCTGTGCGA ACGTGCCCAC CCAGCAACCA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA AAGACCGGCT ACAGCGGTA TCCTGGGTAT CGCATTCTAGA TGGTTGCTGA TCCTGGGTAT CGGATTCCTG 68 Protein CGGATGTCCT 11 AGDGRLRLAR AARTVKCVNR SLVSLTYVSF MVTWLKETEV LIGAIFLLVI	#: EOS Sec. 7 21	GCCGGGGACG GCGTGTTCTC GCGTGTTCGG GCAGCGCGCA GCCTACGTGC CTGCGGGGA CTGGAGGACA CCCCACATTA ATGGTGACCT TATCCGGAAA GACCCGATTC ATCAATGCGG ATGATAACA ATCAATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKULH TYPEKMENRVL	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCC CGTGCCTTAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGACC CCTGGTTTTTG CTGCAGACC CTGCAAACC CTGGTTTTTG CTGCAGACC CTGGTTTTG CTGCAGACC CTGCACACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCACACC CTGCACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTGCAC	120 180 240 360 420 540 660 720 780 840 900
5560657075	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCTCAGGC CGCAACCTGA ATGGCACCG ATTGAACTCA TTGTAACTC TATTTGAACC CACATGGAG AGTTCTAACT Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO:	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGGA AGGTGCCCAC ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA TCGTGGGTAT GCGACTGCGA TCCTGGGTAT CGGATGCCA ACGGGTAT ACAGTGCTGA TCCTGGGTAT CGGATGCCT 68 Protein CGGSTGCCT 11 AGGGGTGCCT AGGGTATCATTA CGGATGTCCT SUSLITVSF MYTMLKETEV LIGAIFLLVI 69 DNA sec	#: EOS Sec. 7 21	GCCGGGGACG GCCTGCTGCG GCAGTGTCTC GCCGTGTCCG GCAGCGGCA CTGCGCGGG TCGCTGGTGA ATGGTGACCT TATCCGGAAA ATGCTGACCG ATGCATAACA ATGCATAACA ATCATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMRNRVL MHNIRDACRE	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCC CGTGCCTTAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGACC CCTGGTTTTTG CTGCAGACC CTGCAAACC CTGGTTTTTG CTGCAGACC CTGGTTTTG CTGCAGACC CTGCACACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCACACC CTGCACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTGCAC	120 180 240 360 420 540 660 720 780 840 900
5560657075	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA ATGGCACCG ATTGGAACTCA TTGGAACTCA TTGTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHABL SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGGCGCGTT CGCTGTGCGA ACGTGCCAC ACCTGGACTT CACATCTAGA TGCGTAGGT TGCGACTGCA ACGTGCTAGT ACAGTGCTGA TGCGACTGCA ACGTGCTGA TCCTGGGATT CGAAGGGGAT GGAAGGGGAT GGAAGGGGAT TCCTGGTAT GGAAGTGCTGA TCCTGGTAT TCGGATGTCCT 68 Protein TGGSATGTCCT AAGDGRLRLAR AAGTVKCVNR AAGTGCTGA TUTLAGT SLUSLTYVSF AVTWLKETLVI LIGAIFLLVI 69 DNA sectid Accession	#: EOS Sec. 7 21 GGGCCCCGCC CTGGGTTCC CTGGGTTCC GTGCTCCGAG GGACCTGCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAA CATGGCAGAC CACCTGTGCA CACCTGTGCA CACTGTGCA AAAAAGTGG CAGATATGAA CGAGTGA SEQUENCE EOS SEQUENC 21 LALVLLGWVS NLTEVPTDLF RNLTHLESLM VQGKDRLTCA YLNRKGIKKW	GCCGGGGACG GCCTGCTGCG GCAGTGTCTC GCCGTGTCCG GCAGCGGCA CTGCGCGGG TCGCTGGTGA ATGGTGACCT TATCCGGAAA ATGCTGACCG ATGCATAACA ATGCATAACA ATCATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMRNRVL MHNIRDACRE	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCC CGTGCCTTAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGACC CCTGGTTTTTG CTGCAGACC CTGCAAACC CTGGTTTTTG CTGCAGACC CTGGTTTTG CTGCAGACC CTGCACACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCACACC CTGCACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTGCAC	120 180 240 360 420 540 660 720 780 840 900
556065707580	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AATCTGACCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA ATGGCACCG ATTGGAACTCA TTGGAACTCA TTGTATGTCT TATTTGAACC CACATGGAAG AGTTCTAACT Seq ID NO: Protein Ac 1 MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHABL SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG CGGCGCGTT CGCTGTGGA AGGTGCCCAC ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCGA TCGTGGGTAT GCGACTGCGA TCCTGGGTAT CGGATGCCA ACGGGTAT ACAGTGCTGA TCCTGGGTAT CGGATGCCT 68 Protein CGGSTGCCT 11 AGGGGTGCCT AGGGTATCATTA CGGATGTCCT SUSLITVSF MYTMLKETEV LIGAIFLLVI 69 DNA sec	#: EOS Sec. 7 21 GGGCCCCGCC CTGGGTTCC CTGGGTTCC GTGCTCCGAG GGACCTGCC CTTCCTTTAC AAGTAATAAT AAGCCTCCAA CATGGCAGAC CACCTGTGCA CACCTGTGCA CACTGTGCA AAAAAGTGG CAGATATGAA CGAGTGA SEQUENCE EOS SEQUENC 21 LALVLLGWVS NLTEVPTDLF RNLTHLESLM VQGKDRLTCA YLNRKGIKKW	GCCGGGGACG GCCTGCTGCG GCAGTGTCTC GCCGTGTCCG GCAGCGGCA CTGCGCGGG TCGCTGGTGA ATGGTGACCT TATCCGGAAA ATGCTGACCG ATGCATAACA ATGCATAACA ATCATGCGG SSSPTSSASS AYVRNLFLTG LEDNALKVLH YPEKMRNRVL MHNIRDACRE	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT FSSSAPFLAS NQLASNHFLY NGTLAELQGL LELNSADLDC	GCTGGCGCGA GCTGCCGGAC CCTTACCGC CCTACCGGC CCAACTGCCC CGTGCCTTAC GGACAACAAT AACAGAGGTA TCGGGTCCTC CCTGCAAACC CCTGGTTTTG CTGCAGACC CCTGGTTTTTG CTGCAGACC CTGCAAACC CTGGTTTTTG CTGCAGACC CTGGTTTTG CTGCAGACC CTGCACACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCAGACC CTGCACACC CTGCACC CTGCACACC CTGCACACC CTGCACACC CTGCACACC CTGCAC	120 180 240 360 420 540 660 720 780 840 900
5560657075	Nucleic Ac Coding sequil ATGCCTGGGG CTAGCGCTGG TTCTCCTCT CAGTGCCCCG AACCAGCTGG AGCCTCAGGC CGCAACCTGA AATGGCACCC CCCTGGGTCT GTGCAGGGCA TTGTAGTCTCT TATTTGAACCT CACATGGAACTA Seq ID NO: Protein Ac I MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVCDCHMAL SSNSDVLE Seq ID NO: Nucleic Ac Coding seq	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG CGCGCGCGTT CGCTGTGCGA ACGTGCCAA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCCA ACAGTGCCAA ACGTGGGTAT GCGACTGCCA ACAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT CGCATCCT 68 Protein CGSATGTCCT AAGDGRLRLAR SLVSLTYVSF MYTWLKETEV LIGAIPLLVI 69 DNA sectid Accessic quence: 26.	#: EOS Sec. 7 21	GCCGGGGACG GCCTGCTGCC GCAGTCCC GCAGTGCC GCAGTGCC GCCTGGGGACA CCCCACATTC TATCCGGAAA GACCCAATTC CTGATAGCG ATGATAGCG ATGATAGCG ATGCATACA ATCATGCGG ATGATACA ATCATGCGG ATGATACA ATCATGCGG ATGCATACA ATCATGCGGA ATCATGCGGA ATCATGCATACA ATCATGCGGA ATCATGCATACA ATCATGCGGA ATCATGCATACA ATCATGCGGA ATGCATACA ATCATGCGA ATGCATACA ATCATGCATACA ATCATGC	GGCGTCTGCG CCAGCCCCC CAGTCAAGTG GCAACCTGT ATGTGCTGGC GCCTCAACGA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC TCAGAGATGC ACCCCAGATT 41 FSSSAPFLAS NQLASMHFLY NGTLAELQGI LELNSADLDC HMEGYHYRYE	GCTGGCGCGA GCTGCCGGAC GCTGCCGGAC CCTTAACCGC CCTAACTGCCC CCTGCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTTC CCTGCAAACC CCTGGTTTTTG CTGCAGAGAC AACAAACCT 51 AVSAQPPLPD LPRDVLAQLP PHIRVIDINN DPILPPSLQT INADPRLTNL	120 180 240 360 420 540 660 720 780 840 900
556065707580	Nucleic Ac Coding sequit ATGCCTGGGG CTAGCGCTGGG ATCTCACCC AATCTGACCG AATCTGACCG AACCAGCTGG ACCACCTGG ACCTCAGGC CGCAACCTGA TTGGAAGCGC TTGTATGTCT TATTTGAACC CACATGGAA Seq ID NO: Protein AC I MPGGCSRGPA QCPALCECSE SLRHLDLSNN PWVDCHMAD SYVFLGIVLA SSNSDVLE Seq ID NO: Nucleic Ac Coding seq	id Accession uence: 1-92' 11 GGTGCTCCCG TACTCCTGGG TACTCCTGGG CGCGCGCGTT CGCTGTGCGA ACGTGCCAA ACCTGGACTT CACATCTAGA TGGCTGAGTT GCGACTGCCA ACAGTGCCAA ACGTGGGTAT GCGACTGCCA ACAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT GCAAGTGCTGA TCCTGGGTAT CGCATCCT 68 Protein CGSATGTCCT AAGDGRLRLAR SLVSLTYVSF MYTWLKETEV LIGAIPLLVI 69 DNA sectid Accessic quence: 26.	#: EOS Sec. 7 21	31 GCCGGGGACG GCCTGCTCTCTC GCCGTGTCCG GCAGCGCGCA GCCTACGTGC CTGCCGGGG TCGCTGGTGA ATGGTGACCT TATCCGGAAA ATCCAGAAA ATCAATGCGG 31 SSSPTSSASS AYVRNLFLTG LEDNALKULG MHNIRDACRE	GGCGTCTGCG CCAGCCCCC CCAGCCCCC CAGTCAAGTG GCAACCTCTT ATGTGCTGGC GCCTGACCTA ATGCCCTCAA GGGTTTTCCT GGCTCAAGGA AAATCAGGAA ATTCCCCCATC CTATTTTCCT TCAGAGATGC ACCCCAGATT 41 FSSSAPFLAS NQLASANELY NGTLAELQGL LELNSADLDC HMEGYHYRYE	GCTGGCGCGA GCTGCCGGAC GCTGCCGGAC CCTTAACCGC CCTAACTGCCC CCTGCCTTCAC GGACAACAAT AACAGAGGTA TCGGGTCCTTC CCTGCAAACC CCTGGTTTTTG CTGCAGAGAC AACAAACCT 51 AVSAQPPLPD LPRDVLAQLP PHIRVIDINN DPILPPSLQT INADPRLTNL	120 180 240 360 420 540 660 720 780 840 900

	CACCACCCAC	CTCCCCCCC	CCGCCATGGT	CCCCCACACC	CCTCCCTTC	ттстсстсас	60
			CCGGACAGGG				120
			AGGAAACCAA				180
	CCCCCACCAC	COCCACA	TCACGTTCCT	CARARACACE	CTCATCCACT	CTCACCCCTC	240
5	CCGCCAGCAG	GI CAGGGAGA	GCACCGGCCT	DAMAMACACO	GIGNIGGAGI	TOTA CTCCCC	300
,			GCACCGGCCT				360
			CGGGCAACGG				420
	CCCCTGCCCC	GCGGGCTTCA	CGGGCAACGG	TATION ACTOR	ACCORCGICA	TCCCCTCCCA	480
	CGCCCACCCC	TGCTTCCCCC	GAGTCCGCTG GCGGCCCCAC	TATCAACACC	AUCCCCGGGG1	TCCGCTGCGV	540
10	GGCTTGCCCG	CCGGGGTACA	GEGGECCEAC	CCACCAGGGC	P CCCCCCT P C	ATTA A CTIC CCCAM	600
10	GGCCAACAAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	#CCGGGCAAC	CCCACCCCC	660
			ACACCCGGGG				
	CTTCGTGGGC	GACCAGGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720
			AGCATGCAGA				780
1.5	GTGCGTGTGT	CGCGTTGGCT	GGGCCGGCAA	CGGGATCCTC	TGTGGTCGCG	ACACTGACCT	840
15			AGCTGCGCTG				900
			GGCAGGAGGA				960
			ACGGGGTCCC				1020
	GAACCCAGAC	CAGCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACTGCCG	1080
00			AAAAGGACAC				1140
20	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
	CTCAGACCAG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
			CGGATGTGGA				1320
	CGATCAAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGGTGCC	1380
	TAACAGTGCC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCCTGCG	ACGACGACGA	1440
25	CGACAATGAC	GGAGTCCCTG	ACAGTCGGGA	CAACTGCCGC	CTGGTGCCTA	ACCCCGGCCA	1500
			GCGTGGGCGA				1560
	GGTGGTAGAC	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCACGCTCA	CCGACTTCAG	1620
			TGGACCCGGA				1680
	GGTGCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
30	GGGTTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1800
			TCATCTTTGG				1860
			AAACGTATTG				1920
			CTGTGAAGTC				1980
	CCCTCTCTCC	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
35			AGAAGTCCTA				2100
55			TCTATGAGGG				2160
	GGGCIACAIC	AGGGTGCGAT	GTGGCCGCCT	CCCCCCCCCCC	TECTTOTO	AGGAGAACAT	2220
	CITGGACACA	ACCATGCGGG	ACCGCTGCAA	TCACACCATC	CCACACGACT	ATGAGACCCA	2280
	CATCIGGGCC	AACCIGCGII	GACCAGGGTG	ACCACCACC	CCAGAGGACI	CACCCTCACC	2340
40			CACCCAGCCC				2400
40					CGICCIGAGG	GGGAAGIGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAGGG			
	a TD NO	no Bunkala					
		70 Protein					
15	Protein Ac	cession #: 1	NP_000086.1		43	E3	
45				31	41	51 I	
45	Protein Acc	cession #: 1 11 	NP_000086.1 21 	1	1	1	£0
45	Protein Acci	cession #: 1 11 LTLAALGASG	NP_000086.1 21 QGQSPLGSDL	GPOMLRELQE	 TNAALQDVRD	 WLRQQVREIT	60 120
45	Protein Ac	cession #: 1 11 LTLAALGASG ACGMQQSVRT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH	 GPQMLRELQE CAPGFCFPGV	 TNAALQDVRD ACIQTESGGR	 WLRQQVREIT CGPCPAGFTG	120
	Protein Actin MVPDTACVLL FLKNTVMECD NGSHCTDVNE	cession #: 1 11 LTLAALGASG ACGMQQSVRT CNAHPCFPRV	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR	GPQMLRELQE CAPGFCFPGV CEACPPGYSG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD	120 180
45 50	Protein Act NVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN	CESSION #: 1 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH	120 180 240
	Protein Act	11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT	GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ	120 180 240 300
	Protein Act	11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL	GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK	120 180 240 300 360
	Protein Acci 1 MVPDTACVLL FLENTVMECD NGSHCTDVNE INECETGQHIN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA	CESSION #: 1 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV	GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD	120 180 240 300 360 420
50	Protein Act	CESSION #: 1 ITLAALGASG ACGMQGSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT	 GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS	120 180 240 300 360 420 480
	Protein Act	CESSION #: 1 LTLAALGASG ACGMQQSVRT CVARPCFPRV CVPRSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV	NP_000086.1 21	GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC	I TNAALQDVRD ACIQTESGGR PTEQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDNC HDGGGDACDNC HDGGGDACDDC PENAEVTLTD	 WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD	120 180 240 300 360 420 480 540
50	Protein Act	CESSION #: 1 LTLAALGASG ACGMOQSVRT CNABPEFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVUNQGREI	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQIMNSDFGL	GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVILTD DFESTFHVNT	I WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI	120 180 240 300 360 420 480 540
50	Protein Act	Cession #: 1 LTLAALGASG ACCMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEBADRIGV WVVLNQGREI VVMWKQMEQT	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAPNGV AEFGLQLKAV	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act WYPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD	CESSION #: 1 LTLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMKQMEQT PRNVGWKDKK	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEFGLQLKAV QVGYLRVRFY	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540
50	Protein Act WYPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD	CESSION #: 1 LTLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMKQMEQT PRNVGWKDKK	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEFGLQLKAV QVGYLRVRFY	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act	CESSION #: 1 LTLAALGASG ACGMOQSVRT CNABPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMKQMEQT PRNVGWKDKK NIIWANLRYR	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLDVC AVGYTAFNGV AEFGLQLKAV QVGYLRVRFY	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act MVPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQILPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO:	Cession #: 1 LTLAALGASG ACGMQGVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act	CESSION #: 1 LTLAALGASG ACGMOQSVRT CNARPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVINGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CCAPGPGYSG PGFYGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP CQRGAQRFCD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENABVTLTD DPEGTFHVNT KSSTGFGEQL EGPELVADSN	WLRQQVREIT CSPCPAGFTS AKANKQVCTD DSSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 300 360 420 480 540 600
50 55 60	Protein Act	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA	I TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN EDGGDACDNC HDGQGDACDD PERAEVILTD DFEGTHVNT KSSTGFGEQL	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT	120 180 240 300 360 420 480 540 600
50	Protein Act	Cession #: 1 LTLAALGASG ACGMQGSVET CNARPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDFGL YWQAMPFRAV SYRWFLQHRP CNDTIPEDYE uence #: NM_024 919 21	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVFFY THQLRQA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPCCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVTLTD DFEGTFHVNT KSSTGFGEQL EGPELVADSN	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG	120 180 240 360 420 480 540 660 720
50 55 60	Protein Act MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLIVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Act Coding seq GAGTCACCAA	LTLAALGASG ACGMOQSVRT CAMAPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCDDDIDGDRI DSDQDQDGDG GCEDADRDGV VVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PCFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY TEQLRQA 626 31 CTCAGCCAGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP CREDEWGDACDN DGIGDACDNC HDGQGDACDD DFENABVTLTD DFESTFHVNT KSSTGFGEQL EGPELVADSN	wlrqqvreit cgpcpagftg akankqvctd dgspsecheh ncvtvpnsgq crsqknddqk pqksnpdqad dddndgvpba vtdddyagfi rnalwhtgdt vvldttmrgg 51 gctgggaacc	120 180 240 300 360 420 480 540 660 720
50 55 60	Protein Act MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDROGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Act Coding seq 1 GAGTCACCAA	Cession #: 1 LTLAALGASG ACCMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGC	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 62.6 31 CTCAGCCAGT CCTCTTCTGG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPGCRKD EDKWGDACDN DGIGDACDNC HDGGGDACDD PENAEVTLTD DFBETFHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC ACCCAGATAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHER NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT	120 180 240 300 360 420 480 540 660 720
50 55 60	Protein Act	Cession #: 1 LTLAALGASG ACGMQGSVRT CNAMPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVINGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGC ATGGCTACCC GGAGCAATTGCC GGAGCAATTGCC	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDFGL YWQANFFRAV SYRWFLQHRP CNDTIPEDYE uence 1 #: NM_024 919 21 GGGGGGGGGGGGGAGTTCCA TGGGGGGAGAT CACTCATCAT	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAPNGV AEPGIQLKAV THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECKEGDACDN DGIGDACDN DGIGDACN ACCCAGATAC AGCATAATTA ATTTCAGGGA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCUTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT	120 180 240 300 360 420 540 600 720
50556065	Protein Act MVPDTACVLL FLENTYMECO INGSHCTUVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1 GAGTCACCAA TTCCCCCAGCC TATTCTGGCT CCCAGGCC TATTCTGGCT CCCAGGCCT I	LTLAALGASG ACGMOQSVRT CAMAPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGC ATGGCTTCCC GGAAGCAATCC	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PCFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKLIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGG CATTGGGGAG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN DFERNAEVTLTD DPEGTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC	120 180 240 360 420 540 600 720
50 55 60	Protein Act MVPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FEGDAQIDPN FEGURALLWKD RLGVFCFSQE Seq ID NO: Nucleic Act Coding seq GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GODDIDGDRI DSDQDQDGDG GQEDADRGBV VVVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 11 DNA seq id Accessio uence: 71 11	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGG CGTTTGGGGAG CGTGATACAA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP EDKWGDACDN DGIGDACDNC HDGQGDACDD DFENABVTLTD DFESTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGAATCC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACICCAC AAGGTGTTTT	120 180 300 360 420 480 540 660 720
50556065	Protein Act MVPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTGAACCT AGGCTTGGTC	Cession #: 1 LTLAALGASG ACCMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GODDIDGDRI DSDQDQDGDG GQEBADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NITWANLRYR 71 DNA seq 1d Accessio uence: 71 11 GGAAGGCAGC GGAAGCAGC GGAGCAATTG ACTGTCGCCT GGACATCAAAC GACATCAAAC CCATGAGTTCA	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG PGFVGDQASG VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAGA AGATGAGCTG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVTLTD DFECTPHVNT KSSTGPGEU EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA TGGCTGAAGG TCGGAGCAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDNDGVVDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT	120 180 240 360 420 540 660 720
50556065	Protein Act MVPDTACVLL FIENTYMECI NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq I GAGTCACCAA TTCCCCAGCC TATTCTGGCT TTTTGAACCT AGGCTTGGTC CAGAGGCCGGCGCGCGCGCCGCCGCCGCCGCCCGCCCGC	LILLAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDDDQDGDG GQEDADRDGV WVVLNGGREI VVMKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGGC GGAGGCAATTG ACTGTCGCCT GACATCAAAC CATGAGTTCA	NP_000086.1 21	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG CGTGATACAA AGATGAGCTG AGTGATAGTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECHWGDACDN DGIGDACDN DGIGDACDN DETGAEVILITD DFETFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGGAATCC TGGCTGAAGG GCCAATGCC GGCAATGCC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT	120 180 240 360 420 540 600 600 720
50556065	Protein Act MVPDTACVLL FILINTYMECD INGSHCTDVNE INSCETTGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLIVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Act Codding seq GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT AGGCTTGGTC CAGAGCCCG GAAAAACCTG	Cession #: 1 LTLAALGASG ACGMOQSVRT CAMAPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCDDDIDGDRI DSDQDQDGDG GCEDADRDGV VVVINGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PCFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGG CGTGATACAA AGATGATGTT CTACAAATGT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDN DFERAEVTLTD DPEGTFHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGCAGATGCC TGGGGGCAGG GGCAATGCCT TATATCATCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG	120 180 300 360 420 480 540 660 720 60 120 180 240 360 420 480
5055606570	Protein Act MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGAGGCCGG GAAAAACGTG CAAGGGGAAT	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGC ATGGCTTCCC GGAGCAATTG ACTGTCACAC CATGATCAAAC CATGACTCACAG GCTAACCTTGC GCATACATGC GCATACATGC GCATACACG GCTAACCTTG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AUGTTAFNGV AUGTTAFNGV AUGTTAFNGV THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAA AGATGATAGTT CTACAAATGT TGGAGCCTTC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPGCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVTLTD DFECTPHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA TGGGTGAAGG TCGGAGCAGG GGCAATGCCT TATATCATCA AGCATTACTCA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDNDQVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTTGCGGCT ACTCAAAGG AAGTGAATGTT	120 180 240 360 420 540 660 720 60 120 180 240 300 420 420 430 540
50556065	Protein Act	LTLAALGASG ACGMOGSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVULNGGREI VVMKKQMEQT PRNVGWKDKX NIIWANLRYR 71 DNA seq id Accessio uence: 71 11	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDFGL YWQAMPFRAV SYRWFLQHRP CNDTIPEDYE 1	GPQMLRELQE GPQMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PMSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG CGTGATACAA AGATGAGCTG AGTGATAGTT CTACAAAATGTT GGGGTGTGAGGCCTT GGGTGTGAGGCCTT GGGTGTGAGGCCT GGGTGTGAGGCCT GGGTGTGAGGCCT GGGTGTGAGGCCT GGGTGTGAGGCCT	ITMAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECKEGDACDN DGIGDACDN DGIGDACDN DGIGDACDN DGIGDACDN DGIGDACDN ACIQTESGR HDGQGDACDD PENAEVILID DFEGTPHVNI KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGCAGAGG TCGGAGAGG GCCAAGGCCG GCCATGCCG AGCATGCCG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTT CTTTGCGGCT CTTTTAAAGG AAGTGAATGT TCCCCCAGCC	120 180 240 360 420 540 600 720 60 120 180 240 300 3420 480 540
5055606570	Protein Act MVPDTACVLL FLENTYMECI INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGCAAA GGAAAACGTG CAAGGGGAAT GGACTATAT CCCAGGGCAA CCAAGGGCAAT CCACAGGGCAAC CCAAGGGCAAT CCACAGGTCACT CAAGGGGAAT CCACAGTGCACT CAAGGGCAAT CCACAGGTCACT CACAGTGCACT CAAGGGCAAT CACAGTGGTC CAAGGGCATAT CACAGTGGTC CACAGTGCTC CACAGTGCACT CACAGTCACT CACAGTGCACT CACAGTGCACT CACAGTCACT CACAGTGCACT CACAGTGCACT CACAGTCACT CACAGTGCACT CACAGTCACT	Cession #: 1 LTLAALGASG ACGMOQSVRT CNAMPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 1 GGAAGGCAGCC ATGGCTTCCC GGAGCAATTCAA ACAGCAGTGT GACATCACAG CATGACTTCG GCAGCACTCG TGGGCATCCCC	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG CATTGGGGAG CGTGATACAA AGATGAGCTTG CTACAAATGT CTACAAATGT CTGAGCCTCC GGGGGCCAAC	TNAALQDVRD ACIOTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPQCRKD EDKWGDACDN DGIGDACDNC DGIGDACDNC DEGGDACDNC DFERAEVILID DPEGTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGAGACCC TGGCGAGAGG TCGGAGCAGG TATATCATCA AGCATCCGGA CCCCGATGGT TTCTCCGAAGG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC	120 180 300 360 420 480 540 660 720 60 120 180 360 420 480 540 660
5055606570	Protein Act MVPDTACVLL FLKNTVMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGS DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq I GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGAGGCCAG GAAAACGTG CAAGTGATATAT CCAGGTTTTAGA CCAGTTCTTAGA CCAGTTCTTAGACCT CAGAGGGGAAT CGACTTTTAGA CCAGTCCT CAGAGGCCTGC CAGAGGCCTGC CAGAGGCCTGC CAGAGGCCTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCGTTTTAGACCT CAGCTTTTAGACCT CAGCTTTTAGACT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTTTAGACCT CAGCTT CAGCTT CAGCTT CAGCTT CAGCTT CAGCT CAGCTT CAGCT C	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAHPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GODDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNQGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG VPNSAQEDSD DKVVDKIDVC AVGTTAFNGV AVGTTAFNGV THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT AGTGATAGTA AGATGATGGT TGGAGCCTTC GGGAGCCAAC CGTGATAGGT TGGAGCCTTC GGGAGCCAAC CGTGATAGGT TGGAGGCTT CGGGAGCCAAC CGAGAAGGTT	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCF RCPEPGCRKD EDKWGDACDN DGIGDACDNC HDGQGDACDD PENAEVTLTD DFECTPHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGTAGGAGCG CCCCATGGT TTCTCCGAAG GTGTCTGTGC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGAGGG AAGTGATGT TCCCCCAGCC TCTCCAATAC	120 180 240 360 420 540 660 720 60 120 180 240 360 420 420 420 450 660 540 660 720
5055606570	Protein Act	LILLAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVWHKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGG GGAGAATTG GGAAGTTCACAG ACAGCATGTG GCAGCTCAGG GCTAACCTTG GCAGGCTCAGG CTGAACTCTG GCAGCTCAGG CTGAACTCTG CTGAACTCTG AACACATACTG AACACATACTG AACACATACTG AACACCATACTG ACACCATACTG AACACCATACTG ACACCATACTG AACACCATACTG AACACCATACTG ACACCATACTG AACACCATACTG ACACCATACTG AACACCATACTG AACACCATACTG ACACCATACTG AACACCATACTG AACACCATACTG AACACCATACTG ACACCATACTG AACACCATACTG AACACCA	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDFGL YWQAMPFRAV SYRWFLQHRP CNDTIPEDYE 1 GGCAGCTCCA GGCAGCTCCA CAGCTGGGAA TTGTCTGATAT AGGAGCAA TTGTTGATAT AGGAGCAA TTGCTGGTCCA AGTATAAAAC AGACCTTGCG AGATTGACG AGAATGTGAC	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV GVGYTRVFY THQLRQA 31 CTCAGCCAGT CCTCTCTGG TGGCTTTGGT CATTGGGGAG CGTGATACAA AGATGAGGTT GGGGGCCTT GGGGTTCAGGCTT CGGGTTCAGAATGTT CTACAAATGT TGGAGCCTT GTGTGAGGCCT CGTGTGAGGCCT CGTGTGAGGCT CTAGAAATGT TGGAGGCCT CGTGTGAGGCT TGGAGGCCT CGTGTGAGGCT TGGAGGCT TGGAGGCCT TGGAGGCCT TGGAGGCCT TGGAGAAATGAC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECKEGDACDN DGIGDACDN ACCCAGATAC AGCATAATTA ATTTCAGGGA GGCAATACCT TATATCATCA AGCATGCCGG CCCCGATGGT TTCTCGGAAG GGTGTCTGGC ATTGCCAAAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCUTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AGGCTGTTT ATGAAATGTT CTTTGCGGCT TCTCTAAAGG TCCCCCAGCC TCTCCAATAC TCTACAATGT TCACACGGGA	120 180 240 360 420 540 600 720 60 120 180 240 300 420 480 540 660 720
50 55 60 65 70	Protein Act MVPDTACVLL FLENTYMECI MVPDTACVLL FLENTYMECI INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq 1 GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT CACAGTCACT CAGAGGCCGG GAAAAACGTG GGACTATAAT GCACTAAAT CACAGTGACT CAGGTTTGAG TACCAAAAGGCT TATCAAAGTC TATCAAAAGTC TATCAAAACTC TATCAAACTC TATCAACTC TATC	Cession #: 1 LTLAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GCDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 1 GGAAGGCAGCC ATGGCTTCCC GGAGCAATCCC GCAGCTCAGC CAGCTCAGC TCAACCCTCAG TGGGCATCCC GCTGAACCTCG AACACCATCCT ACAGAATCCG AACACACTCT AACACATACCT AACACT AA	NP_000086.1 21	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVRFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG CGTGTTAGTA AGATGAGCTT CTACAAATGT CTACAAATGT CTGAGCCTTC GGGGGGCCAAC GGGAGCCAAC GGGAGCCAAC GGGAGTCAA	TNAALQDVRD ACIOTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPPCCRKD EDKWGDACDN DGIGDACDN DGIGDACDN DETGDACND DFERAEVILID DPEGTFHVNT KSSTGFGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGA GATGGAATCC TGGCTGAAGG GCCAGATGGT TTTTCCGAAGG CCCCGATGGT TTTTCCGAAGG GTTTTTCCCGAAGG CCCCGATGGT TTTTTCCAAAG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCACCAGCC TCTCCAATAC TCACAGGGGA TCACAGGGGA TCACAGGGGA TCACAGGGA TCACAGGGA TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTATAC TCACAAGGTAAA	120 180 300 300 420 480 540 660 720 60 120 180 360 420 480 540 660 720 780 840
5055606570	Protein Act MVPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDHOFVGDAC RDHOFVGDAC ROMENLLWED FGYQDSSFY ESQVELLWED Seq ID NO: Nucleic Act Coding seq ID GAGTCACCAA TTTCCCCAGCC TATTCTGGCT CACAGTCACT CAGAGGCCAGT CAGAGGCCAGT CAGAGGCAT CAGAGTCACT CA	Cession #: 1 LTLAALGASG ACGMQQSVRT CNAMPCFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDDIDGDRI DSDQDQDGDG GQEDADRDGV VVVLNGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio Usence: 71 1 GGAAGGCAGC ATGGCTTCCC GGAGTATTCA CACTCAGG CTGACTCAGG GCTAACCTTG GCACTCAGG GCTAACCTTG GCACTCAGG GTGACTCCTG GCAGTCCAGG GTGACCTTG GCAGTCCAGG GTGACCTCTG GCAGTCCAGG TGGGCATCCCG CTGAACCTCTG GCAGCTCAGG TGGGCATCCCG CTGAACTCCTG ACAGAATCCGG TACAGAATCCGG TACAG	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PMSDQEDSD DKVVDKIDVC AVGTTAFNGV AEPGIQLKAV QVGYIRVFFY THQLRQA 62.6 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAGCTT CTACAAATGT TGGAGCCTTC GGGAGCCAAC CCATGAAGGTT TGGAAATGT TGGAAGT TGGAAATGT TGGAAGT TGG	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPGCRKD EDKWGDACDN DGIGDACDNC HDGGGDACDD PENAEVTLTD DFBETFHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC ACCCAGATAC AGCATAATTA ATTTCAGGGA GATGGATGCC TGGCTGAGG CCCCGATGGT TTTCTCGGAG GTGTCTGTGC ATTGCCAAAG CTACAGTGC GCACTTCCG	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSCQ CRSQKNDDQK PQKSNPDQAD DDNDQVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AAGGTGTTTT ATGAATGTT CTTTGAGGC AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTACAATGT CAACAGGGGAA CTCTACAATGT CAACAGGGGAA CTCTCAGACC TCTACAATGT CAACAGGGGAA CTCTCAGCCC	120 180 240 360 480 540 660 720 60 180 240 420 420 420 420 420 420 420 420 42
50 55 60 65 70	Protein Act MVPDTACVLL FILINTYMECI MVPDTACVLL FILINTYMECI INECETGQHIN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq In Coding seq Coding seq Coding seq CAGGTCACCA CAGGTCAC	LILLAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVMKKQMEQT PRNVGWKDK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGG GGAGGATTGA CAGGATTGA CAGGATTGA GCAGCTCAGG GCTAACCTTG GCAGCTCAGG GCTAACCTTG GCAGCTCAGG TGGGCATCCG CTGAACTCTG ACAGCATCG CAGGATTCG CAGGATTCG CAGGATTCG CAGACTACG CTGAACTCTG CACACTACG CTGAACTCTG CACACTACG CTGAACTCTG CACACTACG CTGAACTCTG CTACACTTG CTACACTTCG CTGGGCTCCTG CTGGGCTCCTG CTGGGCTCCTG CTGAACTCTG CTAAACTACT CTAAACTACT CTGAACTACT CTGACTACT CTGAACTACT CTGAACTACT CTGAACTACT CTGACT CTGAACTACT CTGACT CTGC CTGC	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDFGL YWQAMPFRAV SYRWFLQHRP CNDTIPEDYE 1 GGCAGCTCCA GGCAGCATCAT CACTCATCAT CACTCATCAT AAGAAGCAA TTGCTGATCAT ATGCTGGCACA ATTGCTGATCAT AGAACCAA ATGCTGGCAC AGAATGTGAC AGGATGTACAA AGACTTGCG AGAATGTGAC AGGATGTACAC AGGTCACAC AGGATGTACAC AGGATGTACA	GPOMLRELQE GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG PGFVGDQASG DLDGFPDEKL VRNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV GVGYTAFNGV THQLRQA 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGGAG CGTGATACAA AGATGAGGTG AGTGATAGCTT GGGAGCCATC GTGTGAGGCTT GTGTGAGGCTT GTGTGAGGCTT TGGAGGCTT TGGAGGCTT TGGAGGCTT TGGAGGCTT TGGAGGCT CCATGAAGGTT TGAAAATGAC GCGGAGTCAA CCATCAGCTGG CACAAAAAAA	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECKEGGRACACH EDKWGDACDN DGIGDACDN DGIGDACDN DGIGDACND ECKEGGRACACH ECKEGGRACACH HDGQGDACD DFEATAVILTD DFEGTPHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GAGCAGGGGCAGGGCCCCGATGGT TATATCATCA AGCATGCCGG CCCCGATGGT TTCTCGGAAG GGTGTCTGGC ATTGCCAAAG CTTACAGCTGC CGCACTTCTGC GCACTTCTGC CATGCAAAGT	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT TGAGCTGCAC AGGTGTTTT CTTTGCGGCT TCTCAAAGG TCTCCAATAC TCTACAATGT TCACACGGGA TCAACAGGGGA TAAACTCAAT CAACAGGGGA TAAACTCAATAC CTCTCAGCCC CATTGTTACA	120 180 240 360 420 540 600 720 60 120 180 240 300 420 420 420 480 540 660 720 840 900
50 55 60 65 70	Protein Act MVPDTACVLL FLENTYMECI MVPDTACVLL FLENTYMECI INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP FGYQDSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq In Cod	LILLAALGASG ACGMOQSVRT CMARPEFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVINGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGC CATGAGTTCAC GACATCACAG CATGAGTTCAC CAT	NP_000086.1 21	GPOMLRELQE GPOMLRELQE CAPGPCFPGV CEACPPGYSG PGFVGDQASG DLDGFPDEKL VNNPDQRNTD PNSDQKDSDG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEFGIQLKAV QVGYIRVFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG CGTGATACAA AGATGAGCTG AGTGATACAT CTACAAATGT CTACAAATGT CTGGGTGAGGCCTG GGGGGCCAAC GGGAGCCAAC CATGAGGCTG GGGAGTCAC GGGGGGCCAAC CATGAGGCTG GGGGGCCAAC CATGAGGCTG GGGGGCCAAC CATGAGGCTCAC GGGGGCCAAC CATCAGCTGC CACAAAAAAC GCGAAAAAAAC GATATGACCTC	TNAALQDVRD ACIOTESGGR PTHQGVGLAF CQRGAQRFCP ECKEDENGGDACDN DGIGDACDN DGIGDACDN DETGAEVILID DPEGTPHVNT KSSTGPGEQL EGPELVADSN 41 ACCCAGATAC AGCATAATA AGTTCAGGA GGCAATGCC TATATCATCA AGCATGACCC TATATCATCA CCCCAGATGC TTCTCGGAAGG CCCCCGATGGT TTCTCGGAAGG CCCCCAATGGT ATTCACCAAGC CATGCCAAAGT AGCATTATTA	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTCAATGT CAACAGGGGA TAAACTCAAA CTCTCAGCCC CATTGTTACA	120 180 300 360 420 480 540 660 720 60 120 180 360 420 480 540 660 720 780 840 900 900 900
50 55 60 65 70	Protein Act MVPDTACVLL FLENTYMECD NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVVNP FGYQDSSFY ESQVELLWKD RLGVFCFSQE Seq ID NO: Nucleic Act Coding seq I GAGTCACCAA TTCCCCAGCC TATTCTGGCT CACAGTCACT TTTTGAACCT AGGCTTGGTC CAGGGGGAAA CCTG GAAAAACCTG CAGGTTTGAG CTACGATTACAAGTACTACAAGGATCAAAAGTACAAGGATTCAAATGAATTACAAGGATTCAAATGAATTACAAAGGAATTACAAATTACAAAGGAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAAGTACTATACAATTACAATTACAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAGGAATTAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAGGAATTAAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAATTACAATTACAAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAATTACAAAAAA	Cession #: 1 LTLAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPDADGDG GODDIDGDRI DSDQDQDGDG GOEDADRDGV VVVINGGREI VVMWKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq 1d Accessio Uenice: 71 11 GGAAGGCAGC ATGGCTTCCC GGAGCAATTCC GACATCAAC CATGAGTCAA CAGCAGTGT CAACTCACGG TGACACTCTG GCAGCTCAG TGACACTCTG CACAGAATCAG TGGGATCCAG TGACACTCTG ACAGAATCAG TGACACTCTG ACAGAATCAG TGACACTCTG ACAGAATCAG TGTGACTCTG ACAGAATCAG TGTGACTCTG ACAGAATCAG TGTGTCTTG ACAGAATCAG TGTGTCTCTTG ACAGAACTCAT ACAGAAC	NP_000086.1 21 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE LENCE 1 GGCAGCTCCA CAGCTGGGAA TTTCTGATAT AAGAAGGCAA TTGCTGGTAC AGTATAAAAC AGACTTGGCAC AGTATAATAC AGACTTGCAC AGTATAAAAC CCTTCTTTGC CCTTTTGCC CTTCACCAC CTTCACCAC CTTCACCACCAC CTTCACCACCACCACCACCACCACCACCACCACCACCACC	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPPGYSG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PGFVGDQASG PNESDQEDSD	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP RCPEPGCRKD EDKWGDACDN DGIGDACDNC HDGGGDACDD PENAEVTLTD DFBETFHVNT KSSTGFGGQL EGFELVADSN 41 ACCCAGATAC ACCCAGATAC AGCATAATTA ATTTCAGGGA GGCATGGT TTTCTCGGAG GCCCCGATGGT TTTCTCGGAG GTGTCTGGG CTACAGCTGC AGCATGAT TTCTCAGAG GTGTCTGTGC ATTGCCAAAG CTACAGATGC CCATGCTT AGTTTTATAT AGCAAGAAAAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHER NCVTVPNSCQ CRSQKNDDQK PQKSNPDQAD DDNDQVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT ATGAATGTT CTTTGAGGCT CTCTCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC TCTCCAATGC CAACAGGGGAA CTCTCAGCCC CATTGTTACAA TTAACTGCAA TTCTCAGCCC CATTGTTACA TTAGGGGGG AAAAAGAAGC	120 180 240 360 420 480 540 660 720 180 240 420 420 420 420 780 840 960 960 1020 1080
50 55 60 65 70 75	Protein Act MVPDTACVLL FILINTYMECI NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq I GAGTCACCAA TTCCCCASCC CACAGTCACT TTTGAACCT CACAGTGGTC CAGAGGCCGG GAAAAACCTGC CAGAGGCTATAAT CACAGTGTC CAGAGGTCACA TATCAAAGTC TATCAAAGTC TATCCTGATC ACAGGGATC ACAGGGATC ACAGGGATC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAACAATCAACTC CAAAAACCAACTC CAAAAAACAATCAACTC CAAAAAACAATCAACTC CAAAAACCAACTC CAAAAACCAACTC CAAAAACCAACTC CAA	Cession #: 1 LILAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPADAGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVWHKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGG ACTGCAGG ACTGCAGG CATGAGTTCA CAGGAATCAG GGCAGCTCAGG GCTACACCT GCAGGTTCA CAGGACTCAGG GCTACACCT CTGAACTCACAG CTGAACTCAGG TGTGTCTCTT CTAAAATAAT ACAGAACTAT ACAGAACTAT ACAGAACTAT CTAAAATAAT ACAGAACTAT ACAGAACTAT ACAGAACTAT ACAGAACTAT ACAGAACTATAGAA AGGCTCCAAT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE 1 GGCAGCTCCA 1 GGCAGCTCCA 1 TGGGGAA 1 TTCTGATCA 1 AGGACGACA 2 AGGTTGACCA 3 AGGTTGACCA 4 AGATTGACCA 5 AGGTTGACCA 5 AGGTTGACCA 6 CCTGTATGAC 6 CGTGCTGGGC 7 TTCACCACCE 7 GTGCCTCGGC 7 TTCACCACCC 7 GTGCCTCGGC 8 ATGACAAGG	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG FGFVGDQASG FGFVGDQASG PGFVGDQASG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVFFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAGC TGGATACAA AGATGATCTT CTACAAATGT TGGAGCCAGT CATGAAAGGTT TGAAAATGAC CATGAAAGGTT TGAAAATGAC CATCAGCTGG CATGACGCTGC CATGAGCTGC CATGACGCTGC CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGC CACCAGCTGG CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCACACCTGC CACCACACCTGC CACCACACCTGC CACCACCTGC CACCACACCTGC CACCACACCTGC CACCACCTGC CACCACCTCC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCT CACCACC CACCACC CACCACC CACCACC CACCACC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECPEPQCRKD EDKWGDACDN DGIGDACDNC EDKWGDACDN DEIGDACDNC FERAEVTLTD DFECTFHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGAGTGGAGCAGG TCGGAGCAGG CCCCGATGGT TTTCTCGGAAG CTTCTCGGAAG CTTCTACAGCTGC GGACTTCTGC CATGCTAAAGAAAC TTCAAAGAAAC TTCAAAGAAAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCUTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNDGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT ATGAAATGTT CTTTCAATGC ACCATCAATGT CAACAGGGGA TAAACTCAAT CTCTCAAATGT CAACAGGGGA TATTGAAGG TCTTCAGCC CATTGTTACA TCTTGGGCT CTTTCAGCC CATTGTTACA TTCTGGGAGG AAAAAAGAGC TATTTGAGGC TATTTGAGGC TATTTGAGGC TTCTTGGGCT CAATGT CAACAGGGGA TATTAGAAGG TATTAGAAGG	120 180 240 360 420 540 660 720 60 120 180 240 300 420 420 420 420 420 420 420 420 420 600 600 600 720 720
50 55 60 65 70	Protein Act MVPDTACVLL FILINTYMECI NGSHCTDVNE INECETGQHN ADCVLERDGS EDVDRDGIGD DTDQDGRGDA VDHDFVGDAC RDNCRLVPNP PEGDAQIDPN FGYQDSSSFY ESQVRLLWKD RLGVFCFSQE Seq ID NO: Nucleic Ac Coding seq I GAGTCACCAA TTCCCCASCC CACAGTCACT TTTGAACCT CACAGTGGTC CAGAGGCCGG GAAAAACCTGC CAGAGGCTATAAT CACAGTGTC CAGAGGTCACA TATCAAAGTC TATCAAAGTC TATCCTGATC ACAGGGATC ACAGGGATC ACAGGGATC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAGCAGATCAACTC CAAAAAACAATCAACTC CAAAAACCAACTC CAAAAAACAATCAACTC CAAAAAACAATCAACTC CAAAAACCAACTC CAAAAACCAACTC CAAAAACCAACTC CAA	Cession #: 1 LILAALGASG ACGMOQSVRT CNAMPGFPRV CVPNSVCINT RSCVCRVGWA ACDPADAGDG CDDDIDGDRI DSDQDQDGDG GQEDADRDGV WVVLNGGREI VVWHKQMEQT PRNVGWKDKK NIIWANLRYR 71 DNA seq id Accessio uence: 71 11 GGAAGGCAGG ACTGCAGG ACTGCAGG CATGAGTTCA CAGGAATCAG GGCAGCTCAGG GCTACACCT GCAGGTTCA CAGGACTCAGG GCTACACCT CTGAACTCACAG CTGAACTCAGG TGTGTCTCTT CTAAAATAAT ACAGAACTAT ACAGAACTAT ACAGAACTAT CTAAAATAAT ACAGAACTAT ACAGAACTAT ACAGAACTAT ACAGAACTAT ACAGAACTATAGAA AGGCTCCAAT	NP_000086.1 21 QGQSPLGSDL GLPSVRPLLH RCINTSPGFR RGSFQCGPCQ GNGILCGRDT VPNEKDNCPL RNQADNCPRV HQDSRDNCPT GDVCQDDFDA VQTMNSDPGL YWQANPFRAV SYRWFLQHRP CNDTIPEDYE 1 GGCAGCTCCA 1 GGCAGCTCCA 1 TGGGGAA 1 TTCTGATCA 1 AGGACGACA 2 AGGTTGACCA 3 AGGTTGACCA 4 AGATTGACCA 5 AGGTTGACCA 5 AGGTTGACCA 6 CCTGTATGAC 6 CGTGCTGGGC 7 TTCACCACCE 7 GTGCCTCGGC 7 TTCACCACCC 7 GTGCCTCGGC 8 ATGACAAGG	GPOMLRELQE GPOMLRELQE CAPGFCFPGV CEACPFGYSG FGFVGDQASG FGFVGDQASG PGFVGDQASG VPNSAQEDSD DKVVDKIDVC AVGYTAFNGV AEPGIQLKAV QVGYIRVFFY THQLRQA 626 31 CTCAGCCAGT CCTCTTCTGG TGGCTTTGGT CATTGGGAGC TGGATACAA AGATGATCTT CTACAAATGT TGGAGCCAGT CATGAAAGGTT TGAAAATGAC CATGAAAGGTT TGAAAATGAC CATCAGCTGG CATGACGCTGC CATGAGCTGC CATGACGCTGC CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGG CATCAGCTGC CACCAGCTGG CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCAGCTGC CACCACACCTGC CACCACACCTGC CACCACACCTGC CACCACCTGC CACCACACCTGC CACCACACCTGC CACCACCTGC CACCACCTCC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCTC CACCACCT CACCACC CACCACC CACCACC CACCACC CACCACC	TNAALQDVRD ACIQTESGGR PTHQGVGLAF CQRGAQRFCP ECPEPQCRKD EDKWGDACDN DGIGDACDNC EDKWGDACDN DEIGDACDNC FERAEVTLTD DFECTFHVNT KSSTGFGEQL EGFELVADSN 41 ACCCAGATAC AGCATAATTA ATTTCAGGGA GGAGTGGAGCAGG TCGGAGCAGG CCCCGATGGT TTTCTCGGAAG CTTCTCGGAAG CTTCTACAGCTGC GGACTTCTGC CATGCTAAAGAAAC TTCAAAGAAAC TTCAAAGAAAC	WLRQQVREIT CGPCPAGFTG AKANKQVCTD DGSPSECHEH NCVTVPNSGQ CRSQKNDDQK PQKSNPDQAD DDDNGVPDS FRAFQTVVLD VTDDDYAGFI RNALWHTGDT VVLDTTMRGG 51 GCTGGGAACC GCATCATCAT GACACTCCAT TGAGCTGCAC AAGGTGTTTT CTTTGCGGCT CTTCTAAAGG AAGTGAATGT TCCCCCAGCC TCTCCAATAC TCTCAATGT CAACAGGGGA TAAACTCAAA CTCTCAGCCC CATTGTTACA	120 180 240 360 420 480 540 660 720 180 240 420 420 420 420 780 840 960 960 1020 1080

5	CATTGGCAAA TATCGGGCAC CTGATGGGAT CAAGCCAAGT TAGATCTCCA TGAAGCACAC AATGAAGCTT GTTAACCACT	GGGCCTGGAA TAAGCATTCT CAGGATAACA TATCTTCAGC TCTGTAAGAG GACCCTGCCT ACAGACTTTT TGAAGGAAAA GCCTTCCTGG TAGAGTTCTG A	GTCTCTTGG TCTCTCAGTG TTGTTGAGCT AAATGCCTGA GGCCACAATT GAAAGCAAGG GAATACTTTG ACCTTGGAGC	CTGCTGCCTC AACAGAGTTG TCTAAGTTTC GTTCTAGCTC CAAATTAAGG ACAATGACTG TTTCCAGCCC CACGGTGACT	AGCACAGAGA ACAAGGCCTA TTTCCCTTCA AGGTTTTCTT CAACAAACAT CTTGAATTGA CCTTCCCACA GTATTACATG	GCCAGAACTC TGGGAAATGC TTCTACCCTG ACTCTGAAT ATACCTTCA GGCCTTGAGG CTCTTCATGT TTGTTATAGA	1260 1320 1380 1440 1500 1560 1620 1680 1740 1800
15	Protein Acc 1 MASLGQILFW	72 Protein cession #: N 11 SIISIIIILA	IP_078902 21 GAIALIIGPG				60
20	QLTDAGTYKC WASQVDQGAN	WLKEGVLGLV YIITSKGKGN FSEVSNTSFE LQLLNSKASL	ANLEYKTGAF LNSENVTMKV	SMPEVNVDYN VSVLYNVTIN	ASSETLRCEA NTYSCMIEND	PRWFPQPTVV	120 180 240
25	Nucleic Act	73 DNA sequid Accession lence: 143	1 #: XM_0570				
30	1 GGGAGGGAGA CGCGGCGGAG	11 GAGGCGCGCG CCAGACGCTG	21 GGTGAAAGGC ACCACGTTCC	TCTCCTCGGT	CTCCTCCGCC	TCCAGCTCCG	60 120
30	CCGCGGCCTC CCCCAAGGGG AATGTGCTTA	CAGCCGGGAG CTGCTGCTCC AAGCAAAAGG CAAGGGCCAG ACACCTGGGA	TGCTGCTGCA CGCAGCTCCG CAGGAGTGCC	GCTGCCCGCG GCAGAGGGAG TGGTCGAGAC	CCGTCGAGCG GTGGTGGACC GGGAGCCCTG	CCTCTGAGAT TGTATAATGG GGGCCAATGG	180 240 300 360 420
35	TCTGAGGGAA ATTGAATTAT AAATAGTGCT	AGCITTGAGG GGCATAGATC CTAAGAGTTT TGGTATTTCA	AGTCCTGGAC TTGGGAAAAT TGTTCAGTGG	ACCCAACTAC TGCGGAGTGT CTCACTTCGG	AAGCAGTGTT ACATTTACAA CTAAAATGCA	CATGGAGTTC AGATGCGTTC GAAATGCATG	480 540 600 660
40	CACTTCTTCT CTGGGTTGGC TTCTCGCATC TTTTTTTATT	TATTTGGACC GTGGAAGGAC ACTTGTTCAG ATTATTGAAG ATGCCTTGGA	TTTGTGAAGG ATTACCCAAA AACTACCAAA ATGGTTCACT	AATTGGTGCT AGGAGATGCT ATAAATGCTT TAAATGACAT	GGATTAGTGG TCTACTGGAT TAATTTTCAT TTTAAATAAG	ATGTTGCTAT GGAATTCAGT TTGCTACCTC TTTATGTATA	720 780 840 900 960
45	TTTAAATCTA TGGTTAGAAT GGTCTTTTGT TGTACAATTT	AAAAGCAAAG GCATTATTCA ACTTTCTTCA TTTTTCTCTT GTAAATGTTA	TTTTGCTTCA TAGTCACATT AGTATAGCAT AGAATTTTT	ATCAAAAGTG CTCTCAACCT TTTTAAAAAA	GTTTCAATAT ATAATTTGGA ATATAAAAGC	TTTTTTTAGT ATATTGTTGT TACCAATCTT	1020 1080 1140 1200 1260
50	CAACCTTAAA	ааааааааа	AAAA				
30		74 Protein cession #: 2		31	41	51	
55	 MRPQGPAASP GVPGRDGSPG GKIAECTFTK GSPEMNSTIN	QRLRGLLLLL ANGIPGTPGI MRSNSALRVL IHRTSSVEGL	PGRDGFKGEK FSGSLRLKCR	GECLRESFEE NACCORWYFT	SWTPNYKQCS FNGAECSGPL	WSSLNYGIDL PIEAIIYLDQ	60 120 180 240
60	LPK						
	Núcleic Ac	75 DNA seq id Accession uence: 248.	n #: BC0104	23			
65	1	11	21	31	41	51	
03	AGCTACGGCT CAAGTGCGAG	GGGTGTGTAG AGGCAAGAAC	AACGGGGCCG TCTGCAGCTT	GGGCTGGGGC	TGGGTCCCCT GGGTCAGTTC	TCTTGGGGGT AGTGGAGACC CTTATTCAAG	60 120 180
70	TTCAACCATG GCTGCTACTG CGTGGTAACT CGGCGAGCAA	CCCCTGTCCC CTGGCATCAT GTGGTGCTGG GTGGGGCAAG	TGGGAGCCGA TTACAGGCCG GCCAGGACGC TGGCATGGGC	GATGTGGGGG GTGCCCGCG AAAACTGCCC TCGGGTGGAC	CCTGAGGCCT GGTGAGCTGG TGCTTCTACC GCGGGCGAAG	CAGTCTGCCT GGCTGCTGCT AGACCTCAGA GAGGGGACTC GCGCCCAGGA	300 360 420 480
75	GGAGCAGCCG GCAGGCGGAT GGCGCGGCTG ACTAGAAGAG	CCGCCCCAC GAGGGCGAGT CGGCTCCGAG GGCCAGGGCC	GCAACCCCCT ACGAGTGCCG TGCTGGTGCC TGACCCTGGC	GGACGGCTCA GGTCAGCACC TCCCCTGCCC AGCCTCCTGC	GTGCTCCTGC TTCCCCGCCG TCACTGAATC ACAGCTGAGG	AGGGCCGCGT GCAACGCAGT GCAGCTTCCA CTGGTCCAGC GCAGCCCAGC	600 660 720 780
80	CTCCCGCTCT GCAGCCACTG CATCCTCCAC GTGGCACATT	GCTGCCGTCA ACTTGTGTGG GTGTCCTTCC GGCAGAGAAG	CCTCAGAGTT TGTCCCATCC TTGCTGAGGC GAGCTATGCT	CCACTTGGTG TGGCCTGCTC CTCTGTGAGG CAAGTGCCTG	CCTAGCCGCA CAGGACCAAA GGCCTTGAAG AGTGAAGGGC	CCTTCAAGCA GCATGAATGG GGATCACCCA ACCAAAATCT AGCCCCCTCC	900 960 1020 1080
85						TGGATGGGGA GCCATGTCAG	1140 1200

					GTTCTTGACC		1260
					GTGGTGGGTG		1320
					TCCCGATACC		1380
_	GGCCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAGGG	AGAACTCCAT	1440
5	CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
	GAGAGCCGAG	GGCCACCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
					AGGGAGATAG		1620
					GAAGATCAGG		1680
					CTACGGGCCA		1740
10					CCCAGGCCTG		1800
10							1860
					CATCTTGGGG		
					ACTGCTTGAC		1920
					CTCCCACCAT		1980
					ACTGTGTGTG		2040
15					TATGCTGTCA		2100
	AAGTGAACTG	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACTGTCAGG	2160
					TGAAAAAGCA		2220
					GAGAGGTGGA		2280
					CTCCGGTGTG		2340
20							
20	TCTCCTACCA	CTTCGGAGCC	ATGGGGGCAA	GIGIGAAGCA	GCCAGTCCCT	GGGTCAGCCA	2400
	GAGGCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
	ACATATTTTC	TGTAAATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
	ACTTTTAATT	TTTTTCTTTT	TTTTTTCTTG	CCCTTTCCAT	TAGTTGTATT	TATTATTAT	2580
	TTTTATTTTT	ATTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCCTGT	2640
25		ACCAAAACCC					
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	Sea ID NO.	76 Protein	semience				
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				7.1	41	51	
20	i	11	21	31	47	21	
30	1		1	1	<u> </u>	1	
					TVVLGQDAKL		60
					PPPPRNPLDG		120
	DEGEYECRVS	TFPAGSFOAR	LRLRVLVPPL	PSLNPGPALE	EGQGLTLAAS	CTAEGSPAPS	180
	VTWDTEVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGOP	LTCVVSHPGL	LODORITHIL	240
35					NWTRLDGPLP		300
33					KQVDLVSASV		360
							420
					LHSHHTDPRS		
					LSPGSGRAEE	EEDQDEGIKQ	480
40	AMNHFVQENG	TLRAKPTGNG	IYINGRGHLV				
40							
	Sea ID NO:	77 DNA sequ	ience				
		id Accession		474.2			
	Coding sem	ience: 37	3036				
		uence: 37			41	51.	
45	Coding sequ	uence: 37	3036	31	41 1	51	
45	1	11 	21 	31 	1	1	60
45	1 CACTAACGCT	11 CTTCCTAGTC	21 CCCGGGCCAA	31 CTCGGACAGT	 TTGCTCATTT	 ATTGCAACGG	60
45	1 CACTAACGCT TCAAGGCTGG	11 CTTCCTAGTC CTTGTGCCAG	21 CCCGGGCCAA AACGGCGCGC	31 CTCGGACAGT GCGCGACGCA	 TTGCTCATTT CGCACACACA	 ATTGCAACGG CGGGGGAAA	120
45	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC	TTGCTCATTT CGCACACACA GCGGGCCGTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT	120 180
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC	31 CTCGGACAGT GCGCGACGCA CAGCGGCGGC CTCCGGTCGC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC	120 180 240
45 50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC	31 CTCGGACAGT GCGCGACGGA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG	120 180 240 300
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG	11 CTTCCTAGTC CTTGTCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG	31 CTCGGACAGT GCGCGACGGA CAGCGGCGGC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG	120 180 240 300 360
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG GCCGGTGCTC	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTGGCGAGG GATGGTGCAG CAGCGCGCCC TGCTCGCGCCC	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG	31 CTCGGACAGT GCGCACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGA TCCCCGCCC CGAGGGGTGA	TTGCTCATTT CGCACACACA GCGGCCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA	120 180 240 300
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG GCCGGTGCTC	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTGGCGAGG GATGGTGCAG CAGCGCGCCC TGCTCGCGCCC	21 CCCGGGCCAA AACGGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG	31 CTCGGACAGT GCGCACGCA CAGCGGCGGC CTCCGGTCGC CGGGCCCGA TCCCCGCCC CGAGGGGTGA	TTGCTCATTT CGCACACACA GCGGCCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA	120 180 240 300 360
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGACGATGG GCCGCGTGG GCCACGGTGCTC GCTGATGAAG	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCCGCCC TGCTCAGTGC	21 CCCGGGCCAA AACGGCGGGC TAGAAGAGCT CAGGAAATCC CGCTGCCGGC GCTGCCCGGC CTGCCGAGGCC	31 CTCGGACAGT GCGCGACGCA CAGCGCCGAG CTCCGGTCGC CGAGGGTGG CGAGGGTGA AGTGGGGACC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAGC	120 180 240 300 360 420
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGGTGG GCGACGATGG GCGGTGCTC GCTGATGAAG TTCGACTCCA	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTCGCCGAG GATGGTGCAG CAGCGCGCCC TGCTCAGGCC TTGTCAGTGC AGAATCATCC	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATC CGCTGGCGG GCTGCCGTG CTCGCTGGGAGGCC CTCTGTTCGG AGAAGTGCTG	31 CTCGGACAGT GCGCGACGCA CAGCGCGCGC CGGGCCCGAG TCCCCCGCC CGAGGGGTGA AGTGGGACC AATATTCGAC	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGA TCTGGATCCC TACAACGGA	ATTGCAACGG ATTGCAACGG CGGGGGAAC CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGGACA AATGAAGAACA AAGCAAAGAA	120 180 240 300 360 420 480 540
	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCCGGTGG GCGCTGATGG GCTGATGAAG TTCGACTCCA TTCGACTCA	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCGCGCC TGCTCAGTGC ATGTCAGTGC ATCTGGAAAG	21 CCCGGGCCAA AACGGCGGC TAGAAGTATCC CGCTCGCCGTG GCTGCCGGTG CTGCGAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT	31 CTCGGACAGT GCGCGACGCA CAGCCGCGGC CCGGCCCCAG TCCCCGCCC CGAGGGGTGA AGTGGGGACC AATATTCGCA	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTTCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCC GCTCGCCCTG CGAAGGAAGA AGTGAAGAAGA AGCAAAGAA GGAAACCCAC	120 180 240 300 360 420 480 540
50	1 CACTAACGCT TCAAGGCTGG CTITTITIAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCTGATGAAG TTCGACTCCA CTGATCATAA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCAGG GATGGTGCAG TGCTCAGTGC AGCATCAGTCA ATCTGGAAG ACGGTACTGA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGG CTGCCGGT CTGCGAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC	31 CTCGGACAGT GCGCGACGCA CAGCGCGGGC CTCCGGTCGC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCAC GCTCGAAATT	TTGCTCATTT CGCACACACA GCGGCCCTGG AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT	ATTGCAACGG CGGGGGGAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAAGA AGTGAAGAACCA CTCTGGGTCAC	120 180 240 300 360 420 480 540 600 660
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG GCGATGATGATG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGTG CTCTGTTCGG AGAACTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT	31 CTCGGACAGT GCGCGACGCA CAGCGCCGCC CTCCGGTCGC CGGGCCCGAG TCCCCCGCCC CAATATTCGAC CTCATTGCCA ACTCGAAACT TCTCGAATCAG	TTGCTCATTT CGCACACAC GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG CGAAGGAAGA AGTGAAGGAC AAGCAAAGA CGAAACCCAC TCTGGGTCAC CAGCACGTCT	120 180 240 300 360 420 480 540 600 660 720
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGGTGGT GCGACGATGG GCGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTCA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT GGGGACTTAT	21 CCCGGGCCAA AACGCGGGC TAGAAGAGCT CAGGAAATC CGCTGGCGG GCTGCCGTG CTGCTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA	31 CTCGGACAGT GCGCGACGCA CAGCCGGGCCCGAG TCCCCGCCC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCCA GCTCGAAATT TCTGATTCGA AATGAAAGCT	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCTTATGGAA TCTGGATCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCAT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGACA AGTGAAGACA TCTGGGTCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA	120 180 240 300 360 420 480 540 660 720 780
50 55	1 CACTAACGCT TCAAGGCTGG CTITTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCTGATGAAG TTGACTCAA TATCTGCAAG TGTTACTACC TCTGGTTCTCA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATCC CGCTCGCCGC GCTGCCGGG CTCGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGATAT TGTGTTTCCCAA	31 CTCGGACAGT GCGCGACGGC CAGCGCCCCCCCCCCCC	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCCGGC AGCTGCTACA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCAGTTTACAC ACACGGTAAT CAGTCAGTCA ACACGGTAAT CAGTCAGTCA ATGTCATAGA TGAAAAGCGT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGAGA AGTGAAGAAGA AGGAAAGA AGGAAAGCCAC TCTGGGTCAC CAGCACGTGT CCAATGAAA CCGGGGATCA	120 180 240 300 360 420 480 540 660 720 780 840
50	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCGCGTGGG GCGACCATGG GCTGATCAAA TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACA TCTGGTCTCA AGTGCAACCA TGTGGATCACA TGTGGATCACA TGTGGATCACA TGTGGATCACA TGTGGATCACA TGTGGATCACA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA	21 CCCGGGCCAA AACGCCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGC CTCTGTTCGG AGAACTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCCA	31 CTCGGACAGT GCGCGACGCA CAGCGCCGCCC CGGGCCCGACG AGTATTCGAC CTCATTGCC AATATTCAAC ATGAATAT TCTGATTCAG AATGAAAGCG GCTCGAAAGAG GCTCGAAAGG GCTCGAAAGG	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCATGCC ATGTCATGCC ATGTCTTAGA TGAAAAGGGT ATGTCTTAGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG CGAAGGAAGA AGTGAAGAAC AAGCAAAGAA GGAAACCCAC CTCTGGGTCAC CAGCACGTGT ACCAATGAAA ACCGACCTCT	120 180 240 300 420 480 540 600 720 780 840 900
50 55	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGG GCCGGTGGG GCGACGATGG GCCGGTGCTC GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA CTGGACACCA CCAGACATGGG	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTGCCGGG GCTGCCGTG CTGCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCAA ACCAAACCTC	31 CTCGGACAGT GCGCGACGCA CAGCCGGCCCGAG TCCCGGCCCAA AGTGGGGACAT ACTCTCATTGAC GCTCATATT TCTGATTCAG GCTGAAAAGCT GCGAAGAAGCA GCTCAAAGGCAGAGAAGCA ACCCTCAAGGCAAAGCA ACCCTCAAGGCAAAGCA ACCCTCAAGGCAAGAAGCAAGCAAGAAGCAAGAAGCAAGAAGCAAGAAG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA ATGTCTTAGA TGTGATTCC CAACTAAGTA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGC AAGTGAAGAGC TCTGGGTCAC TCTGGGTCAC ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGAGCCT	120 180 240 300 420 480 540 660 720 780 840 900 960
50 55	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCTGG GCGACCATGG GCCGACTGAAA TTCGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA TGTGGATCAC GGACATGG GTGATCGTGG	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ACTCGAAAG ACGGTACTGA ATGGACATAT ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACAC CAGACAACAC	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATC CGCTCGCCGC GCTGCCGGC CTCTGTTCGG AGAACTGCTG TAGTCTCCCTC ACGGGATAT TGTCTTCCCAACCAACCTC TAAAAGAGT TAAACAAACTC TAAAACAGT	31 CTCGGACAGT GCGCGCGCG CTCCGGTCGC CGGGCCCGAG TCCCCGCC CGAGGGGTGA AGTGGGACC AATATTCGA GCTCGAAATT TCTGATTCAG GCTGAAAGA ACCCTCAAGG ACCCTCAAGG ACCCTAAGG ACCCTAAGG ACCCTAAGG ACCCTAAGG ACCCTAAGG ACGCAAGGAAGAAGA	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTTCAC ACACGGTAAT CAGTCATCT ATGTCTTAGA TGAAAAGCGT ATGTGTTTCC CAACTAAGTA AAGATCTGGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCT CGAAGGAGA AGTGAAGAAG AGCAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAGGTTAAG	120 180 240 300 420 480 540 660 720 780 840 900 1020
50 55	1 CACTAACGCT TCAAGGCTGA CCGAGCTGA GCCGCGTGGG GCGCGCTGCT GCTGATCAAAG TTCGACTCCA CTGATCATAA TATCTCCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA AGTGCAACCA CGGACATGGG GTGATCATGG CAGCATGGG CAGCATTGA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACCG TAGACAATTGC TAGACAATTGC TAGACAATTGC TAGACAATTGC	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGTG AGAAGTGCTG AGAAGTGCTG ACGGGGATAT TGTCTCCCCA ACCGAGGCT TAAAACAGAGA AGAGTTCAG TAAATCACGTT	31 CTCGGACAGT GCGCGACGCA CAGCGCCGCCC CGGGCCCAGG TCCCCCGCCC CAGAGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGG ACCCTCAAGGA ACCCTCAAGGA ACGCAAGGAA AGGCAAGGAA	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGCGT ATGTCTTAGA AAGATCACGTAAT ATGTCTTAGA AAGATCACGTAAT ATGTCTTAGA AAGATCAGCACACT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG CGAAGGAAGA AGTGAAGAAC AAGCAAAGAA CCAACGATC ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAAGTTAAG AAAACTTAAG AAAACTTAAG AAAACTTAAG AAAATTCGG	120 180 240 300 420 480 540 660 720 780 840 900 960
50 55 60	1 CACTAACGCT TCAAGGCTGA CCGAGCTGA GCCGCGTGGG GCGCGCTGCT GCTGATCAAAG TTCGACTCCA CTGATCATAA TATCTCCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA AGTGCAACCA CGGACATGGG GTGATCATGG CAGCATGGG CAGCATTGA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA CAGACAACCG TAGACAATTGC TAGACAATTGC TAGACAATTGC TAGACAATTGC	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGTG AGAAGTGCTG AGAAGTGCTG ACGGGGATAT TGTCTCCCCA ACCGAGGCT TAAAACAGAGA AGAGTTCAG TAAATCACGTT	31 CTCGGACAGT GCGCGACGCA CAGCGCCGCCC CGGGCCCAGG TCCCCCGCCC CAGAGTATTCGAC CTCATTGCA GCTCGAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGG ACCCTCAAGGA ACCCTCAAGGA ACGCAAGGAA AGGCAAGGAA	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGAAAAGCGT ATGTCTTAGA AAGATCACGTAAT ATGTCTTAGA AAGATCACGTAAT ATGTCTTAGA AAGATCAGCACACT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG CGAAGGAAGA AGTGAAGAAC AAGCAAAGAA CCAACGATC ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAAGTTAAG AAAACTTAAG AAAACTTAAG AAAACTTAAG AAAATTCGG	120 180 240 300 420 480 540 660 720 780 840 900 1020
50 55 60	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACGATGG GCGACGATGCATCATAA TATCTGCAAC TCTGGTCATCA TGTGTACTACC CTGGTCACA AGTGCAACCA AGTGCAACCA CGACAATGGG GTGATCATCA AGTGCAACCA AGTGCAACCA AGTGCAACCA AGTGCATCAC CAGACATGGG GTGATCCTGA ATCCTGTTGG	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGAACATTAT ACAGATACAA CCAAGAAGGCA CAAGAAGGCA TAGAAATTGC TAGGCATTGGA	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCGGC GCTGCCGTG CTGCTTGGAAGGCC AGAATGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCAC TAAAAGAGAG AGAGTTTCAG TAAAAGAGAG TAATCACGTT AGTGTGAAATCACGTT AGTGTGGAAAT	31 CTCGGACAGT GCGCGACGGC CAGGGCCCGAG TCCCCGCCC CGAGGGCTGA AGTGGGGACC ATATTGGAC CTCATTGCA GCTCGATATA ATGATCGA ATGATAGA ACCTCAAAGA ACCTCAAGG AGCAAGAAGA ACCTCAAGG AGCAAGAAGAAGAAGAAGAAGAAGAAGAAAGATTTT GACATGGACAAGAACACA	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTTCAC ACACGGTAAT CAGTCATCT ATGTCTTAGA TGAAAAGCGT ATGTGTTTCC CAACTAAGTA AAGATCTGGA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAGAGA CAGCAACGAACCCAC TCTGGGTCCA ACCACCCTCT ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGAGCTG AAAAGTTAAG AAAAGTTAAG AAAACTTCAGAAA	120 180 240 300 360 420 480 660 720 840 900 900 900 1020
50 55	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCTGG GCGACCATGG GCTGATCAAA TTCGACTCCA TGTTACTACC TCTGGTCTAC TGTTGCACC TCTGGTCTAC TGTGGACCAC TGTGGACCAC TGTGCAACCA TGTGCAACCA TGTGCAACCA TGTGCATCAC TCTGGTCTCG CAGCATTGG CTGTCTTGG CAGCCATTGA ATCCTGTTGG CCATTCACCA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ACTGCAAAG ACGGTACTGA ATGGACATGT ACAGATACAAC CAAGAAGGCA CAGACAACAC CAGACACCG TAGGCATTGT ACAGAACGC TAGGACATGC TAGACATGCA ACGCCTAGAGAGGCA CAGACACCG TAGGCATTGC TAGGCCTTGA GCCTCCATGA	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATC CGCTCGCCGC GCTGCCGGC CTCGTTCGG AGAACTGCTG AAATGAAGGT TGTCTCCCT ACGGGATAT TGTGTTTAA ACTCTTCCCA ACCAAACCTC TAAAAGAGA TAATCAGTT AGTGTGAAT AGTGTTCAG TAATCAGTT AGTGTGAAT AGTGTGGAAT ATTTCTGGAC	31 CTCGGACAGT GCGCGACGGC CAGCGGCCCGACGGCCCCCCCCCC	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCTCATGCA TCTGGATCCC TACAACGGA GCAGTTTCAC ACACGTAAT CAGTCATTTAGA TGTATAGA TGAAAAGGT ATGTCTTAGA ACACACTAGA ACACACCACT AAGACCACT AAGACCACT TGAAAGCTCT TGAAGCTCT TGAAGCTCT	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CACACCCTCT TCGTGAGCTCA ACCACCACCTCT AAAAGTAAG GAACATTCAG GAACATTCAG GAACATTCAG AACTTCAG AACTTCAG AACTTCAG AACTTCAGAAA	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140
50 55 60	CACTAACGCT TCAAGGCTGA CACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCTGATCAAAG TTCGACTCCA TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGGATCACA CGGACATGGG GTGATCATGA ATGTCGATCACA TGTGGATCAC CAGACATGGG CTGATCATGA ATCGTGTGG CAGCCATTACA TCCCATCACA TCCCATCACA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCAGG GATGTGCAG CAGCGCGCC TTGTCAGTGC ATCTGGAAG ACGGTACTGA ATGGACATGT ACAGAAGACAC CAAGAAGGCA CAGACAACCG TAGGCGTGCT AGGCGTGCA ATGCCAGCACACCG AGGCCTGCA ATGCCAGCACACCG AGGCCTGCA ATGCCCAGCA ATGCCCAGCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGT GCTGCCGTG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACCTTTCCCA ACCAAACCTC TAAAAGAGAG AGAGTTTCAGT AGTGTGAAA ATTTTCAGAC TTTCAGTGAAACTCT TATTCAGGTT AGTGTGAAAACTCT TATTCAGGTT AGTGTGAAAACTCT TATTCAGGAC TGTCAGTGGG	31 CTCGGACAGT GCGCGACGGC GCGCGCGCC CGAGGGGGGACAGCA AGTGGGGACC AGTATTCGAC GCTCGAAATT TCTGATTCAG AATGAAAGC GCTGAAAGA ACCCTCAAGA ACCCTCAAGG ACCCTCAAGG ACCACAAGGAA GCAAGGTTT GACAAGGAAG GACAAGTTTT GACATGAAGA TGGAGAAGAG GTTATTTCCC	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA ACACGGTAAT CAGTCAGTCA TGGATATGCA TGGATATGCA ATGTCTTAGA TGAATAAGCGT ATGTGTTTCC CAACTAAGTA AAGATCTGGA ACAGACCACT AATGCTCTGGA TGAAAGCCACT AATGCTCTCT AAGGCACCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACC AAGCAAGAA GGAAACCCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGGTCAC TCTGGAGCTCT TGTGGAGCTG TAAAGTTAAG GAACATTCGG AAGTCAGGAC ACCTCGCAAA CATCGGCATG	120 180 240 300 420 540 600 660 720 780 840 900 1020 1080 1140 1260
50 55 60	1 CACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGGG GCGACGATGA GCCCGGTGCTCA CTGATCATAA TATCTGCAAC TCTGGTCTAC TCTGGTCTAC AGTGCAACCA CAGACATGGG GTGATCATGA AGTGCAACCA AGTGCAACCA CAGACATGGG CAGCGATTGA CAGCGATTGA CCCATGACCA TCCCATGACCA CCCCATGAC GCCCAATCA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGAACAT CAAGAACAC CAAGAAGGCA CAGACAACCA TAGGCATGGC TAGGCGTGGA GCCTCCATGA ATGCCCATGA ATGCCCATGA TGAGCATGTG	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGTG CTGCAGGCC TGTGTTGGG AGAATGCT AAATGAAGGT TGTCTCCCTC ACGGGGATAT TGTGTTTGAA ACTCTTCCAC TAAAAGAGAG TAATCACGTT AGTGTGGAAT TGTGTTGAA TATTCTGGAC TATTCTGGAC TATTCTGGAC TATTCTGGAC TAGTGGAAT ATTTCTGGAC CCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCGCAGAC CCCCCCCAC CCCCCCCC	31 CTCGGACAGT GCGCGACGCA CAGCCGAC CGGGCCCGAG TCCCCGGCC CGAGGGGCACA AGTGGGGACC AGTATTGGAC CTCATTGCA TCTGATTCA ATCGACACA GCTCAAAGA ACCCTCAAGG ACCCTCAAGG ACCACACACTT GACAAGTT GACAAGTT GACAAGTT GACATGGACA TGGAGAACA TGGAGAACA TGGAGAACA CTTTATTCC CAGTCTCGGGG	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA ACACGGTAAT CAGTCAGTCT ATGTCTTAGA TGTGATTTCCC CAACTAAGTA ACAGACCACT AATGCTCTGT TGAAGCTCT TGAAGCTCT AATGCTCTGGA ACAGACCACT AATGCTCTGGA CGAATTGTCT CAACTAAGTA ACAGCACCACT AATGCTCTGT TGAAGCTCTCT TGAAGCTCTCT CAACGGAACCACT AATGCTCTGT TGAAGCTCCACT CAACTAAGTA CAGACCACT CAACTAAGTA CAGACCACT CAACTAAGTA CAGACCACT CAACTAAGTA CAGACCACT CAACTAAGTA CAGACCACT CAACTACTCTCT CAACGGAACCACC CAATTCTCAT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAGAGA CAGCACGTGT ACCAATGAAA CCGGGGGATCA TCTGGGTCTA TCTGGAGCTG AAAAGTTAAG ACCACCTCT TGTGGAGCTG AAAAGTTAAG CAACGCTCA AAAGTTAAG CAACGCTCA AAAAGTTAAG CAACGCTCA CAACTCAGCAAC ACCTCGCAAA ACCTCGCAAA ACCACCTCG	120 180 240 360 420 540 660 720 780 900 960 1020 1140 1260 1320
50 55 60	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCCGCTGG GCGACCATGG GCTGATGAAG TTCGACTCCA TGTTACTACA TATCTGCAAG TGTTACTACA TGTTACTACA TGTGCAACCA TGTGGATCAC CAGACATGGG GTGATCGAC CAGCATTAA ATCTGTTGG CCATTGAC TCCCATGACA GCCCAATCAC GCCCCAATCA TCCCATGACA GCCCCAATCAC	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTC ACGAATCATCC ACTCGAAAA ACGGTACTGA ACGGTACTGA ACGGACTTAT ACAGATACAA CCAGAGAGCA CAGACAACCG TAGAGATGCA TAGAGATGCA ATGCCCATGA ATGCGCAGCT TGAGACTGCA TTGGAGATGCA TTGGAGATGCA TTGGAGATGCA TTGGAGATGCA TTGGCAGCT TGAGCATGCA TTGGCTGCAGCT	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATC CGCTCGCCGC GCTGCCGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCTC ACCGGGAAACT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGG TAATCAGGT TAGTGTGAA TAGTGTGAA TAGTGTGAA TAGTGGAAT AGTGTGAAT AGTGTGGAAT TGTCAGTGGG CGCGCCAGC CGTGACCCTG	31 CTCGGACAGT GCGCGACGGA CAGCGGCGCCCGACGGA AGTGGGGACAC AATATTCGAC GCTCGAAATT TCTGATTCAG GCTGAAAGA ACCTCAAGG ACCACACAGA ACCACTCAAGG ACCACAGAGA ACCACTCAAGG ACGACAGAAG CGCACAGGAG CGCACAGGAGAGAG CGCACAGGAGAGAG CGCACAGGAGAGAG CGCACAGGAGAGAG CGCACAGGAGAGAGA	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATCATAGAA ATGTCTTAGA ATGTCTTAGA AAGATCTGGA ACACACCACT ATGTCTTGT AATGTCTGT AATGTCTGT AATGTCTGT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGTCTGT TGAAGTCTGT TGAAGTCTGT TGAAGCTCTCT TGAAGCTCTCT TGAAGCTCTCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCT TGAAGCTCCACA	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAAGA AGTGAAGACA AGTGAAGACA AGCAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCTCT TGTGGGCTG AAAGTTAAG GAACATTCAG AACTTCGGCAAA CATCGGCATC TTTCGGAAC TTTCGGATTC TTTCGGATTC TTTCGGATTC TTTCGGATTC	120 180 240 300 480 540 600 780 900 960 1080 1140 1200 1200 1320 1380
50 55 60 65	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA GCCGGGGCGTGG GCGACGATGG GCCGCTGCTCG GCTGATCAAA TTCGACTCAA TGTTACTACC TCTGGTTCTCA AGTGCAACA TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC GCGATTAA ATCGTGTTGC CAGCAATCAG GCCATTCACCA GCCCAATCA GACAATCCC GACAATCCA AATCATGACA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGGCTGGA ATGGCGTGGA ATGGCATGAC TAGGCATGGC TAGGCATGCA CCATGACACC CAGCACATGC CAGCACATGC CAGCACACGC CTGGACATGC CTGGACACGC CTGGACACGC CTGGACACGC CACTGGACACGC CACTGGACAGCC CACTGGACAGC CACTGGACAGCC CACTGGACAGC CACTGGACACAC CACTGACACC CACTGGACACACC CACTGGACACAC CACTGACACC CACTGCACACC CACTGACACC CACTGCACACC CACTGACACC CACTGCACACC CACTGCACACACC CACTGCACACC CACTGCACACC CACTGCACACC CACTGCACACC CACTGCACACC CACTGCA	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG CTGCTCGCAGGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCAC ACCGAACCTC TAAAAGAGAG TAATCACGT TAAACGAG TAATCACGT AGTGTTGAA TTCTGGAC TAATCACGT AGTGTGGAC TGTCAGTGGGC CACGGCAGAC CGTGACCCTG GGGCTGTAGC	31 CTCGGACAGT GCGCGACGGC GCGGCCCGAGGGCCGAGG AGTGGGGGGGCAAGT AGTGGGAAAT TCTGATTCGAC GCTCATAGCA AATATCAAGG AATGAAAGGT AACGTAAGAG ACCTCAAGG ACCTCAAGG ACCACAGGAAGAAG GCTGCAAGGAAGAGC GCTGCAAGGAAGAGGC GCTGCAAGGA GCACTCAAGG GCGCACTGGGGAAGAG GCACATGGGG GCTCAAGGAGAGAGGC GCTCAAGGGAAGAGG GTTTATTCC CAGTCTGGGG GCACATGAGG GCACATGAGG TGTCAAATGG	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTTACA ACACGTAAT CAGTCATTTACA TGAAAAGCGT ATGTCTTAGA ACAGACCACT AAGACCACT AATGCTCTG AAGACCACT TGAAAGCTCT AATGCTCTGA ACAGACCACT TGAAGCTCT TGAAGCTCCT TGAAGCTCCCACA CGAATTGTCACA CGGTTGAGAA	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTCT ACCAATGAAA CCGGGGATCA ACCACCCTCT TGTGGGCTG AAAGTTAAG GAACATTCAG GAACATTCAG CAGCACGTCT TGTGGAGCTG AAAGTTAAG GAACATTCAG CACCCCTCT TGTGGGATG AAAGTTAAG GAACATTCAG CACCCCTCT TGTGGGATG AAAGTTAAG GAACATTCAG CACCCCTCT AAAAGTTAAG GAACATTCAG CACCCCTCT AAAAGTTAAG GAACATTCAG CACCCCCTCT AAAAGTTAAG CACCACCCCTCT AAAAGTTAAG CACCACCCCTCT AAAAGTTAAG CACCACCCCTCT AAAAGTTAAG CACCACCCCTCT AAAAGTTCAGGATG AACATTCAGCATG AGGAGGCTGC	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1380
50 55 60	1 CACTAACGCT TCAAGGCTGA CCACTAACGCTGACCTGA GCCCGCGTGG GCGCACCATGG GCCGCTCCCACCACCACCACCACCACCACCACCACCACCACCAC	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TGCTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGCAGTGCA TAGGCAGTGCA TAGGCAGTGCA TAGGCAGTGCA TAGGCAGTGCA CACACCC TAGGCAGTGCA CCCCCGCAGCA CCCCCCCC CCCCCCCCCC	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT TAGAAATCC CGCTCGCCGC GCTGCCCGT GCTGCCGT AGAAGTGCT AAATGAAGGT TGTCTCCCA ACGGGAATAT TGTGTTGAA ACTCTTCCCA ACGAGACTCT TAAAACAGAG AGAGTTTGAA AGTGTTGAA ACTCTTCCGA CGAGGCTGACCT TAGAACCTC TAAAACAGGG CGGGCAGAC CGTGACCTG GGGCTGACCG GGGCTGTAGC GTACCCATTT	31 CTCGGACAGT GCGCGACGCC CGGCGCCCCC CGGGCCCGCC CGAGGGGTGA AGTGGGGACC AATATTCGAC CTCATTGCC GCTCGAAATT TCTGATTCAG AATGAAAGC GCTCGAAATG GCTCAAAGA ACCCTCAAGGA ACCCTCAAGGA AGCAAGGAA GACAAGTTTT GACATGGACA TGGAGAAGG GTTTATTCC CAGTCTGGCG CTGTCAATGC CTGTCAAGGA TGGAGAAGGA TGGAGAAGGA TGTTATTCC CAGTCTGGCG TGTCAAATGG	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGA ATGTCTTAGA ACAGACCACT AATGCTCTGT TGAACCGCT CAACTAAGTA ACAGACCACT AATGCTCTGT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGAGCACT AATGCTCTGT TGGAGCTCT TGGAGCTCT TGGAGCTCT TGGAGCTCAT TGGGCCACAA CGGTTGAGAA TCAGCAGTTG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAGACCAC TCTGGGTCAC TCTGGGTCAC ACCACGTTT ACCAATGAAA ACCACCCTCT TGTGGAGCTG AAAAGTTAAG ACACCCTCT TGTGGAGCTG AAAAGTTAAG CACCCTCT TGTGGACTG AAATTCAG AACTCAGGAAC ACCTCGCAAA ACTCAGGAC ACTCGCAAA CATCGGCATG AGGAGGCTGC AGGAGGCTGC AGGAGGCTGC AGCAGGAAG	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1500
50 55 60 65	1 CACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCGCGTGGG GCGACGATGGG GCGACGATGA GTCGATCATAA TATCTGCAAG TGTGATCACA TGTGATCACA CTGGTCTCA AGTGCAACCA CCGACTACA CAGACATGGG GTGATCCTGG CAGCCGATTCA CAGCCATTCA CAGCCATTCA CACACACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATCACA ATCATGACA GCCCTAGACA ATCATGACA ATCATGACA ATCATGACA GACTTGGAGA GACTTGGAGA ATCATGACA ATCATGACA GACTTGGAGA	11 CTTCCTAGTC CTTGTGCCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ACGGACATGT ACAGATACAA CCAGACAACAC CAAGAAGGCA TAGGCATGGA ATGCCATGA ATGCCATGGA ATGCCATGGA TGGACATGGC TGAGCATGGC CACTGCACAG CCACTGCACAG CTTCCACCGG CCACCGGCACACCG	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGTG CTGCAGGCC TGTGTTGGG AGAATGCTG AAATGAAGGT TGTCTCCCTC TACAGGGCATTCAG TATCATCGG TATCACGTG AGAGTTTCAG TATCACGTT AGTTTGAAA TTTCTGGAC TATCACGTT GCGCGGAGAC CGTGACCTG GGGCTTTAGC GTACCCATTT GAAAGGAAT GTACCATTT GAAAGGAAT GTACCCATTT	31 CTCGGACAGT GCGCGACGGA CAGCCGGCCCGAG CCGGGCCCGAG AGTGGGGACAT AGTGGGACAT TCTGATTCGA GCTCGAAATT TCTGATTCGA GCTGCAAGGA AGCCTCAAGG ACGCACGAGAGAGA ACCCTCAAGG ACGCACGAGAGAGA CGCTGCAAGGA ACCTTGATTGCCC CGATCTGAGG CGCACAGGAA CCCTCAAGG CGCACAGGAA CGCTCAAGG CGCACATGAGC CGGTCTGGGG CCCATGGGG CCCATGGGG GCACATGAGC CCCATGGTGT GGGGTGTGCC	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT ATGTCTTAGA ACAGTAGT AAGGTCTC TAGAACGGTA ACAGTCTC AAGGTCTCC CAACTAAGTA ACAGCACT AATGTCTCGT TGAAGCCTCT TGAAGCTCTC TGAAGCTCTCT TGAGGCTCTC TGAGGCCACAC TCGGGCCACAC TCGGCTTAGAA TCGGCCACAC TCGGCTTAGAAA TCAGCAGTTG TGGTTTAACCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAGAGA AGTGAAGAGA CAGCACGTCT ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AAGTCAGAGA CATCAGGACT TATTCAGGACT ATTCAGGACT TTTCGGAAT CATCGCATT TTTCGGATT ACCACCATT TTTCGGATT ACGACGATT ACGACGATT AGGACGATT AGGACGATT AGGACGAGAGC CCGCAGAGTC GCCGGAAGTC	120 180 240 300 480 540 660 780 900 960 1080 1140 1200 1380 1440 1360
50 55 60 65	CACTAACGCT TCAAGGCTGG CTTTTTTAAA GCCGGGGTGG GCGACGATGG GCGACGATGG GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTCCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGTACAC TGTGGATCAC TGTGGATCAC TCCGATCAGAC TCCCATGACA TCCCATGACA GCCCAATCA GCCCAATCA GACAATCAC GACTTGAACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA AGGGAGTCTT	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ATGTCAGTGC ATGTCAGTGC ATGTCAGTAG ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGGGTGGA ATGGCGTGGA ATGGCGTGGA ATGCGCATGC TAGGCATGC CACTGGACAGC TGGACATGC TGGACATGC TGGACATGC TGGACATGC TGGACATGC CACTGGACAGC CTCCACCGG CCACTGGACAGC TCGGCGGCCCACAGCCTGGA TCGGGGGGCCCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGT GCTGCCCGT AAAGGAT TGTCTCCCA ACGAACTCT TAGAAGAGT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TAATCAAGT TAATCAAGT TATCTCGAA TGTGTTGAA TATTCTGGAAT AGTGTGGAAC CGTGACCCT GGGCTGTAGC GGGCTGTAGC GGACCCT GAAAGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGAATG GAAGAATG GAAGAATG GAAGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAG	31 CTCGGACAGT GCGCGACGGC GCGCGCCCCCCCCCCCC	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTACA ACACGTAAT CAGTCATTTAGA TGAAAAGGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT TGAAAGCTCT TGAAGCTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCTGT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGAAGAAGAG TTAACCT TGGAAGAAGAG	ATTGCAACGG CGGGGGGAAA CGCGGGGGCT CCCGCTCGGC CTGAAGGCCG CGAAGGAGA AGTGAAGACA AGTGAAAGAA GGAAACCCAC TCTGGGTCAC CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCTCT AAAAGTTAAG GAACATTCAG GAACATTCAG CATCGGCAT ACTCGGCATC ACTCGGCATC ATTCGGGATC ACTCGGCATC ACTCGGCATC ACCACCTCT AAAGTTAAG CAACATTCGGAAC CATCGGCATC ACCACGAGAC CATCGGCATC ACCACGAGACT CAGCAGGAATC AGCAGGAATC ACGAGGAATC ACGAGGAATC ACGAGGAAGTC ACGAGGAAGTC ACGAGGAGTCT	120 180 240 300 480 540 660 780 900 960 1080 1140 1200 1380 1440 1360
50 55 60 65	CACTAACGCT TCAAGGCTGG CTTTTTTAAA GCCGGGGTGG GCGACGATGG GCGACGATGG GCTGATGAAG TTCGACTCCA CTGATCATAA TATCTCCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGGATCAC TGTGTACAC TGTGGATCAC TGTGGATCAC TCCGATCAGAC TCCCATGACA TCCCATGACA GCCCAATCA GCCCAATCA GACAATCAC GACTTGAACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA AGGGAGTCTT	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTGC ATGTCAGTGC ATGTCAGTGC ATGTCAGTAG ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGGGTGGA ATGGCGTGGA ATGGCGTGGA ATGCGCATGC TAGGCATGC CACTGGACAGC TGGACATGC TGGACATGC TGGACATGC TGGACATGC TGGACATGC CACTGGACAGC CTCCACCGG CCACTGGACAGC TCGGCGGCCCACAGCCTGGA TCGGGGGGCCCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCCGT GCTGCCCGT AAAGGAT TGTCTCCCA ACGAACTCT TAGAAGAGT TGTCTTCCCA ACCAAACCTC TAAAAGAGA TAATCAAGT TAATCAAGT TATCTCGAA TGTGTTGAA TATTCTGGAAT AGTGTGGAAC CGTGACCCT GGGCTGTAGC GGGCTGTAGC GGACCCT GAAAGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGAATG GAAGAATG GAAGAATG GAAGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAGGAATG GAAGGAATG GAAGAATG GAAG	31 CTCGGACAGT GCGCGACGGC GCGCGCCCCCCCCCCCC	TTGCTCATTT CGCACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGA GCACTTACA ACACGTAAT CAGTCATTTAGA TGAAAAGGT ATGTCTTAGA ACACTAAGTA AAGATCTGGA ACAGACCACT TGAAAGCTCT TGAAGCTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCT TGAAGTCTGT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGAAGAAGAG TTAACCT TGGAAGAAGAG	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GGAAGGAAGA AGTGAAGAGA AGTGAAGAGA AGTGAAGAGA CAGCACGTCT ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AAGTCAGAGA CATCAGGACT TATTCAGGACT ATTCAGGACT TTTCGGAAT CATCGCATT TTTCGGATT ACCACCATT TTTCGGATT ACGACGATT ACGACGATT AGGACGATT AGGACGATT AGGACGAGAGC CCGCAGAGTC GCCGGAAGTC	120 180 240 300 480 540 660 780 900 960 1080 1140 1200 1380 1440 1360
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA TCGACTCCA TGTCATCAAG TGTTACTACC TCTGGTCTCA AGTGCAACCA TGTGCATCACA AGTGCAACCA TGTGCATCACA ACCATCACCA CAGACATGGG CAGCCATTACA ACCATCACCA ACCATCACCA ACCATCACCA ACCATCACCA ATCATCACCA ATCATCACCA ATCATCACCA ACCATCACCA ACCATCACCA ACCATCACCA CGCCATCACCA CGCCATCACCA CGCCATCACCA CGCCATCACCA CGCCATCACCA CGCCCATCACCA CGCCCCATCACCA CGCCCCTCCCCACCA CCCCCCCCCC	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTGCCCAGG GATGTGCAG CAGCGCGCC TTGTCAGTGC AGCATCATCA ATGAATCATCC ATCTGGAAG ACGGTACTGA ATGACATCAT ACAGATACAA ATCACAACAC CAAGAAGGCA GCTCCATGA GCTCCATGA ATGGCCTGGA GCTCCATGA CTGGTCCAGG CCACTGGACAG CTCCACGG CCACTGGACAG CTTCCACCGG CCACTGGACAG ATCGGGGGCCA AGCCAGAGGAA TCGGGGGCCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT TAGAAATCC CGCTCGCCGC GCTGCCCGT GCTGCCGGC CTGTTCGG AGAAGTGCT AAATGAAGGT TGTCTCCCA ACGAGACCTC TAAAACAGAGA AGAGTTTCAG AGAGTTTCAG AGAGTTCAG TAATCACGTT AGTGTGAAA ATTTTCTGAA ACTCATTCAGT GGGCTGTAGC GGGCTGTAGC GGGCTGTAGC GTACCCATTT GAAAGGAAG AGAGTTTAGA ATTTATAAA	31 CTCGGACAGT GCGCGACGCG GCGCGCGCGCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCAGTCT ATGTCTTAGAA AGATCTTCCC ATGTCTTAGAA AGATCTGGA ACACACT ATGTCTTGGA ACACACT ATGTCTTGGA ACACACT ATGTCTTGGA ACAGTCTCT CGAGTATT CGGCCACACA TGAAGTCTGT TGGACACTCT TGGACACTCT TGGACACTCT TGGACACTTGT TGGACACTTGT TGGACACTC TGGACACACT TGGACACTTGT TGGACACACT TGGACACACT TGGACACACT TGGACACACT TGGACACACT TGGACACACT TGGACACACC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC GCTCGCCTG CGAAGGAAGA AAGCAAGAAGA AAGCAACGAC CCACATGAAC CCACATGAAC ACCACCTCT TGTGGAGCTG AAAAGTTAAG AACCACCTCT TGTGGAGCTG AAAAGTTAAG AACTCACGATCA ACCACCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AACTCAGGAAC ACCTCGCAAA CCTCGCCAAA CATCGGCATG GGACCATTCA TTTCGGGTTC CAGCAGGACG CCGGAAGTC CAGCAGGAAGTC CAGCAGGAAGTC CAGAGGAGGGTG CTGTACCCTG	120 180 240 360 420 480 540 660 720 780 900 900 900 1020 1260 1260 1320 1440 1500 1620
50 55 60 65 70	1 CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGGG GCGACCATGG GCGACCATGG GCGACCATGG TTCGACTCCA TCTGGTCTAA TATCTGCAAG TGTTACTACC TCTGGTCTAC AGTGCAACCA CCGACATGAC CAGCATTCA CAGCATTAC TCCCATGAC GCCCAATCA GCCCCAATCA ATCATGACA GCCCCAATCA ATCATGACA GACTTGGAGA ATCATGACA ATCATGACA GACTTTGGAGA AGGCGCGACG AAGCCCGACG	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCC TTGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTAA ACGACACAC CAAGAAGGCA TAGACAACAC CAAGAACACC TAGGCAGCT TAGGCATGCA ATCACCATGAA ATCACCATGCA ATCACCATGCA CAGCAACGG CTCCATGA CTGGCAGGC CTCCCATGA CTGGCGCCC CTGGGCCCAGC CTCCCGGGCCCA CTGGGGCCCAGC CCCGGCCCGG	21 CCCGGGCCAA AACGCCGCC TAGAAGAGCT CAGGAAATCC CGCTCGCCGC GCTGCCGGC GCTGCCGTG AGAAGTGCTG AGAAGTGCTG AGAGTGCTG ACGGGGATAT TGTCTTCGG ACGGGGATAT TGTGTTTGAA ACTCTTCCCT TAAAAGAGAG TAATCAGTT AGTGTGAAT AGTGTCAGTGGG CACGGCAGAC CGTGACCTG GGACCTG GGACCTG GGACCTG GGACCTTAGAAAGGAGA ATGTGGGGAAAC ATGTGGGAAAC ATGTGGGAAAC ATGTGGGAAAC ATGTGGGAAAAC ATGTGGGGAAAAC ATGTGGGAAAAC ATGTGGGGAAAAC ATGTGGGGAAAAC ATGTGGGGAAAAC ATGTGGGGAAAAC ATGTGGGAAAAC ATGTGGGGAAAAC ATGTGGGGAAAAC ATGTGGGGAAAAC ATGTGGGAAAAC ATGTGGAAAAC ATGTGAAAAC ATGTGAAAAAC ATGTGAAAAC ATGTGAAAAAC ATGTGAAAAAC ATGTGAAAAAC ATGTGAAAAAC ATGTGAAAAAC ATGTGAAAAAAAAAA	31 CTCGGACAGT GCGCGACAGCA CAGCCGGCCCGAGGGCCCGAG AGTGGGGACAGCA AGTGGGGACAT TCTGATTCGAC GCTCGAAATT TCTGATTCGAC GCTGCAAAGCA GACAGCAGAAGCA GACAGCTTTT GCATGGACA AGCCATGACAC CGCTCAAGGA ACCCTCAAGGA CGCTACAAGGA CGCTACAAGGA CGCTACAAGGA CGCTACAGGA CGCACAGGAAGA CGCACAGGAAGA CGCTCCAAGGA CGCACATGAGC CCAGCTCGGG CCCAGCTGGGG CCCAGCTGGGG CCCATGAGGA CCCATGGGGA CCCATGGGGA CCCATGGGGA CCCATGGGGA CCCAGCTGTGAAGGA CCCCAGCTGCA CCCCCTGCCA CCCCTGCTGCAA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA CAGCTCATAC ACGGTAAT ATGTCTTAGA ATGTCAGTT AATGTCTTGA ACAGCACT TAGAGCACT TAGAGCACT TAGAGCACT TAGAGCACT TAGAGCACT TAGAGCACT TGGAGCACT TGGGCCACAA CGGTTAGAG TCGGACTTGGA TGGGCACACA TGGGCACACA TGGGCACACA TGGGCACACA TGGGCACACA TGGGCACACA TCAGCAGTTGG TGGAGAGAGGA ATGCCACCAC ATGCCACCAC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAGAGA CAGCACGTGT ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGAGCTG AAAAGTTAAG GAACATTCAG AAGTCAGGAC ACCTCGCATA CATCAGGAC ACCTCGCATA CATCAGGAC ACCTCGCATA CATCAGGAC ACCTCGCAAA CCTCGCAAA CCTCGCAAA CCTCGCAAA CCTCGCAAA CCTCGCAAA CCTCGCAAA CCTCGCAAA CTTCGGATC AGGACGATC AGGACGATC AGGAGGATC AGGAGGATC CAGCAGGAAG CCTGCAAGCTC CAGCAGGAAG CCTGCACCTC GAAGCCTGCA	120 180 240 360 420 480 540 660 720 780 900 960 1140 1200 1320 1320 1440 1500 1560 1680
50 55 60 65	1 CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCTGG GCGACCATGG GCCGACCATGG GCTGATCAAA TTCGACTCCA TGTTACTAC TGTTACTAC TGTGCTCCA TGTGCACCA TGTGGATCAC TGTGCATCAC TGTGCATCAC TGTGCATCAC TGTGCATCAC TGTGCATCAC TCCCATGACA TCCCATGACA GCCATTCACA TCCCATGACA GCCCAATCA ATCATGACA GACAATCAC ATCATGACA AGGAGTCTT GACTGTGGGG AAGCCGGAC AGGAACAGCGT GGAACAGCGT	11 CTTCCTAGTC CTTGTGCAG AATGAAAGGC CTCGCCGAGG GATGGTGCAG GAGGCGCCC TTGTCAGTGC AGGAATCATCC ATCTGGAAAG ATGGACATGT ACAGATACAA ATCACAACAC CAAGAAGACGC TAGGCGTGGA ATGGCATGT AGGCATGTG ATGGCATGC ATGCGCAGGC TAGGCATGGA ATCGCAGCA	21 CCCGGGCCAA AACGCGCGC TAGAAGACT CAGGAAATCC CGCTCGCCGC GCTGCCCGTG CTGCTCGCGC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCA ACCAAACCTC TAAAAGAGA TAGTTTCAG AGAGTTCAG TAGTCTGGAAT AGTGTTGGAAT ATTCAGTGGG CACGGCAGAC CGTGACCCTG GGGCTGTAGC GGGCTGTAGC GGACCCTG GAAGGAATC CAAAGGATT CAATGACTCC AATGAATGACCTC CAAAGGAATC CAAAGGAATC CAAAGGAATC CAATGACTCC CACCAAACCTC CACCAAACTC CACC	31 CTCGGACAGT GCGCGACGCA CAGCACGCA CAGCACGCA CCGGCCCCGCCC CCGACGGGCCAAA AGTGGGACAC GCTCGAAATT TCTGATTCAC GCTGCAAAGA AATCAAAGC GCTGCAAAGA ACCCTCAAGG ACGCAAGAAGA GCACAAGGACAGACTTTT GACATGGCAC TGGACAGGACA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT CAGTCATCTTAGA ATGTCTTAGA ATGTCTTAGA ACACACCACT ATGTCTTGTA AATGTCTGT AATGTCTGT AATGTCTGT AATGTCTGT CGAATTAGAA CGGATCAGACACC TGAAGACCACT TGAAGACCACT TGAAGACCACT TGAAGACCACT TGAAGACCACT TGGAAGACAC TCGCACT TGGAAGAAGG ATGCCACCAC ACTGCCAGCT CGAAGTTCTGC	ATTGCAACGG CGGGGGGAAA CGCGGGGGGAAA CGCGCTCGCC CTGAAGGCCG CGAAGGAAGA AGTGAAGACC AGCAAAGAA GGAAACCCAC TCTGGGTCAC CACCACTCT TGTGGATCAC ACCACCTCT TGTGGAGCTG AAAGTTAAG AACATTCGG AACATTCGGAAC ATTCGGAAC ATTCGGCATG ATTCGGATG AACATTCGCAAA CATCGGCATG CGACCACTCT TTTCGGATC TTTCGGATC TTTCGGATC CGCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC CACCAGGAGC CCTTACCCCC CACAGGAGCC CACAGGGCCC CACAGGGCCC CACAGGGGCCC	120 180 240 360 420 480 540 660 720 780 900 900 1020 1020 1260 1320 1440 1500 1620 1620 1620 1620
50 55 60 65 70	1 CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCGA GCCGATCCAA TTCGACTCCA ATGTCATAACA TGTTACTACC CCGATCATCAA AGTGCAACCA AGTGCAACCA CAGACATGGG CCACTCACCA GCCCAATCA GCCCCAATCACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA ACTCTGGGGG AAGCACTCT CACTGGGGGACACGGGACACGGGACACGGACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCGCACA AGCCCCCACT	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTGC ATCTGGAAG ATGACATCA ATCACAGA ATGACATGA ATGACATGA ATCACACAC CAAGAAGGCA CAGCACTGA ATGCCAGCT TAGGCATGA ATGCCAGCT TAGGCATGA ATGCCAGCT CACTGGACAG CTCCATGA ATGCCAGCT CACTGGACAG CTCCATGA CTCCACCGG CCACCTGGACAG CTGCACAGGAC CCACTGGACAG CTGCACAGGAC CCACTGGACAG CCACTGGACAG CCACTGGACAG CCACTGGACAG CCACTGGACAG CCACTGGACAG CCACTGGACAG CCACAGAGAC CCACTGGACAG CCACAGAGAC CCACTGGACAG CCACAGAGAC CCACTGGACAG CCACAGAGAC CCACTGGACAG CCACAGAGAC CCACCCAACCC CCACCCAGCCCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGC CAGCAAACC CGCTGCCGG GCTGCCGG GCTGCCGGG GCTGCCGGG AGAAGTGCT AAATGAAGGT TGTCTCCCA ACGAAACCT TAAAACAGAGA AACGTTCAGG AGAGTTCAG AGAGTTCAG AGAGTTCAG AGAGTTCAG AGAGTTCAGT AGTGTGAAAC ATGTAGAGAA ATGTAGAGAA ATGTAGGG GAAGGAACC CGTGACCTG GAAAGGATG GAAAGGATG ATGTATAAAA ATGTGGGAC CGTACCCTC CAGCAACCCC CGAGAACCCC CGAGAACCCC CGAGAACCCC CGAGAACCCC CGAGAACCCC CGAGAACCCC CGAGAACCCC CGGGACCCC CGAGAACCCC CGGGACCCC CGGGACCCC CGGCACCC CGGGACCCC CGGGACCCCC CGGGACCCC CGGGACCCCC CGGGACCCC CGGGCACCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGCACCC CGGGCACCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGACCCC CGGGCACCC CGGGACCCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGGCACCC CGGCACCC CGGCACCC CGGCACCC CGGCACCC CGGCACCC CGGCACCC CGGCACCC CGGCACCC CGCCACC CGGCACCC CGGCACC CGGCACCC CGGCACCC CGCGCACC CGCCACC CGCGCACC CGCCC CGCGCACC CGCCC CGCCC CGCGCC CGCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	31 CTCGGACAGT GCGCGACGGC GCGCGCGCGC CGGGGGCGCAGCA AGTGGGGGCCAAG AGTGGGGACC AATATTCGAC CTCATTGCCA GCTCGAAATT TCTGATTCAG AATGAAAG ACCTCAAGA ACCCTCAAGA ACCCTCAGGAGA GACAAGATTT CGACACGACA	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGAA TCTGGATCCC TACAACGGGAA CAGCTCAGTCT ATGTCTTAGAA ATGTCTTAGA AAGATCTGGA ACACTAGTA AAGATCTGGA ACACTAGTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGACTACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TAGGACACAC TCGGACACAC TCGGACACAC TCGAAGAAGG ATGCCACCAC ACTGCCACC ACTGCCACCAC ACTGCCACC ACTGCCACCAC ACTGCCAGCTTCC ACTGCCACCAC ACTACAC ACTGCCACCAC ACTCACCAC ACTGCCACCAC ACTCCACCAC ACTCC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC GCTCGCCCTG CGAAGGAAGA AAGCAAAGAA AAGCAAAGAAA CCGACGTCT ACCAATGAAA CCGGGATCA ACCACCCTCT TGTGGAGCTG AAAAGTTAAG AACTCACCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AACTCGCAAA CATCGGCATC ACCACGTGT CACCAGTGT CACCAGTGT CACCAGTGT CACCAGTGT CACCAGTGT CACCAGTGT CACCAGTGT CACCAGGAGC CACCAGGAAGC CCGGAAGTC CACAGGGGCT CACAGGGCC CACAGGGCC CACAGGGCC CACAGGGCC CACAGGGCC	120 180 240 360 420 480 540 660 720 780 960 960 1200 1260 1320 1320 1440 1500 1500 1620 1740 1860
50 55 60 65 70	1 CACTAACGCT TCAAGGCTGA CCACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCGACCATGG GCGACCATCA TTCGACTCCA TCTGGTCTCA AGTGCAACCA TGTGACACCA CAGACATGGG GTGATCACA ACTGCATCCA ACTGCATCACA ACTCATCACA GCCCCAATCA GACAATCCCC AATCATGACA GCCCTCATCT GACTTGGACA GCCTTCGGCA GGACAGCGT AGCCCGCACC GGACACGCGT AGCCCCTCCT GGCCTCCT GGCTACTGGCA GGCCCTCACT GGCCCTCCT GGCTACTGGCA GGCCCTCCT GGCTACTGGCA AGCCCCTCCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCCCTCACT GGCTACTGCT GCTACTGCT GGCTACTGCT GCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTGCT GGCTACTACT GGCTACTACT GGCTACTACT GGCTACTACT GGCTACTACT GGCTACTACT GGCTACTACT GGCTACTA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCGCCC TCGTCAGTGC AGAATCATCC ATCTGGAAAG ACGGTACTGA ATGACATAT ACAGATACAA ATCACAACAC CAAGAAGGCA TAGGCCAGCA CTTGTCAGTGC TAGGCATGCA ATCACAACAC CAAGAAGCA CAGCACT TAGGCCTGGAA CTTGCTCACCAG CTTCCACCAG CCACCAGCAG CTTCCACCAG CCACCAGCAG CCAGCCAGCAG CCAGCCAGC	21	31 CTCGGACAGT GCGCGACGCA CAGCCGGCCCGAGGGCCCGAGGGACGCA AGTGGGGACAGCA AGTGGGGACAC CTCATTGCCA GCTCGAAATT TCTGATTCGA GCGAAGAAGCA AGCCTCAAGG ACCCTCAAGG ACCATCAAGG ACCATCAGGACAAGT CGCAAGAGAGA CGCTCAAGG CGCACAGGAGAGA CGCTCAAGG CGCACAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	TTGCTCATTT CGCACACACA GCGGGCCGTG GACGCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTAAC ACGGTAAT CAGTCAGTCT ATGTCTTAGA ACAGCACT AATGTCTTGGA ACACCACT AATGTCTCG TGAACCACT AATGCTCTGT TGAAGCACT TGAAGCACT TGAAGCACT TGAAGCACT TGAAGCACT TGAAGCTTCT TGAAGCTTCT TGAAGCACT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGAAGCTCCAC TGAAGCTCAC TCGAAGTTGAC TCGAAGACCAC TCGAAGTTGCAC TCGAAGACCAC TCGAAGTTTGCACCACAC ACTGCCACCC ACTGCCAGCT CAGAGTTCTCAC ACTGCCACCC ACTGCCAGCT CAGAGTTCTCAC	ATTGCAACGG ACTGGAGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG CGAAGGAAGA AGTGAAGAGA AGTGAAGACA AGTGAAGACA CCACCACTCT ACCACCTCT TCTGGGTCA AAGCACTCT TCTGGAGCTG AAAAGTTAAG CACACCTCT TCTGGAGCTG AAAAGTTAAG CACACCTCT TCTGGAGCTG AAAGTTAAG CACACCTCT TCTGGAGCTG AAGCACTCA CACCACGGAAC CCACCAGGAAC CCACCAGGAAG CCACCAGGAAG CCACAGGGACC CACAGGGGCC CACAGGGGCC CGAAGGCCTCA CACAGGGGCC CGGATGTGACC CGGATGTGAC CACCAGGGAC CACAGGGGCC CGGATGTGAC CACTGGCAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGAC CACTGGGAC CACTGGAC CACTGGGAC CACTGGAC CACTGCAC CACTGGAC CACTGGAC CACTGCAC CACTGGAC CACTGCAC CACTGGAC CACTGCAC CACTGGAC CACTGCAC CACTGCAC CACTGGAC CACTGCAC CACTCCAC CACTGCAC CACTGCAC CACTCCAC CACTGCAC CACTCCAC CACTCAC CACTCCAC CACTCCAC CACTCCAC CACTCCAC CACTCCAC CACTCCAC CACTCCAC	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1680 1740 1880 1740 1800
50 55 60 65	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCCCATGG GCGACCATGG GCTGATGAAG TTCGACTCCA TGTACCAAC TGTTACTACC TCTGGTCTAC TGTGCACCA TGTGCAACCA TGTGCAACCA TGTGCAACCA TGTGCAACCA TGTGCAACCA TGTGCATCAC CAGCACTAGG CCCAATCAC TCCCATGACA TCCCATGACA GCCCAATCAC ATCATGAACG GACTTGGAGA ATCATGAACA TCATGAACA GACAATCCC AATCATGACA TCATGACA TCAT	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCGAGG GATGGTGCAG CAGCGCCCC TTGTCAGTC ACTGGAAAG ACGAGTACTGA ATGGACATGA ATGGACATGA ATGACATACAA CCAGAGAGGA CTAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGCATGC TGGACATGC TGGACATGC CTCCATGA ATCCCAGCAGGA CCTGCAGGACAG CCAGCCAGAGGA CCTGTGTGCCC GCAGGGACTC GCAGGGACTC GCAGGGACTC GCAGGGACTC CCAGCCAAA ACAATGGCAT	21 CCCGGGCCAA AACGCGCGC TAGAAGAGC CGCTGCCGG GCTGCCGGG GCTGCCGTG CTGCTGCGG AGAACTGCT ACGGAACTCT ACGGGATAT TGTCTCCCC ACCAAACCTC TAAAAGAGT TAGTCTTCAG ACCAAACCTC TAAAACAGG TAATCAGGT TAGTCTGGAG CACGGCAGC CGTGACCCT GGGCTGTAGC GTACCCT GAAGGAT GAAGGAT CATGACCT CAAAGCTCC CGTGACCCT CGGACACCC CGTGACCCT CGAGCACCC CGTGACCCT CAGCACCC CGTGACCCC CGTGACCCC CGTGACCCC CGTGACCCC CTGCCACACC CTGCCACCC CTGCCACC CTGCCACCC CTGCCACC CTCCCC CTGCCACC CTCCCC CTCCC CTCC CTCCC CTCC CTC	S11 CTCGGACAGT GCGCGACGCA CAGCAC CAGCCCCGCC CGACGGGCCAGCA AGTGGGGACAGCA AGTGGGGACAGCA AGTGGGACACA GCTCGATCCC GCTCGAAATT TCTGATTCAG GCTGCAAAGA ACCCTCAAGG ACCATCAAGC ACCATCAAGC CAGTTATTCAC GCACAGCACA	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT ATGTCATAGAA ACAGTAAT ATGTCTTAGA ACAGTAAT AATGTCTGT TGAAGCTCT AATGTCTCT AATGTCTCTGT TGAAGCTCT TGAAGACACA CGGTTTAACCT TGAAGAAGG ATTGCACCACT ACTGCAGCTT CACTGCAGTT CACTGCAGT TCATTCTGC	ATTGCAACGG CGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTGACGCCTG GGAAGAAGA AGTGAAGAGC AAGTGAAGAGC AAGCAAAGAA CCAGCACTCT ACCAATGAAA CCGGGGATCA ACCACCTCT TTTGGAGCTG AAAAGTTAAG GAACATTCAG CACCACCTCT TTTCGGAGCT AACTCAGCAT TTTCGGGATG ACCACGCATCA TTTCGGGATG AGCAGGAGC CACCAGGAGAG CACCAGGAGAG CACCAGGAGAG CACCAGGAGAG CACCAGGAAG CACCAGGAGAG CAGCAGGAAG CACCAGGAGAG CAGCAGGAAG CACCAGGAGAG CACAGGAGCC CAGCAGGAAG CACCTGCA CACCAGGGAC CACCAGGAGCC CACAGGGGCC CACCAGGGGCC CACCAGGGGCC CACCAGGGAC ACCTCTGGGA AGGTGATCCT	120 180 240 360 420 480 540 660 720 840 900 900 1020 1260 1320 1440 1560 1620 1620 1620 1620 1860 1860 1860 1860
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA TCGACTCCA TGGACTCCA TGTCATCAAC TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGGATCATCA CAGACATGGG CCATTCACCA TCCCATCACA ATCCTCTGGCCAATCA GCCCCAATCA ATCATGAACA ATCATGAACA ATCATGAACA ATCATGAACA ATCATGAACA ATCATGAACA AGGAGTCTT GACTTGGGG AAGCCGCA CGGACATCCA CGCCCCACT GCCACTCACT CCAGGTCCTACT CCAGGTCCTACT CCAGGTCCTCACT CCAGGTCCTCACT CCAGGTCCTCACT TATGGCAACT	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTGCCGAGG GATGGTGCAG GAGCGCCCC TGCTCAGTGC AGGATCATCAC ATCTGGANAG ACGGTACTGA ATGACATGA ATGACATGA ATCACACAC TAGACATGC TGGGCCAGC CCACTGGACAG CTTCCACCGG CTTCCACCGG CTGTGTGCGC GCAGGGCCAA ACCTGCCAG ACCAGCCCAA ACCAGCCCAA ACCTGCCCAC CCAGCCCAA ACCAGCCCAA ACCTGCCCAC CCAGCCCAA ACCAGCCCAA ACCTGCCCAC CCAGCCCAA ACCTGCCCAC CCAGCCCAA ACCAGCCCAA ACCTGCCCCAC CGTGGCCAAC CCGTGGCCAAC CCGTGGCAAACGC CTGCCCAC CCGTGGCAAACGC CTGCGCCAAC CCGTGGCAAACGC CTGGCCAAC CCGTGGCAAACGC CTGCGCAACCC CTGCGCCAAC CCGTGGCAAACGC CTGCGCAACCC CCGCGCAACCC CCGCGCAACCC CCGCCCAAC CCGCGCAACCC CCGCCAACCC CCGCGCAACCC CCGCCAACCC CCGCGCAACCC CCGCGCAACCC CCGCGCAACCC CCGCGCCAACCC CCGCGCAACCC CCGCGCAACCC CCGCGCCAACCC CCGCGCAACCC CCGCGCCAACCC CCGCGCCAACCC CCGCCAACCC CCGCCAACCC CCGCCAACCC CCGCCAACCC CCGCCAACCC CCGCCAACCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT TAGAAAATCC CGCTCGCCGC GCTGCCCGTG CTGCCAGG AGAAGTGCTG AAATGAAGGT TGTCTCCCA ACGAACCTC TAAAACAGAG TAATCAAGTT AGTGTTGAA ACCATTCACA ACGAACCTC TAAAACAGAG TAATCAAGTT AGTGTGGAACTC GGGCTGTACCCT GGAAGGATT GTACCCATTT GAAAGGATG CACGCAACC CCTGCAACCT CCTCGCAACCT CTGCCAGACT CCTCGCAGACT CCTCGAAGACT CCTCGAAGACT CCCCGTGTACCCT CTGCCAGACT CCTCGAAGACT CCCCGGAACACCT CCTCGAAGACT CCCCGGAACACCT CTCGAAGACT CCCCGGAACACCT CTCGAAGACT CCCCGAAGACT CCCCCAACC CCCCGAAGACT CCCCCCAACC CCCCCCAACC CCCCCCCCCC	TCCAGACAGT GCGCACAGCA CAGCACAGCA AGTGCGCACCC CCAGGGGGCACAGCA AGTGCGGACACA AGTGCGGACCA AGTATTCGAC CTCATTGCCA GCTCAAAGA AATGAAAGCT ACCTCAAGG ACCTCAAGG ACCATCAGGA GCACAAGAAGA TTTATTCCA CCATCGGGACAGAAGA TGGAGGAAGA CCTCAAGG ACCAGGTT GACATCGGC CCATGGTGT CGGAGATTT CGCTGCACACA CGCTGCTGCACACACACACACACACACACACACACACACA	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGAA TCTGGATCCC TACAACGGGAA TCAGTCAGTCT ATGTCTTAGAA TGAACAGGTAAT AAGATCTGGA AAGATCTGGA AAGATCTGGA ACAGTAGTA TGAACACGTT ATGTCTTGGA ACAGTAGTA AAGATCTGGA ACAGTCTGTT AGGGACCACT AATGTCTGT AGGGACCAC TGAAGTAGTA TGAGCACAC TGAGCACAC CGGTTGAGAA CGGTTCACACAC CAGGTTCTCAC CAGGGTTCTCA CAGGGTTCTCA CAGGGTTCTCA CAGGTTCTCA CAGGTTGTCAC AGTGCACACA CAGGTTCTCAC CAGAGTTCTCAC AGTGTGTCAC AATGCGACAC AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACAC AATGCGACACA AATGCGACACA AATGCGACACA AATGCGACACA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG GCAAGGAAG AAGCAAAGAA GCAAAGAAA CCCAC CTCTGGGTCAC CCACACGTCT ACCAATGAAA CCGGGATCA ACCACCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AAGTCAAGGAC ACCTCGCAAA CATCGGCAT CAGCAGTGT CAGCAGTGT CAGCAGTGT CAGCAGTGC CAGCAGGAAGTC CAGCAGGAAGTC CAGCAGGGAGT CTGTACCCTG GAAGCTTGCA CCCTGGCAAA CCTCGCAAA CCTCGCAAA CTCTGGGAA CCCGGAAGTC CAGCAGGAGTG CTGTACCCTG GAAGCCTGCA ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGGAC ACTCTGGGGAC ACGTGTGACCCT GGAGAGTGCT CGGAGGATGCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGATGCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT GGAGAGTGCT GGAGAGTGCT GGAGAGAGCCT GGAGAGAGCCT GGAGAGAGCCT GGAGAGAGCCT	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1440 1500 1620 1680 1740 1860 1920 1920 1920
50 55 60 65	CACTAACGCT TCAAGGCTGA CACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA CTGATCATAA TTCTGACTCCA TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGCATCACA AGTGCAACCA CAGACATGGG CAGCCATTCACCA ATCATGACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA AATCATGACA AATCATGACA AAGCAGTGCA AAGCAGTGCA AAGCAGTGCA CGCAACCA CGCAATCACA CACAATCACCA AATCATGACA CGCCTCACCA CGCAACCAC CGCAACCAC CGCAACCAC CGCAACCAC CGCACCACCAC CCCACCACCAC CCCACCACCAC CCCACCA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTGCCGAGG GATGTGCAG CAGCGCGCCC TGTCAGTGC AGAATCATCC ATCTGGAAGA ATGGACATGA ATGGACATGA ATGGACAACAC CAAGAAGCA CCAGCAGCT TGGCCAGGA CTCCATGA ATGGCATGAA ATGCACACAC CACGGACAGCA CCACCAGCAG CTTCCACCAG CCACCAGCAG CTTCCACCAG CCACCAGCAG CTTCCACCAG CCACCAGCAG CCACCAGCAGA CCACCAGCAGA CCACCAGCAGA CCACCAGCAAA ACATGCCCC GGCCAAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACTGCCCC GTGGCAAACT AAACTGCCCC	21 CCCGGGCCAA AACGCCGCCAA AACGCCGCCCAAACCCCCCTCTTTCGG AGAAGTCCTGCAGGCCCTTGTTCGA AACTGATGATTGATTGATTTGAT	CTCGGACAGT GCGCGACAGT GCGCGACAGCA CAGCCGGCCCGAG CTCCGGTCGC CGAGGGGTGA AGTGGGGACAGCA AGTGGGGACAGCA AGTCGATATCGAC CTCATTGCAA ATTATTCGAC GCTCGAAATT TCTGATTCAG AACGAAGAA ACCCTCAAGG AGCAAGGAA ACCCTCAAGG CGCACAGGACAGCAA GCCAAGGACAGCAA TGCACTCAGGGC CCACTGGTGT GGGGTGTGCC CACCAGGTGTGCCCCACCAGGTGTGCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCCCTG GACGCCCGGC GCTTATGGAA TCTGGATCAC ACACGGTAAT CAGCTAATT CAGTCAGTCT ATGTCTTAGA ATGTCTTAGA ACACGACACACACACACACACACACACACACACACA	ATTGCAACGG ACTGGAGGGAAA CGCGGGGGGAAA CGCGGCCTG CCTGAAGGCCG GCTCGCCTG CGAAGGAAGA AGTGAAGAC ACTGAGAGAA AGTGAAGAC TCTGGGTCAC CAGCACGTTA ACCACCCTCT TGTGGACTCA ACCACCCTCT TGTGGACT AAAAGTTAAG ACACCCTCT TGTGGACT AAAAGTTAAG CACACCCTCT TGTGGACT AAAAGTTAAG CACCCCTCT TGTGGACT AAAAGTTAAG CACCCCTCT TGTGGACT AAAAGTTAAG CACCCCTCT TGTGGACT AAAGTCAGAAC CACCCCCCC AACTCAGAAGC CACCAGGAAGC CACCAGGAAGTC CACCAGGGAC CACAAGGGCC CACAAGGGCC CACAAGGGCC CACTCGGGA ACTCTGGGA ACTCTGGGGA ACTCTGGGGA ACTCTGGGGA ACTCTGGGGA AGGTGATCCT GAAGAGTGCT GAAGAGTGCT GAGAGATGCT TACCAATGCC	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1680 1740 1880 1980 2010
50 55 60 65 70	CACTAACGCT TCAAGGCTGA CACTAACGCT TCAAGGCTGA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCCA CTGATCATAA TTCTGACTCCA TGTTACTACC TCTGGTTCTCA AGTGCAACCA TGTGCATCACA AGTGCAACCA CAGACATGGG CAGCCATTCACCA ATCATGACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA ATCATGACA AATCATGACA AATCATGACA AAGCAGTGCA AAGCAGTGCA AAGCAGTGCA CGCAACCA CGCAATCACA CACAATCACCA AATCATGACA CGCCTCACCA CGCAACCAC CGCAACCAC CGCAACCAC CGCAACCAC CGCACCACCAC CCCACCACCAC CCCACCACCAC CCCACCA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTGCCGAGG GATGTGCAG CAGCGCGCCC TGTCAGTGC AGAATCATCC ATCTGGAAGA ATGGACATGA ATGGACATGA ATGGACAACAC CAAGAAGCA CCAGCAGCT TGGCCAGGA CTCCATGA ATGGCATGAA ATGCACACAC CACGGACAGCA CCACCAGCAG CTTCCACCAG CCACCAGCAG CTTCCACCAG CCACCAGCAG CTTCCACCAG CCACCAGCAG CCACCAGCAGA CCACCAGCAGA CCACCAGCAGA CCACCAGCAAA ACATGCCCC GGCCAAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACCTGCCCC GTGGCAAACT AAACTGCCCC GTGGCAAACT AAACTGCCCC	21 CCCGGGCCAA AACGCCGCCAA AACGCCGCCCAAACCCCCCTCTTTCGG AGAAGTCCTGCAGGCCCTTGTTCGA AACTGATGATTGATTGATTTGAT	CTCGGACAGT GCGCGACAGT GCGCGACAGCA CAGCCGGCCCGAG CTCCGGTCGC CGAGGGGTGA AGTGGGGACAGCA AGTGGGGACAGCA AGTCGATATCGAC CTCATTGCAA ATTATTCGAC GCTCGAAATT TCTGATTCAG AACGAAGAA ACCCTCAAGG AGCAAGGAA ACCCTCAAGG CGCACAGGACAGCAA GCCAAGGACAGCAA TGCACTCAGGGC CCACTGGTGT GGGGTGTGCC CACCAGGTGTGCCCCACCAGGTGTGCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCCCTG GACGCCCGGC GCTTATGGAA TCTGGATCAC ACACGGTAAT CAGCTAATT CAGTCAGTCT ATGTCTTAGA ATGTCTTAGA ACACGACACACACACACACACACACACACACACACA	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGACG GCTCGCCTG GCAAGGAAG AAGCAAAGAA GCAAAGAAA CCCAC CTCTGGGTCAC CCACACGTCT ACCAATGAAA CCGGGATCA ACCACCTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AAGTCAAGGAC ACCTCGCAAA CATCGGCAT CAGCAGTGT CAGCAGTGT CAGCAGTGT CAGCAGTGC CAGCAGGAAGTC CAGCAGGAAGTC CAGCAGGGAGT CTGTACCCTG GAAGCTTGCA CCCTGGCAAA CCTCGCAAA CCTCGCAAA CTCTGGGAA CCCGGAAGTC CAGCAGGAGTG CTGTACCCTG GAAGCCTGCA ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGAC ACTCTGGGGAC ACTCTGGGGAC ACGTGTGACCCT GGAGAGTGCT CGGAGGATGCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGATGCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT GGAGAGTGCT CGGAGAGTCCT GGAGAGTGCT GGAGAGTGCT GGAGAGTGCT GGAGAGAGCCT GGAGAGAGCCT GGAGAGAGCCT GGAGAGAGCCT	120 180 240 360 420 480 540 660 720 780 900 900 1080 1140 1260 1380 1440 1500 1620 1680 1740 1860 1920 1920 1920
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCCGTGG GCGACCATGG GCGACCATGG GCTGATGAAG TTCGACTCCA TGTTACTACA TATCTGCAAG TGTTACTACA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TCCATGACA TCCCATGACA TCCCATGACA TCCCATGACA TCCTGTTGG CATTCACCA TCCTGTTGG CATTCACCA TCCTGTTGG CCATTCACCA TCTGTGGG ATCATGACG GACTTGGAGA AGGGAGTCTT GACTGTGGGG AGCCGACT GGCACTGCGCACT CGGTACTGCT TATGGCACT TATGGCACT TATGGCACT TATGGCACT TATGGCACT AAATGTGGAA TCCAGGTGCTA	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTCGCCAGG GATGTGCAG GATGTGCAG CAGGCGCCC TTGTCAGTGC AGAATCATCC ATTGGAAAG ACGGTACTGA ACGGACTTAT ACAGATACAA CCAGAGAGA ATGCCAGGC TAGGCAGGC TAGGCAGGC TAGGCAGGCA CAGCCAGGCA ATGCGCAGGC CCACCTGGACAG CCACCTGGACAG CCACCTGGACAG CCACCTGGACAG CCACCTGGACAG CCACCTGGACAG ACAGCAGGACA CCGGCCAAA ACAACGC CGCCAAAGCAC CTGGCAAAGC CTGGCAAAGC CTGGCAAAGC CTGGCAAACC CGCCAAACCC CGCAAACCC CGCCAAACCC CGCCAAACCC CGCCAAACCC CGCCAAACCC CGCAGCAAACCAC AACCTGCCCC CGCCAAACCAC AACCTGCCCC CGCCAAACCAC AAACCAACCAC AAACCAACCA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGC CGCTGCCGG GCTGCCGGG GCTGCCGGG GCTGCCGGG GCTGCCGGG CTGGTTCGG AGAAGTGCT ACGGGGATAT TGTCTCCCC TAAAAGAGT TGTCTTCCAA ACCAAACCTC TAAAACAGT TAGTCTGGAA TATCAGGTT AGTGGAACT TGTGAAGAGG GGACCTG GGGCTGTAGG GGACCTG GAAGTGTGGG ATTATAAAT ACATGGCTG CAGCACAC CGTGAACCTC CGGGAACTCC CGTGTACCTG CTGCCAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC	CTCGGACAGT GCGCGACGGA GCGGCGACGGA AGTGGGGGCCGAGG AGTGGGGGCCGAG AGTGGGGACAGT AGTGGGGACAGT TCTGATTGCA GCTCGAAATT TCTGATTGAC GCGACGGAGAGAGA AGCCTCAAGG AGGAGAGAGA AGCCTCAAGG AGCAAGAGAGA GCAAGGAGAGA GCAAGGAGAGA GGCAAGGAGAG GCAAGTTTT GCATTGGGG GCACATGGGG GCACATGGGG TGCAGGGGGGG TGCAGGGGGGGGGG	TTGCTCATTT CGCACACAC GCGGCCGTG GACGCCGGC AGCTGCTGCA GCGCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGTTTCAC ACACGGTAAT ATGTCTTAGA ACAGTCAT ATGTCTTAGA ACAGTCAT AATGTCTCGT TGAACGCCC GAATTGTCAC GGATTGTAGA TCAGCACTCAC GAATTGTCAC CGAATTGTCAC CGAATTGTCAC CGAATTGTCAC CGATTAGAA CCGGTTAGAA TCAGCACTC ACGCACTCAC CGATTCACC CGATTCACC CGATTCACC CACCTCACC CACCT	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC CTGAAGGCCG GCTCGCCCTG GGAAGAAGA AGTGAAGAGA AGTGAAGAGA AGTGAAGAGA CAGCACGTCT ACCAATGAAA CCGGGGATCA ACCACCCTCT TCTGGGGTCAC TCTGGAGCTG AAAAGTTAAG GAACATTCAG AACTCAGCAT TTTCGGATCA ACCTCGCATA TTTCGGGATG AGGAGGCTGC CAGCAGGAGG GCCGGAAGTC AGGAGGAGTCA CACCACGCAG CACCAGGGAG GCCGGAAGTC GAAGCCTGC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGGCC CACAGGGCC CCGGGGACC CCCGGGGGCC CCCGGGGGCC CCCGGGGGCC CCCGGGGGCC CCCGGGGGCC CCCGGGGGACC CCCGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGGACC CCCGGGGACC CCCGCGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCGGGGACC CCCCCCCC	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1680 1740 1880 1980 2010
50 55 60 65 70	CACTAACGCT TCAAGGCTGG TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCGCGTGG GCGACCATGG GCCGATCGA TTGACTCCA CTGATCATAA TATCTGCAAG TGTTACTACC TCTGGTTCTCA AGTGCAACA TGTGAACA TGTGAACA TGTGAACA TGTGAACA AGTGCAACA ATCGTGTTGG CAATCAGA ATCATGAACA TGACTGTGGGG AAGCCGCACT GGCTACTGCCACT GGCTACTGCT CCAGGTGCTA TATGGCAAC TAATGGCAAC CACGTTCATCA AATGTGGAA GTTTCCATAG	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTGCCGAGG GATGGTGCAG GAGCGCCC TGCTCAGTGC AGGATCATCAC ATCTGAAAA ATGACATACAA ATCACACAC TAGGACTGT ACAGATACAA ATCACACAC TAGGACATGT TAGGACATGC TAGGCGTGGA ATGCGCAGCATGA CTCCATGA ATGCGCAGCA CTCCACCAGA CTCCACCAGA CTCCACCAGA CCACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CACTTGGACAC CCACTTGGACAC CCACCTGGACAC CCACCTGGACAC CCACCTGGACCAA ACAATGCCAT AAACCAGCC CGTGGCAAACT AAACCAGCC CGTGGCAAACT AAACCAGCC CACGCACCAA ACAATGCCAT AAACCAACCAT AAACCAACCAT CAAACAAACAA	21 CCCGGGCCAA AACGCGCGC TAGAAGAGCT TAGAAAATCC CGCTCGCCGG GCTGCCCGTG CTGCAGGCC CTCTGTTCGG AGAAGTGCTG AAATGAAGGT TGTCTCCCAA ACCAAACCTC TAAAACAGAG TAATCAAGTTCAG TAATCAAGTTCAG TAATCAAGTTCAG TGCAGAGCC CGTGACCTG GGGCTGTAGC GTACCCTG GGGCTGTAGC CATGACCTG CAGGAACTC CTGCAAACTC CTGCAAACTC CTGCAAACTC CTGCAAACTC CTGCAACTC CTGCAACTC CTCGAACACT CCCCCCTGCACCT CCCCCCCCCC	31 CTCGGACAGT GCGCGACGGC GCGCGCCCCCCCCCCCC	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA TCTGGATCCC TACAACGGGAA TCTGGATCCC TACAACGGGAA TCAGTCAGTCT ATGTCTTAGAA TGACTAGTCAGTCT ATGTCTTAGAA AGATCTGGA ATGTCTTGCC AATGTCTTGCC AATGTCTTGCC AATGTCTTCCC AAGCACACT AATGTCTTGGA ACAGCACT TGAAGCTTCT AGGGACCAC TCAGTCAGTA TCAGCAGTTG CGGTTCAGA TCAGCAGTTG ATGTCTTGCA CGGTTCAGAA CGGTTCAGAA TCAGCACTC AATGCCACCAC ACTGCCACCAC ACTCCATCTCCAC ACTCCATCTCAC ACTCCATCTCCAC ACTCCATCTCCAC ACTCCATCTCCAC ACTCCATCTCCAC ACTCCACCAC ACTCCAC ACTCCACCAC ACTCCACCAC ACTCCACCAC ACTCCAC A	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC GCTCGCCTG GCAAGGAAGA AGCAAAGAA GGAAACCCAC CTCTGGGTCAC CCAGCACGTCT ACCAATGAAA ACCACCTCT TGTGGAGCTG AAAAGTTAAG AACCACCTCT TGTGGAGCTG AAAAGTTAAG AACTCACGCATC AACCACTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACTCGCAAA TTTCGGGATG AGGAGGTGC CAGCAGGAGTG CTGTACCCTG GAAGCCTGCAC CCTGCACAC CCTGCACAC CTCTTCGGAAGTGCT CTGTACCCTG GAAGCCTGCA ACTCTGGGGAC CCCGGAGTGCC CCGGAGTGCC CCGGAGTGCC CCGGAGTGCC CCGGAGTGCC CCCGGGGGCC CCCGGGGCC CCCGGGACCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGATGTGGCC CCCGGGGGCCC CCCGGGGGCCC CCCACAAAGTGTC	120 180 240 360 420 480 540 660 720 780 900 900 900 1080 1140 1260 1380 1440 1500 1680 1740 1860 1980 2040 2100 2100 2100 2100 2100 2100 210
50 55 60 65 70	1 CACTAACGCT TCAAGGCTGA CCACTAACGCTT TCAAGGCTGA GCCGGTGGG GCGACCATGG GCGACCATGG GCCGATCAACA TTCGACTCCA AGTGCATCACA AGTGCAACA AGTGCAACA AGTGCAACA ATCATGAACA ATCATGAACA ATCATGAACA ATCATGAACA ATCATGACA CACTATGACA AGCCGCACT CACTGGGGG AAGCCCCACT CACTGGGGG AAGCCCCACT AGCCCTCACT CCAGGTGCTA TATGGCAACT AAATGTGGAAC GTTTCCATAC CACGTGTACA CACGTACA CACGTGTACA CACGTAC CACGTACA CACGTAC CACG	11 CTTCCTAGTC CTTGTGCAG AATGANAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCGCC TTGTCAGTGC AGCAGTACTAG ATGAATCATCC ATCTGGAAG ATGACATGA ATCACACAC CAAGAAGGCA CAGCACTGA ATCACACAC CAAGAAGGCA CTGCCCAGC CACTGGACAG CTCCATGG CTCCATGG CTCCATGG CTCCATGG CTCCATGG CTCCACGG CTGCACAGG CTTCCACCGG CCACTGGACAG CTGCCCCAG CCACTGGACAG CTGCACAGGAC CACTGGACAG CTGCCCC CGCCCTGGACGA CTGGGCGAC CCCCTGGACGG CCCCTGGACGG CCCCCCC CGCCCCGCCC	21 CCCGGGCCAA AACGCGCGC TAGAAGAGC CAGCAAACTC CGCTCGCCGG GTTGCCGGG GTTGCCGGG GTTGCCGTG AGAAGTGT TGTCTCCCA ACGGGATAT TGTCTTCCCA ACCAAACCTC TAAAACAGAGA AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG AGAGTTTCAG CACGCAGAC CGTGACCTC GAAACGAGG GAACGCGC CGTGACCTC CGGGAGAC CGTGACCTC CGGGAGAC CGTGACCTG CAGCAGC CGTGACCTG CAGCAGC CGTGACCTG CCGCGAGAC CGTGACCTG CCGCGAGAC CGTGCCGGAC CTGCCAGACT CCCCCTGCAG CCTCCAGAGGT CCCCCCGGAC CGTGCCGGAC CGTGCCGGAC CGTGCCGGAC CCTCGCAGACT CCCCCTGCAG CCTCCGCAGCG CCTCGCAGACT CCCCCTGCAG CATGCCGGAC CGTGCCGGAC CGTGCCGGAC CCTCGCAGACT CCCCCTGCAG CCTCGCAGACT CCCCCTGCAG CATGCCGGAC CGTGCCGGAC CGAATCGTCCGGAC CGAATCGTCCAG CATGCCGGAC CGAATCGTCAG CATGCCGGAC CGAATCGTCAG CATGCCGGAC CGAATCGTCAG CAGAATCGTCAG CAGAATCGTC	S1 CTCGGACAGT GCGCGACGGA CAGCGACAGCA AGGCGGCCCGAG CCGGGCCCGAG AGTGGGGACAGCA AGTGGGGACAGCA AGTGGGACAGCA AGTGGGACAGA ACTCATTGCA GCTCAAATT TCTGATTCAG AATGAAAGCT GCGAAGAAGCA ACCCTCAAGG AGCAAGGAAGA ACCCTCAAGG AGCAAGGAAG GCAACAGTTTT GACATGGACA TGGAGGAGAG CCCATGGTGT GGGGTTCGAAGT TGTGAACT CCCATGGTGT CCCATGGTGT CCCATGGTGC CACGAGTAGCA CCCACGAGCAGC CCACGAGCAGC CCACGAGCCGG CCACGAGCCT CCCACGAGCCT CCCACGCCT CCCACGACCT CCCACCACGAC CCCACGACCT CCCACACCC CCCACGACCT CCCACACCC CCCACGACCT CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACACCC CCCACCC CCCACACCC CCCACACCC CCCACCC CCCACCC CCCACACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACCC CCCACC CCCACCC CCACCC CCCACC CC	TTGCTCATTT CGCACACACA GCGGCCCTGG GACGCCCGGC GCTTATGGAA ACCGCTACACACACACACACACACACACACACACACACAC	ATTGCAACGG ACTGGCCTGGC CTGAAGGCCG GCTCGCCTGGC CTGAAGGCCG GCTCGCCTG GCAAGAAAA AGTGAAGAA AGTGAAGAA AGTGAAGAC TCTGGGTCAC TCTGGGTCAC CACCACGTTT ACCAATGAAA CCGGGATCA ACCACCCTCT TGTGGAGCT AAAGTTAAG AAGTTAAGAA ACTCAGCATCA ACACCCTCT TGTGGAGCT AAAAGTTAAG GAACATTCGGAAA CATCGGCAAA CATCGGCATG AGGAGGCTGC AGAGGATGT CTGTACCCTG GAAGCTGCC CACCAGGGAC CACCAGGGAC CTCTGGGGA CCTCTGGGAAG CCCGGAAGTCC TCTTACCCTG GAAGCCTGCA ACTCTGGGGA CACCAGGGAC CCCGGAAGTCC CTCTACCTG GAAGCTGCC CGGATGTGGAC CCCGGAGTGCC CGCAAAGTGCT TACCAATGCC CCCGGGGACC CCCACAAAGTGT TGGGGTTCAC TGGGGGACC CCCACAAAGTGT TGGGGTTCAC TTGGGGTTCAC CCCCACAAAGTGT TGGGGTTCAC	120 180 240 360 420 480 540 660 720 780 900 1080 1140 1200 1320 1340 1560 1740 1860 1920 1980 2160 2220
50 55 60 65 70	CACTAACGCT TCAAGGCTGG CTTTTTTAAA CCGGAGCTGA GCCCCCATGG GCGACCATGG GCTGATGAAG TTCGACTCCA TGTTACTACA TATCTGCAAG TGTTACTACA TGTTACTACA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TGTGCATCA TCCCATGACA TCCCATGACA TCCCATGACA TCCCATGACA TCCTGTTGG CCATTCACCA TCCTGTTGG CCATTCACCA TCCTGTTGG CCATTCACCA TCCTGTTGG CCATTCACCA TCCTGTTGG TCCTTGGGGA AGCCGCACT GGCTACTGCT TATGGCACT TATGGCACT TATGGCACT TATGGCACT TATGGCACT TATGGCACT CCAGGTGCTA TATGCACT CAGGTGCTA CACGTGTACT C	11 CTTCCTAGTC CTTGTGCCAG AATGANAGGC CTGCCGAGG GATGTGCAG GATGTGCAG CAGCGCCCC TTGTCAGTC TTGTCAGTC TTGTCAGTC AGAATCATCC ATTGGACAT ACAGAACAC CAGAGAGAA ATCACAACAC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGATGC TAGAGCACCG CTCCATGA ATCCCACGG CTACCAGGC CCACCCAAA CCGCCCAAA ACAACGC TCGGGGCCAA TCGGGGACTC GCAGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACTC TGGGGGAACCA TAAACCACCC TTGGACAACCA TAAACCACCC TTGGACAACCA TAAACCACCC TTGGGGGAACCA TAAACCACCC TTGGGGGAACCA TTGCGTGCCC TTGCAGTGCCC TTGCAGTGCC TTGCAGTGCCC TTGCAGTGCCC TTGCAGTGCCC TTGCAGTGCCC TTGCAGTGCC TTGCAGTGC TTGCAGT TTGCAGTGC T	21 CCCGGGCCAA AACGCGCGC TAGAAGAGC CGCTGCCGG GCTGCCGGG GCTGCCGGG GCTGCCGGG GCTGCCGGG CTGGTTCGG AGAAGTGCT ACGGGATAT TGTCTCCCT ACGGGGATAT TGTGTTTGAA ACTCTTCCCA ACCAAACCTC TAAAAGAGG TAATCAGGT AGTGTGGAA TATTCTGGAA TATTCTGGAA TATTCTGGAA GGGCTGTAGG GGACCTG GGGCTGTAGG GTACCCTG GAAGGTGT CAGGCAGAC CTGGCAGAC TGGGAACTCC CTGGAAGACT TGGGAACTCC CTGGAAGACT TGGGAACTCC CTGCAAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC CTGCAAGACT TGGGATCTGC CTGCAAGACT TCAAGGAGGT CCCCTGCAC CATGCCCGCAC CCGCACAC CCCCTGCAC CCGCACAC CCCCTGCAC CCGCACAC CCGCACAC CCGCCACAC CCCCCCCC	CTCGGACAGT GCGCGACGGA GCGGCGACGGA AGGCGGGCCGAGG AGGTGGGGCCGAGGA AGGTGGGGACAGT TCTGATTCGA GCTCGAAATT TCTGATTCGA GCTCGAAATT TCTGATTAGA GCGAGGAGAAGA AGCCTCAAGG AGGAGAAGA ACCCTCAAGG AGGAAGAAGA GCAAGGAAGA GCAAGGAAGA GCAAGGAAGA TTTTGCAT GCATGGGG GCACATGAGC CAGGTGTGAAG TGCAGGAGAAGA TTTTCTCGATTCGGG CCAGGTGTGAG TGCTGAGGAGAGAAGA TTTTCAAATGG CCAGGTGTGAG TGCTGCAGG CCAGGGCTGC CAGGCTGCG CCAGGCTGC CCAGGCTGCG CCAGGCGCG CCAGGGCAGC CCAGGGCAGC CCAGGGCAGC CCAGGGCAGC CCAGGGCAGC CCAGGGCAGC CCAGGGCAGC CCAGGGCGCC CCAGGGCTCC CCAGGGCACC CCAGGCACC CCAGCC CCAGGCACC CCAGGCACC CCAGCC CCACC CCC	TTGCTCATTT CGCACACACA GCGGCCGTG GACGCCCGGC AGCTGCTGCA GCGCCCTCCT GCTTATGGAA TCTGGATCCC TACAACGGGA GCAGCTAACA CAGCTCATAC ATGTCTTAGA ATGTCTTAGA ACAGTCATT AATGTCTTGT TGAACGCCC TACAACGGAAC ACACCACT AATGTCTTAGA ACAGCACT TGAAGCTCT TGAAGCTCT TGAAGCTCT TGGAGGACCAC TGGAGGACCAC TGGAGGACCAC TGGAGGACCAC TGGAGGACCAC TGGAGGACCAC TGTTTAACCT TGGAGGACCAC TGGAGGACCAC TGTTAACCT TGGAGGACCAC TGTTTAACCT TGGAGGACCAC TGATCTCAC TGGAGGACCAC TGATCTCAC TGGAGGTCTCAC TGAGGTCTCAC TCAATTCTCC TGAATTCTCC TCAATTCTCC TCAATTCCAC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCAATTCCAC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCAATTCTCC TCACTCC TCAATTCTCC TCAATTCC	ATTGCAACGG CGGGGGGAAA CGCGAGGGCT CCCGCTCGGC GCTCGCCTG GCAAGGAAGA AGCAAAGAA GGAAACCCAC CTCTGGGTCAC CCAGCACGTCT ACCAATGAAA ACCACCTCT TGTGGAGCTG AAAAGTTAAG AACCACCTCT TGTGGAGCTG AAAAGTTAAG AACTCACGCATC AACCACTCT TGTGGAGCTG AAAAGTTAAG GAACATTCGG AAGTCAGGAC ACTCGCAAA TTTCGGGATG AGGAGGTGC CAGCAGGAGTG CTGTACCCTG GAAGCCTGCAC CACAGGGACG CACATGGAC CCCGGAAGTC CTGTACCCTG GAAGCTTGCA ACTCTGGGAC CACAGGGCC CGGATGTGGAC CCCGGGACC CCCGGGACC CCCGGGACC CCCGGGACC CCCGGGACCC CCCGGGACCC CCCGGGACCC CCCGGGGCCC CCCGGGGCCC CCCGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGGGGCCC CCCGGACGCC CCCGGGGGCCC CCCACAAAGTGCT	120 180 240 360 420 480 540 660 720 780 900 900 900 1080 1140 1260 1380 1440 1500 1680 1740 1860 1980 2040 2100 2100 2100 2100 2100 2100 210

GGCCCCATICC GGCAGAGGA TACCAAGGT TTACCATAGGA GAACTCTOTA ACCARCTOT 2460 TOTOTTCTTC GTCCCAGAGTT TOTOCTTATA CACAAGGTT GACACTCTCT 2460 TOTOTTCTCT CACACAGTT CACAAGGTT TOCACACTCTC CACACACCACC 2460 GCCCCCCAGA CACCACCACACACACACACACACACACA								
TTTACANATA AGAGGACCAC CATTGAMAMA CTAAGGTTGT GORACAGCTC COGCCACCT 2580 COGCCGOTTC ACCTCTCCCC GAGGACATCT COCACCACCT GATAGGAM 2440 COCCCGOTTC ACCTCCCCC AGAGGACAT CCCAGGAGAT TOCTCCAGT TCAAATCTT 2740 CACATCACC CACCCCTCAA GAGGACAT CCCAGGAGAT TOCTCCAGT TCAAAACCT 2740 CACATCACCC CACACCCC TAAGGACCAC CACCCCCCCC AGAGCCCCCCAG 2840 CACATGGAGA CTGGGCTCCC CCTGGCACCC CTCAGACCTC CTCCCAGAT CCCCCCCCAGA CACCCCCAGGA CACCCCCAGGA CACCCCCAGGA CACCCCAGGA CACCCCCAGGA CACCCCAGGA CACCCCAGGACCCC CACCACACACA								
TTTACANATA AGAGGACCAC CATTGAMAMA CTAAGGTTGT GORACAGCTC COGCCACCT 2580 COGCCGOTTC ACCTCTCCCC GAGGACATCT COCACCACCT GATAGGAM 2440 COCCCGOTTC ACCTCCCCC AGAGGACAT CCCAGGAGAT TOCTCCAGT TCAAATCTT 2740 CACATCACC CACCCCTCAA GAGGACAT CCCAGGAGAT TOCTCCAGT TCAAAACCT 2740 CACATCACCC CACACCCC TAAGGACCAC CACCCCCCCC AGAGCCCCCCAG 2840 CACATGGAGA CTGGGCTCCC CCTGGCACCC CTCAGACCTC CTCCCAGAT CCCCCCCCAGA CACCCCCAGGA CACCCCCAGGA CACCCCCAGGA CACCCCAGGA CACCCCCAGGA CACCCCAGGA CACCCCAGGACCCC CACCACACACA		TGTCTTCTTG	CTGCCGGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
CONGROTTEC AACCITGICA GGCTCACCTC GGCCACCTTG GAAAAGGCCT GATAGGAAG 2200 GACATCAGCA GACCCCACCA GAGCACCACAT CCCCAGGAGAT TACTCACGAGT CACAAAGGCCT CACAGGACAT CCCCAGGAGAT TACTCACCAGT CACAAGGCCTCCCACC GCCACACAACT CCCCAGGAGAT TACTCACCAGT CACAACTCACCACC GACACCACCACC GCCCACCACACC CCCCAGGACACC CCCCAGGACACC CTCCGAGCACC CTCCGAGCACC CTCCGAGCACC CTCCGAGCACC CTCCGAGCACC CTCCGAGCACC CTCCGAGCACC CTCCGACCACC CTCCACCACCACC CTCCGACCACC CTCCACCACCACCACCCCACC								2580
CCGCCAGATT CCTACCCACC GAAGGACAT CCCAGGAGAT TECTCAGGG TCAGATCTT 2760 GAATGAGGA GACCCTCAA GTCCCTACATA GTCCCTCAGC CCAGATCACT CTACCCAGT 2760 CTTCCTCCCC TCACCCGGGC CCCACGTGGA CCCACGTGGC CCAGATCAC TCACCCAGT 2760 CTTCCTCCCC TCACCCGGGC CCCACGTGGA CCCACGTGGCC CCATCAGGCC CCATCAGGCC CCACGTGGACC CCAGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGGCC CCAGGGCC CAGGGCC CCAGGGCC CCAGGGCCCAGGCC CCAGGGCC CCAGGCCC CCAGGGCCC CCAGGGCCC CCAGGGCCC CCAGGGCCC CCAGGGCCC CCAGGGCCCCAGGCCC CCAGGGCCC CCAGGGCCC CCAGGGCCC CCAGGCCCCACGCCCCACGCCCCCCCC								
GRAPTCHICCE TEACCECTCAA GGGCTTAAT GTCCCTCAGC CCCATCAAC TCACCAGCT 2760 CTTCCCCCC TTAGGCAGG CCCAGGGGACC TGTAAGCCAA CCCTCCCCCC 2820 AAGCCTGCAC TTAGGCAGG CCCAGGGGACC TGTAAGCCAA CCCTCCCACC 2820 AAGCCTGCAC TTAGGCAGG CACAGGGACC TGTAAGCCAA CCCCCCCCCC	_	CGTGGCTTCC	AACCCTGTCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GAIGAGGAAG	
GRAPTCHECC FICACCECTANA GROCCTTANG COCARTENA CTACCACATE 2760 CTOCCCCC TRAGECAGE COCARGERAC TOTALOCCAN COCARGE CONTECCACE 2810 ADOCTRICAC TRAGECAGE COCARGERAC TOTALOCCAN ACCECCTO ADMICTET 2810 COCACACAC TRAGECAGE CACAGGRAC TOTALOCCAN ACCECCTO ADMICTET 2810 COCACACAC TRAGECAGE CACAGGRAC TOTALOCCAN ACCECCTO ADMICTET 2810 COCACACAC COCACACAC CACACACAC CACACACAT TOTALOCCAN 3000 GROCCCAGAT CACACACAC CACACACACA ACTIVATA TACACACACA 3000 GROCCCAGAT CACACACACA CACACACACA ATTIVATA TACACACACA 3000 GRATITITI TANITITAN ACATALITA CITALOCTAG GITTITATA CACACATATA 13120 GRATITITI TANITITAN ACATALITA CITALOCTAG GITTITATA CACACATATA 13120 GCAGAATOTI GATTACACTI COCACAGACAT TITALOCTAC CACAGTATA TATALITATI 31240 CACACACACACACACACACACACACACACACACACACA	2	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2700
CTTCCTCCCC TCACCGGGGC CCAGGGGCA CTAGGGTCC TCTCCAGACC CTTCCGAMC CCTCCCCCAGACCCCCTCCAGACCCCCCCCCCCCCCCC		GACATCAGCA	GACCCCCCAA	CCCCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
AGGCTGGAC TTAGGCAGG CONGGGACC TGTAAGCCAAA ACCCCCTCAG ASAGCCTCTCAGACTCTCAGCCTCAGACTCTCAGCCTCAGACTCAGCCCAGACTCAGCCCAGACTCAGCCCAGACTCAGCCCAGACTCAGCCCCAGACTCAGCCCCAGACTCAGCCCCAGACTCAGCCCCAGACTCAGCCCCAGACTCAGCCCCCAGACTCAGCCCCCAGACTCAGCCCCCAGACTCAGCCCCCAGCCCCCCACACTCAGCCCCCAGCCCCCAGCCCCCCAGCCCCCCAGCCCCCCAGCCCCCC		GAGAICAGCA		COCCIONI	0100010100	QQQQQQQQ	COTTCCCTACCC	
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CONTROLATE CICTOGCAGA ACANCTOGG CICACTCATG CCTIGGCAGA SACCCAGGA 2940		AAGCCTGCAC	TTAGGCAGGC	CCAGGGGACC	TGTAAGCCAA	ACCCCCCTCA	GAAGCCTCTG	2880
CANTIGGRADA CTGGGCTCCC CTCGGACCC CTCGGACTC TCCACATA TCCACACA 3000 TGAAGGCAGA AGTTTGCACT ATCTTTCACC TCCATTGCAC TGAAGGCAGA AGTTTGCACT ATCTTTCACC TCCATTGCAC TTTTCACCT TGAAGGCAGA AGTTTTCTCAC TCCATTGCAC TCCATTGCAC TTTTCACCT TCCATTGCAC TCCA		COTCOLOREC	Officer Court	BACKACTCCC	CTCACTCATC	CCTTCCCCCAG	GACCCCAGGA	2940
GTGCCCAGAC GCCTATATT AGGGAGAGA GTGCACCTT TITTCAACG 3066 GARTTTTTT TAATGTTTAA AACATCATTA TATGTTTAA AACATCATTA TATGTTTAA AACATCATTA TATGTTTAA AACATCATTA TATGTTTAA TATGTTTAA AACATCATTA TATGTTTAA TATGTTTAA AACATCATTA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAA TATGTTTAAC TATGTTAACATTA TATGTTAACATTAAAAAAAAAAAAAAAAAAAAAAAAAAA	10	CCIGCAGAIC	CICIOGCCAG	MACMACICOG	CICACICAIG	CCLIGGCCNO	OACCCCAGGA	
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TGANGACGA AGITTICACT ATCTITCAGC TCCGTTGGA GTTTTTTGTA CAACTTTTA AJAGAC TTGACACTAC TOCGTCGAT 13120 GCGTGTGTGT GCTATGGTGC TCTGTCTACT TGCACGGTA CTGTAANT ATTAATTAT CCATGGCAGG AAGGCTTGTT GCACGGTA CTGTAANT ATTAATTAT ATGGCAGAACTTC GCACAGGTA GTTTTTGCTT CGACAGGTA ACCTGAANT ATTAATTAT ATGGCAGACTTC GCACAGGTA GTTTTGCTT CGACAGGCA CTGTAANT ATCTGCTTC ACGGCAGG AAGGCTTGTT GTGCTTTTGTT CTGATCAGG CCTTATGGA ACCTGAANT ATCTGCTCC CCACCACACCC CCACCTGTGC CTGACGAGCA AACCTGAAAT ACCTGACAC CCACCACACCC CCACCTGGAGCA CTGACCACACACACACACACACACACACACACACACACAC		GTGCCCAGAT	CCACCCACAC	CCCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
15 GCGGGATGTTT TANDSTTAN ANCASCATTA CTATANGANC TYTUACCTAC TOCCOTOCS 1180 GCGGATGTT GATTACAGTG CAGGGCGTA CTAGTAGGCAT TYTTACAAT ATTATATTAT 1300 ACCORDER ANGAGCAT GATGGCAG ANGAGCTTGT GATTACAGTG CAGGGCAG ANGAGCATTAT CAGGGAT TITTAGGAT ACTAGGAT 1420 CCAAGGATGT GGACGAGAAC CAGGGATTAT GATTACAGTG CAGGGATGT GATGGCAG ANGAGCATC CAGGGATGT 1420 CCAAGGATCAC CAGGGATGT CAGGGATGC CAGGGATGT 1420 CCAAGGATGT CAGGGATGCAC CAGGGATGT 1420 CCAAGGATGT CAGGGATGCAC CAGGGATGT 1420 CCAAGGATGT CAGGGATGT 1420 CCAAGGATGT CAGGGATGT 1420 CCAAGGATGT 1420 CCAAGGATGT CAGGGATGT 1420 CCAAGGATGT		OTOCCCAGA1			maga ammaga	Ommonmoom's	CCAACCOOCA	
15 GCGGTGCGGG GCTATGGTGC TCTGTCTACT TGCALGGGGT CTGTAAATT ATTAATTAT 1240 CAGAGATGT GTTAAAGTG CATGGCAGG AAGGCTGGT GTGCTTTAAG TATTTAGTG AACTCAACA CAGAGATGT GTGCTTTAGTGCAGG CTATTTAGTGA AACTCACAC CAGAGATGT GTGCTTTAGTGCTT CTGACAGAGG CAACACATTATTAGTAGA AACTCACACACACACACACACACACACACACACACACA								_
15 GCGGTGCGGG GCTATGGTGC TCTGTCTACT TGCALGGGGT CTGTAAATT ATTAATTAT 1240 CAGAGATGT GTTAAAGTG CATGGCAGG AAGGCTGGT GTGCTTTAAG TATTTAGTG AACTCAACA CAGAGATGT GTGCTTTAGTGCAGG CTATTTAGTGA AACTCACAC CAGAGATGT GTGCTTTAGTGCTT CTGACAGAGG CAACACATTATTAGTAGA AACTCACACACACACACACACACACACACACACACACA		GGATTTTTTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTCAGT	3180
15 GCAGANTSTT GNTTACAGTS CAGTGGGSTS TAGTAGGCAT TITTACCATC ACTGAGTTTT 3300 ATGGGATCT GGACAGGATS TATTAGTAM ACTGGATT 3300 ATGGGATCT GGACAGGATS TATTAGTAM ACTGGATTA ATGGGATCT GGACAGGATS TATTAGTACA AGAGATCC CACACTTAGT TITTAGTACA AGAGATCC CACACTTAGT TITTAGTACA AGAGATCC CACACTTAGT TITTAGGTACA AGAGATCC CACACTTAGT CACACTTAGTACA GGCCAGAGCAC CACACTGACA AGACTCCAC GACAGATCACAT TATTAGGATA AGACTCACAG GACAGACACAT AGACTCACAG GACACACACAT TATTAGGATA AGACTCACAG GACACACACAT TATTAGGATA AGACTCACAG GACACACACAT TATTAGGATAGAT 3400 AGACTCACAG GACACACACACAT TATTAGGAT AGACTCACAGA AGACTCACACACACACAT TATTAGGAT GACACACACACACACACACACACACACACACACACACAC								3240
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ATGGGATTCT GARCAGGATG TITTAGTTC CHARTCAGG CTATATEGA AMGCASTCC 3420		CCATGGCAGG	AACCCTTCTT	CTCCTTTTAG	TATTTTAGTG	AACTTGAAAT	ATCCTGCTTG	3360
CCARGTHACT TITCGGATA COCCATICA GEOCOAGGC NAGAGAITC CAATTACAAT 3480 1000								
CTCAGTTGAT TITCTGGATT COCCATTCTCA GGCCAGGCAG AGGGGGGGGGGGGGAGGAGAGAGAGA								
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1000 1000		CTCACTTCAT	ምምምምም	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
ACACCTOGGA GAANTCTGC TICTGCCAG GAAGCTTGT GAGAACTG GATTCCAGACA AGACTTTA AGACTGTAGAC AGACTGCAGAACT TOTACCAGATAT AGACTGCAGACTCT TOTACCAGATAT AGACTGCAGACTCT TOTACCAGATAT AGACTGCAGACTCT TOTACCAGATAT AGACTGCAGACTCT TOTACCAGATAT AGACTGCAGACTCC AGACTGCT TOTACCAGACTCC CAGACTCCT TATACCACTA AGAACTCCACACACTCCAGACTCCAGACTCCAGACTCCCAGACCTCCAGACTCCATTCCAGCTGCAGCACCACACTCCAGACCTCCACACCCCAGACCTCCACACCCCAGACCTCCACACCCCAGACCTCCACACCCCACACCCCACACCCCACACCCCACACCCCACA	20	CICAGIIGAI	TITCIGGATI	ccccarcrar		MC-0100011	COMOCON CCC	
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AGGARCTIA AGGTURACC ACACCAGGAT AGGACTIGA ACACTAGACA AGCCAGACT TIGACCAGAC GRIGACATOT TIGAGAGGG TETURAGAT CACTCAGGG GRIGCTIGAT AGAARGCCA AGCACTICTI TITICAGAGGGG TETURAGAT CACTCAGGG GRIGCTIGAT AGAARGCCA AGCACTICTI TITICAGAGGGG TETURAGAGGAGGGG CACAGACCAC TACCAGCACCC ARCTGAGGAGGAGGGG TETURAGAGGAGAGGGGG CATAGACCATTA ACCAGATCTA GRAAAGAGGA TETUCATIGA GACACTACACA AATTAGGCGA ACTGATCAGA AGACTGAGGAGA TITCCAGAGA ACCACACACA TITTAGAGCA AATTAGGCGA ACTGATCAGA GACAGAGGGG TETUCATGAGA ACCACACACAT ATTATAGACCA AATTAGGCGA ACCACTACTA GACACACACA TACACCACA ACTGATATAA AATTAGGCGA ACCACACTA ACCACACACACACACACACACACACACA		ACACCTGGGA	GAAATCTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
25 GENERAL CARGO CONTROLLANCE CONTROLLANCE CARCATTECT TITETCENCET CECTITETCA GACACTICAS 3840								3720
25 CGGTGCTGAT AGAAAGCCA AGCACTTCTT TTTCCGGTG TCCTTTCTAG AGCACTGCCA 3840 CCGCAGGCGCCC ATACTGCTTG GAGAGGTGG TGTTCTGTA AGAACCTGCCAGAGGCA AGCGGTAGATA 3960 CCGCAGACCCC CACCTCCCT ATACTGCTTG GAGCTAGGCA AATGACCACA AACTGTATATA 3960 CATACTACT ATACTGCACA AGCGGTAGAGA ATTCACACCA AACTGTATATA 3960 AATTAGGCAGA ACTGTTATAG CTTGCAAAAA CTTCATTACTG GAAGGTTCA ACTTATTACACACA TATATAGGCAGA ACTGTTTATACACACA ACTGTATATACACACA TATATAGGCAGA ACTCTATATAC CTTGCAAAAA CTCACACCACAC								_
CONGRAGGIT ATTITAGCTITG GANAGGIGS IGTITCTGITA AGANACCIAC TGCCCAGGCA CICANACCIC CACCTCCCT ATACTGCTGTG GACTGAGGA ANTOCACCAA AACTGTATATA CAATGACCCT GATTICAGAC AGATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG TGAACCATTA ACCAGACTA GATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG AATTAGGCAG ACTCTTATAG CTGACAAAA CTCGATATAC AATTAGGCAG ACTCTTATAG CTGCAAAAA CTACAACCAA TGGAATGGA ACTTATTACAC ACCTATTCT TAGCTCATC ATATATCGTA GATATTGGAC AACGAACTA CTCTCATGGGG CATCCTCTT TTCCAACTTG GCTGCAGGAA TCTTTAAAAA AAGAACATC CTCTCATGGGG ACCTATTCT TAAACACTTC CAACCTACCT GTTGGGCATC ACGAGATGGA TATAGGGAATA CCATTGCTT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGGA TATAGGGAATA CCATTGCTT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGTG TAAAGGACATT CAACTTGCATT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGTG TAAAGGACAAT CCAGCACGGA ACCTTCACAGA AACCACACTT ACACGAGACTT TAAAGTGACT CTGCACTGT TATCACATTA GAGAGCAATT GACACACAGTT AACTACATCA CCTGCAGTGT TTTATGAGAAA AATACTCAGA TAAGGTAAAA TGCCATGGAGA CCTTCACCAT TTCACATTA GAGAGCAATT GACACACAGTT AACTACACAC AACACACA AAAAGGGAAC CCCAGCTCAA AACAACACAC AACAACACACA AAACAACAC AAAAAAAA								3780
CONGRAGGIT ATTITAGCTITG GANAGGIGS IGTITCTGITA AGANACCIAC TGCCCAGGCA CICANACCIC CACCTCCCT ATACTGCTGTG GACTGAGGA ANTOCACCAA AACTGTATATA CAATGACCCT GATTICAGAC AGATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG TGAACCATTA ACCAGACTA GATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG AATTAGGCAG ACTCTTATAG CTGACAAAA CTCGATATAC AATTAGGCAG ACTCTTATAG CTGCAAAAA CTACAACCAA TGGAATGGA ACTTATTACAC ACCTATTCT TAGCTCATC ATATATCGTA GATATTGGAC AACGAACTA CTCTCATGGGG CATCCTCTT TTCCAACTTG GCTGCAGGAA TCTTTAAAAA AAGAACATC CTCTCATGGGG ACCTATTCT TAAACACTTC CAACCTACCT GTTGGGCATC ACGAGATGGA TATAGGGAATA CCATTGCTT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGGA TATAGGGAATA CCATTGCTT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGTG TAAAGGACATT CAACTTGCATT ATCAACTTC CAACCTACCT GTTGGGCATC ACGAGATGTG TAAAGGACAAT CCAGCACGGA ACCTTCACAGA AACCACACTT ACACGAGACTT TAAAGTGACT CTGCACTGT TATCACATTA GAGAGCAATT GACACACAGTT AACTACATCA CCTGCAGTGT TTTATGAGAAA AATACTCAGA TAAGGTAAAA TGCCATGGAGA CCTTCACCAT TTCACATTA GAGAGCAATT GACACACAGTT AACTACACAC AACACACA AAAAGGGAAC CCCAGCTCAA AACAACACAC AACAACACACA AAACAACAC AAAAAAAA		GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTTCTAG	AGCACTGCCA	3840
CRICHACCG CACCTCCT ATACTGCTTG MACTGGACA ANTICACCACA ANCTGTATATA ACTACTCT TATACTCAGA ACATGAGGAC TITCCATGGA ACCACACATA TITTCAGATGA ATTAGGCAG ACTACTATA CACAGATCTA GRANICANA TCTGTTTACT GCAAGATTA ACTATTACAC ANTIAGGCAG ACTOTATAG CTTGCAANA CTCACACCACA TAGAACTATATACA ATTAGGCAG ACTOTATAG CTTGCAANA CACACACACTA TATATTAGGAAG ACCACACTATA ACTATTACACCACA ACCATTCTTA TOCACTAG GCTGCAGAGA ATGATTTTACAGA AGGATGTGA ACAGAATGA ACCACACTGACACACACACACACACACACACACACACACA	25	COLOUI COM	A MONTH A COMMO	CONNECCTO	memmercury.	ACA A A COTTAC	TOTOCACOOA	3000
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CANTGATCCT GTATTCAGAC AGATGAGGAC TTTCCATGGG ACCACACTA TTTTCAGATG TGAACCATA ACCAGACTA GTGATCAGA GTGGTTACT GCAGGGTCTA ACTITTAGA 080 AATTAGGCAG ACTCTTATG CTGCCAAAAA CTACAACCAA TGGAATGTGA ACTTTCAGG 140 CATCGCCTTT TTCCAACTG GCTGCAGGAA TCTTTAAAGA ATGGCTTAAA CACGAGTCTGA 120 ACTAGTCCT TTTCCAACTG GCTGCAGGAA TCTTTAAAGA ATGGCTTAA CACGAGGTCTGA 120 CACTGCTCTT TTCCAACTCG CACCTACCT GTTGAGGACT ACCAGGAGT 120 CACTGCTCT ATCAACTTC CAACTAACTA GAGGAGTCTA CACGAAGTAC ATAACACTTA CACGAGGACT 120 CACTGCTCT AACACTTG CACACTACCT GTTGAGGACT ACCACTACTC TAAATGACCT 120 CACTGCTCT AACACTTC CAACTAACTA GACGAGTCT CACAGGAGCA 120 CACTGCTCT AACACTTCC TAAATAATAT GAGAACTATC ACCAGAGTCT AATAGACTTG CACAGAGCCT TAAAGACTAC 1400 CACGACTGC TTCCAATTAC GACCAACCT ACCACTACCT 120 CACGACTGC TTCCAATTAC GACCACACCT 120 CACGACTGC TTCAAATTAC GACCACACCT 120 CACGACTGC TTCAAATTAC GACCACACCT 120 CACGACTGC TTCAAATTAC GACCACACCT 120 CACGACTGC TTCAAATTACAA AACACAACA 120 CACGACTGC TTCAAATTAC GACCACCTCC TTCAACGGT 1400 CACGACCACC AACACAAACA 120 CACCACACACA 120 CACCACACACACA 120 CACCACACACACA 120 CACCACACACA 120 CACCACACACACA 120 CACCACACACACA 120 CACCACACACACA 120 CACCACACACA 120 CACCACACACACA 120 CACCACACACACACA 120 CACCACACACACACA 120 CACCACACACACACACACACACACACACACACACACAC		CTGCAAACCG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTAATA	3960
TGAACCATTA ACCAGARTICA GTCATCANG TCTGTTACT GCAAGGTTCA ACTTATTACG 4810 ATTAGGCCA ACCTITATC CTTGCAACTA CTACATCAA TGGAATGTCA GTGTTACTGG 4140 CATCCTCTTT TCCAACTG GCTGCAGGAA CTCTTAAAGA ATGAATCTTA CAGAGTCTGA 4260 ACCTATTCT TAAACACTTC CACCTACCT GTTGGACATC ACCAGATGT ACCAGTGCTA 4260 ACCTATTCT TAAACACTTC CAACTACCT GTTGGACATC ACCAGATGT ACAGAGTCTGA 4260 CACTGCTT ATACACTCC TAAATATATA GGAATTGGA TAGAGAACT 43260 ACCTGTCTACACTC TCAAATATCA GAGATCTCAAAAA ATGCCTTATAA CAGAGTCTT 4AAAGGAAT 43260 CTCTTCACTC TCAAATGCC TAACTAGGGA GCCATGTTC ACAAGGTCT TAAAGGAAT 4380 CTCTTCACTC TCAAATGCC TAACTAGGGA GCCATGTTC ACAAGGTCT TAAAGGAAT 4380 CTCTTCACCACT TTCAAATTA GAGAACAATT GACAACAGTT ACAATATCA CCTCTGATCT 4500 CTGGACTGGT TTCACAATTA GAGAACAATT GACAACAGTT ACAATATCA CCTCTGAGTCT 4500 TTATCACAAGA ATCTTGGTT GCCTTCCAGA AAAACACAGT ACCATGAAAAAC ACGAGAACAC AAAAGGGACAC AAAAGGGACAC AAAAGGGAAC ACAAGGTTCAC ATGACTATGA TACACTATCA ACCAGGAACAC AAAAGGGACAC AAAAGGGACAC AAAAGGGAAC ACAAGATTACA TACACTATGA GTGCGAAAAA AACACACAC AAAAGGGACAC AAAAGGAATA AACACACACA AAAAGGAACAC AAAAGGGAAC TAACTTAGAT TACACTATGA TGCTGGTAAAA AAACACACAC AAAAGGGACAC TAACTTAGAT TACACTATGA TGCTGGTAAAA AAACACACAC AAAAGGGACAC TAACTTAGAT TACACTATGA TGCTGGTAAAA AAACACACAC AAAAGGAACAC TAACTTAGAT TACACTATGA TGCTGGAAAAA AAAAAAAAAA		CAATCATCCT	GTATTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTCAGATG	4020
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ATARGTICAT GICTICTATIC ATTATTICGTA GARATTIGGAA AAGAACCTI CTCTATGGGG 4260 CATCACTCTIT TICCAACTIG CGTCGGGGAA TCCTTTAAAGA ATGCTTATAA CAGGGTCTGA 4260 ACCTATTICT TAAACACTIC CAACCTACCT GTTGGACATC ACGGATGGA TCACCTAGA 4260 ACCTATTICT TAAACACTIC CAACCTACCT GTTGGACATC ACGGATGGA TCACCTAGA 4360 CTCTTCACTC TICCAACTG CAACCTACCT GTTGGACATC ACGGATGGA TCACCTAGA 4360 CTCTTCACTC TICCAACTG CAACCTACCT GTTGGACATC ACGGATGGAT ACATAGGAAAT 4360 CTCTTCACTC TICCAATTA GAAACACAGTT ACATAGTCAT CCTCTGACTT 4500 CTGGACTGGT TTCTACAATTA GAAGACAAAT TAAGGTAAAA ATACCCACAA TAAACTCACAA ATACCTCACAT CCTTTGATAC CCTCTGAGTCT 4500 TTTATCACAGAA ACCTCTCTTT TGGGGTCACA CATTTTCCAT TGCTTTTCACA TGCTTTCACA TGCTTTCACA CAGAAAATA 4620 TTTATCTCAATA GTTATTAGGA CATAGTATTC ATGCTATCAC TGCTTTTACA CAGGAACACAC 4680 ACACACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA								
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AACTRICAT ATCAACTICC TRATATATAT GRAGATGGC TTGGGCAGCA TCCCCTTGAA 4380 CTCGTCACATC TTCAAATGCC TGGCTAGGGA GCCATGTTC CAAAGTGCT TAGATGGCCT 4500 AATGGCATGG TTTCAAATGCC TGACTAGGGA GCCATGTTCT CAAAGTGCAT 4500 CTGGACTGGT TTTCACATTG GAGACCAATT GACAACAGAT ACCTAAATTCA CTCTGGTGT 4500 TTATATGAGAA AGCCTTCTTT TGGGGTCAAC AGTTTTCCTA TGCTTTGAAA CAGAAAAAT 620 TGTACCAAGA ATCTTGGTTT GCCTCCAGA AAACAAACT GCATTTCACT TTCCCGGTGT 4600 AAACACACCA AAAGGGAAC CCAGCTCTAA TACATTCCAA CACTTAGAA ATCACTCTAT 4700 AAACACACCA AAAGGGAAC CCAGCTCTAA TACATTCCAA CTCGTTATAGA CACCTGGTAC 4800 TTATTCTATA GATACTGATT TCTTTAAAAT GTAAAGCCAT GCTGGTAAAT ATCACTCTAT TACATTCCAA GACATCGTT 4800 TTATACTATA TAAAAGGGTT TACAGAATTT TATGGTGCAT TAGTGCAAACAAA AAAAAACA ACCAAAAAAAA AA Seq ID NO: 78 Protein sequence Protein Accession #: NP_003465 1		ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
TCTITCACTIC TICAMATGCC TGACTAGGGA GCCATGTTIC ACAGGGTCT TAAAGTGACT 4440 ANATACAMA ANATACTAGA TAAGGTAGAMA TGCATGGATG CCTCTGTCTT 4560 TTTATGGAT AGCTTCTTT GGAGGTAATA GAACACAGTA ACATAATTCA CTCTGAGTGT 4560 TTTATGGAA AGCTTCTTT TGGGGTCAAC AGTTTTCCTA TGCTTTGAAC AGAAAAAATA 4520 TGTACCAGAG ATCTTGGTTT GCCTTCCAGA AAACAAACT CAATAATTCA TTCCCGGTGT 4680 ACACACACCAC AAAAGGGAAC CCAGCTCTAA TGCATTCCAA CTCGTATAGC ATCACTGTGA 4680 AGATACATAC AAAAGGGAAC CCAGCTCTAA TGCATTCCAA CTCGTATAGC ATCACTGTG 4860 AGATACATAC AGAATTCATG TAACTGATAT ACACTTCCAA CTCGTATAGC ATCACTATAG 4860 AGATACATAC AGAATTCATG TAACTGATAT ACACTTCAAA TCCATACAAA AAAAAAAAAA								4300
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ATTGGATGG GAAATACAAA AATACTCAGA TAAGGTAAAA TGCATGATGA CTCTGTGTT 4500 CTGGACTGGT TTTCACATTA GAGAGCAATT GACAACAGAT ACATAATTCA CTTGAGTGT 4550 TOTACCAAGA ATCTTGTTT GGGGGCAAC AGTTTTCCTA TGCTTGAAAC CAGAAAAATA 4620 TOTACCAAGA ATCTTGTTT GCGTCCAGA AAACAAACT GCATTCACT TCCCGGTGT 4680 TCCCCACTGT ATCTAGGCAA CATAGTATTC ATGACTATGG ATAAACTAAA CAGGTGACAC 4740 AAACACACCA AAAGGGAAC CCAGGTCTAA TACATTCCAA TGCTATAGC ATCACTCTGT 4800 TTATTCTATA GTATTTACTT TCTTTAAAAT GTAAACCCAT GCTGGAAAAT AAATCTGCTG 4860 AGATACATAC AGAATTACTG TAACTGATTA ACACTGCAA TGCATAACA ACACAACATA 4920 TATATACTAT TAAAAAGGTT TACAGAATTT TATGGTGAT TTGTACTAAG GCCAAACATA 4920 AGATCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCCT CCAATTATAA GAGGATAGA 4920 AGATCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCCT CCAATTATAA GAGGATATGA 5040 **Seq ID NO: 78 Frotein sequence Protein Accession #: NP_003465 1		CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
CIGGACTGGT TITCACATTA GAAGACAATT GACAACAGTT ACATAATTCA CTCTGATCA 4520 TITATGAGAAA AGCCTTCTTT TGGGGTCACA GATTTTCTTA TGCTTTGAAAAAAAAAA	35	AATCCCATCA	GAAATACAAA	ANTACTCAGA	TAACGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
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TOTACCAGGA ATCTIGGITT GCCTCCAGA AAACAAACT GCATTTCACT TCCCGGGGAC 4740 TCCCCACGG ATACTAGGACA CATAGGATTC ATACATCAGA CACGGGACA 4740 TACATCCACAGA ATCTITAGAT TCTTTAAAT TACATTCCAA CTCGTATAGC ATGCATCGTG 4860 AGATACATCA AGAATTCTG TACATGATTA CACTTGGAAAT AATACTGCTG 4860 AGATACATCA AAAAGGAT TACAGAATTT TACAGTGCAT TGCCGTATAGC ATGCATCTGT 4860 AGATACATCA AGAATTACTG TACACTGATTA CACTTGGTAA TGCTGCTAA AATACTGCTG 4860 ACACAAAAAA AAAAAAAAA AA Seq ID NO: 78 Protein sequence Protein Accession #: NP_003465 1 11 21 31 41 51 MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVSASVRSG DLWIPVKSFD 660 SKNHEPVLNI RLQRESKELI INLERNEGII ASSETETHIL QDGTDVSLAR NYTVILGRCY 120 NSKNHEPVLNI RLQRESKELI INLERNEGII ASSETETHIL QDGTDVSLAR NYTVILGRCY 120 SHRNTPNLAA KNYPPPSGT WARRHKRETL KATKYVELVI VADMREPGRQ GKDLEKVKQR 240 DNAQLVSGVY FQGTTIGMAP IMSNCTADOS GGIVMDHSDN PLGAAVTLAH ELGHRFGMN 360 DTLDRGGSGQ MAVEKGGGIM NASTGYPFM VYSSCSKEDL ETSLEKMGWG CLULERSH 300 ACRDSSNSCD LPEFCTGASF HCPANVYLHD GHSCODVBY CNNGLCCHAGG 440 ACRDSSNSCD LPEFCTGASF HCPANVYLHD GHSCODVBY CNNGLCCHAGG 540 ACRDSSNSCD LPEFCTGASF HCPANVYLHD GHSCODVBY CNNGLCCHAG 450 ARCAGGGAATG NASTGYPEN PYSSCSKEDL ETSLEKMGWG CLULERBET 650 ARCAGGGAATG RLLQCCNOUT SRPLINGLINV PQGTGVRUP PLARPARS PRELIDENT AGAGGATT CACCTTAGG GAGAAAAGGA AGAGGGGGA AGAGGGGGA AGAGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGGAG AGAGGGGAGA AGAGGGGGAGA AGAGGGGAGA AGAGGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGACCA AGAGAGATC CAGAGGAGA ACCAATGTT GCCGAGGGAGA AGAGGGGGAGA AGAGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGGGAGA AGAGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGGGGAGA AGAGGG								
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AAACACACA AAAAGGGAAC CCAGCTCTAA TACATTCCAA CTCGTATAGC ATGATTCTTT 4800 ATTATTCTATA GTATTAAAGT TCTTTAAAAT GTAAAAGCATA GCTGGAAAAT AATACTGCTG 4860 AGATACATAC AGAATTACTG TAACTGATTA CACTTGGTAA TTGTACTAAA GCCAACATA 4920 AGATGCCCAA ATCCTTAGT TCAGGATTT TATGGTGCAT TACGTGGGA TTGTCTTTTT 4980 ACCAAAAAAA AAAAAAAAAA AA Seq ID NO: 78 Frotein sequence Protein Accession #: NP_003465 1 11 21 31 41 51 MAARPLPVSP ARALLLALAG ALLAPCEARG VSIMNEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPSVLMI RLQRESKELI INLERNEGLI ASSTTETHYL QDGTDVSLAR NYTVILGHCY 120 YHCHVRGYSD SAVSLSTSCG LRGLIVERNE SVLEPMKSA THRYKLFPAK KLKSVRGSCG 180 SHRNTPNLAA KNVPFPPSOT WARRHKRETL KATKYVELVI VADNREFORQ GKDLEKVROR 240 DTLDRGCSCQ MAVEKGGCIM NASTGYFFFM VFSSCSKRDL ETSLEEGMGV CLENLERVRS ACRDSSNSCD LPETCTGASP HCPANYVLHD GHSCQVDVBY TSLHEFLDWR KMKLLPRKSH 300 AKDASSNSCD LPETCTGASP HCPANYVLHD GHSCQDVDBY CMGICQTHE GQCVTLWBGT 480 AKDASSNSCD LPETCTGASP HCPANYVLHD GHSCQDVDBY CMGICQTHE QQCVTLWBGT 480 AKDASSNSCD LPETCTGASP HCPANYVLHD GHSCQDVDBY CMGICQTHE QQCVTLWBGT 480 AKDASSNSCD LPETCTGASP HCPANYVLHD GHSCQDVDBY CMGICQTHE QQCVTLWBGG 540 AKDAFGICER RWNSAGDPY NCGKVSKSSP AKCRNDAKC GKICLNRQCO NISVFGCHAC 240 AKDAFSVEK KRULIRLIFT NKKITIEKER CVRPSRPRG FOPCQAHLDH LIGKSLMRKPP 780 DSYPKONDR RLLQCONVDI SRPLNGINUP GPGSTORVLP PLBRAPRASP VPARPLPAKP 840 DSYPKONDR RLLQCONVDI SRPLNGINUP GPGSTORVLP PLBRAPRASP VPARPLPAKP 840 DSYPFKONDR RLLQCONVDI SRPLNGINUP GPGSTORVLP PLBRAPRASP VPARPLPAKP 840 ACGGGAAGG GAAAAGGCA GCAAAAAGGA ACAAGGACC CAGGGCGGGAAG GGAGGAAGGG AGCGGAGGGG AGCGGGGGGG CTTGGCCCAG GCGGGGAGG GGAGAAGGAC CCACCCCCAG GGCGGGAAG GCGGGGAGG GGAGAAGGAC CCACCCCAG GGCGGGAAG GCGGGGAAG GCGGGGAAG GCGGGGAAG GCGGGGAAG GCGGGGAAG GCGGGGGAAG GCGGGGAAG GCGAAAAGGAT CCACGCCCAC GCCGCGGGGGG CCGGGGGAGG GAGAAGACCT CCACCCCAGG GGCGCGAGG GAGAAGACTTC ATCAAAGAC CCCCCCCAC GCGGGGGGG AGCGCCTTTCCCAGGAAGAC CCCCCCCAGG GGCCCCACCAG GCGCGGGGGA GCGGGGGAAG GCGCCCTTTCCAAGACCCCAC CCCACCCAGG GGCCCCACCAG ACCCCACCGGG GAACCCTTTCC AGCAAG		IGIACCAAGA	AICIIGGIII		- man ama maa	30033000333	CACCECACAC	
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45 AGATGCCAA ATCCTTAGAT TACAGAATTT TATGGTGCAT TACGTGGCA TTGTCTTTTT 4980 45 AGCAAAAAAA AAAAAAAAAAA AA Seq ID NO: 78 Protein sequence Protein Accession #: NP_003465 1 11 21 31 41 51 MAARPLPUSP ARALLLALGA ALLAPCEARG VSLWNEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSTETTHYL QDGTDVSLAR NTTVILGHCY 120 YHGHVRGYSD SAVSLSTCSG LRGLTVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSGG 180 SHRTPRIAA KNVPPPPSQT WARRIKRETL KATKYVELVI VADNNEERGO (GKDLEXVKG 240 DINAQLVSGVY FGGTTIGMAP INSMCTADOS GGIVMDHSDN PLGAAVILAH ELGHFGMHH 360 DTLDRGCSGQ MAVEKGGCIM NASTGYPFM VPSSCSRKDL ETSLEKGMGV CLFNLPEVRE SFGGKCGNR FVEEGECDG GEPEECMNSC CNATTCTLKP DAVCAHGLCC EDCQLKPAGT 480 ACRDSSNSCD LPEFCTGASP HCPANYLHED GHSQDVDGY CYNGICQTHGG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMBAKC GKIQCQGGAS RPVIGTNAVS 660 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMBAKC GKIQCQGAS RPVIGTNAVS 660 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMBAKC GKIQCAGGAS RPVIGTNAVS 660 AKPAPGICFT RYNSAGDPYG NCGKVSKSSF AKCEMBAKC GKIQCAGGAS RPVIGTNAVS 660 AKPAPGICFT RVNSAGDPYG NCGKVSKSSF AKCEMBAKC GKIQCAGGAS ARGAGGAGGA AGGGGGAGGA AGGGGGA AGGGGG		ITATICIAIA	GITHITMAGI	ICIIIMMA	GIAAAGCCAI	GCIGGAMAA		
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Seq ID NO: 78 Protein sequence Protein Accession #: NP_003465 1		TATATACTAT	TAAAAAGGTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	
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Protein Accession #: NP_003465 1 11 21 31 31 41 51 MAARPLPVSP ARALLALAG ALLAPCEARG VSLWMEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCY 120 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRSSCG 180 SHHNTPNLAA KNVFPPPSGT WARRIKRETL KATKYVELVI VADNREFQRQ KOLLEKVRG, 240 DNAQLVSGYY FQGTIIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMH 360 DTLDRGGSCQ MAVERGGCIM NASTGYPFPM VFSSCSRKOL ETSLEKGMGV CLFALLPEVRE 420 SFGGQKCGNR FVEEGECDC GEPECOMRC CNATTCTLRP DAVCAHGLCC ELFOLLPEVRE 420 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMPDAKC GKIQCQGGAS RPVIGTNAVS 660 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP TRIHEFLDWR KNKLLPRKSH 306 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLIFT NKKTTIEKUR CVRPSRPPRG FQPCQAHLGH LGKGLMRKFP 780 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 75 Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGGAGAGG GAAAAGGCA GCAAAAAGGA ACAAAGGATC CAGGTCTCC GCTTTGGTG 120 GAGGAAAGGC AGGAGGAGGA AGAGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGCGGAG ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GTGGCACCTT TGACCCGGC CGGGGGGACG ACGACAAGGAT CAGGTCCCTG GCTTTGGTG 120 GTGGAATTCG GGGCTTAACT GGGATTTGCA TGACCCTG GCTTTTGTG 136 ACCGGGGATG CCAGCGGA AGCGGGAGG ACGACACGC CCGACCGA ACCACCCAC	15	TATATACTAT AGATGCCCAA	TAAAAAGGTT ATCCTTAGAT	TACAGAATTT CTGGCATGTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
Protein Accession #: NP_003465 1 11 21 31 31 41 51 MAARPLPVSP ARALLALAG ALLAPCEARG VSLWMEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCY 120 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRSSCG 180 SHHNTPNLAA KNVFPPPSGT WARRIKRETL KATKYVELVI VADNREFQRQ KOLLEKVRG, 240 DNAQLVSGYY FQGTIIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMH 360 DTLDRGGSCQ MAVERGGCIM NASTGYPFPM VFSSCSRKOL ETSLEKGMGV CLFALLPEVRE 420 SFGGQKCGNR FVEEGECDC GEPECOMRC CNATTCTLRP DAVCAHGLCC ELFOLLPEVRE 420 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMPDAKC GKIQCQGGAS RPVIGTNAVS 660 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP TRIHEFLDWR KNKLLPRKSH 306 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLIFT NKKTTIEKUR CVRPSRPPRG FQPCQAHLGH LGKGLMRKFP 780 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 75 Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGGAGAGG GAAAAGGCA GCAAAAAGGA ACAAAGGATC CAGGTCTCC GCTTTGGTG 120 GAGGAAAGGC AGGAGGAGGA AGAGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGCGGAG ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GTGGCACCTT TGACCCGGC CGGGGGGACG ACGACAAGGAT CAGGTCCCTG GCTTTGGTG 120 GTGGAATTCG GGGCTTAACT GGGATTTGCA TGACCCTG GCTTTTGTG 136 ACCGGGGATG CCAGCGGA AGCGGGAGG ACGACACGC CCGACCGA ACCACCCAC	45	TATATACTAT AGATGCCCAA	TAAAAAGGTT ATCCTTAGAT	TACAGAATTT CTGGCATGTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
Protein Accession #: NP_003465 1 11 21 31 31 41 51 MAARPLPVSP ARALLALAG ALLAPCEARG VSLWMEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCY 120 YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRSSCG 180 SHHNTPNLAA KNVFPPPSGT WARRIKRETL KATKYVELVI VADNREFQRQ KOLLEKVRG, 240 DNAQLVSGYY FQGTIIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMH 360 DTLDRGGSCQ MAVERGGCIM NASTGYPFPM VFSSCSRKOL ETSLEKGMGV CLFALLPEVRE 420 SFGGQKCGNR FVEEGECDC GEPECOMRC CNATTCTLRP DAVCAHGLCC ELFOLLPEVRE 420 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMPDAKC GKIQCQGGAS RPVIGTNAVS 660 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP TRIHEFLDWR KNKLLPRKSH 306 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLIFT NKKTTIEKUR CVRPSRPPRG FQPCQAHLGH LGKGLMRKFP 780 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 75 Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGGAGAGG GAAAAGGCA GCAAAAAGGA ACAAAGGATC CAGGTCTCC GCTTTGGTG 120 GAGGAAAGGC AGGAGGAGGA AGAGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGCGGAG ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GAGGAAGGG GAAAAGGCA GCGGGGGAGC ACAAAAGGAT CAGGTCTCC GCTTTGGTG 120 GTGGCACCTT TGACCCGGC CGGGGGGACG ACGACAAGGAT CAGGTCCCTG GCTTTGGTG 120 GTGGAATTCG GGGCTTAACT GGGATTTGCA TGACCCTG GCTTTTGTG 136 ACCGGGGATG CCAGCGGA AGCGGGAGG ACGACACGC CCGACCGA ACCACCCAC	45	TATATACTAT AGATGCCCAA	TAAAAAGGTT ATCCTTAGAT	TACAGAATTT CTGGCATGTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
1 11 21 31 41 51	45	TATATACTAT AGATGCCCAA ACCAAAAAA	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
MAARPLPVSP ARALLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSG DLWIPVKSFD 60 SKNHPPSVLNI RLGRESKELI INLERNEGIJ ASSFTETHYL QDGTDVSLAR NYTVILGECY YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180 SHHNTDNLAA KNVFPPSGYT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240 DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360 DTLDRGCSCQ MAVEKGGCIM NASTGYPFM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE 420 SFGGQKGGNR FVEEGECDC GEPEECMNG CNATTCTIKEP DAVCAHGLCC EDCQLKPAGT 480 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYMGICQTHE QQCVTLWGFG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCQGGAS RPVIGTNAVS 600 IENNIPLQQG GRILCRGTHV YLGDDMPDFG LVLAGTKCAD GKICLUNQCQ NISVFGVBC 660 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQSLT IGILVTILLC 720 LAAGFVVYLK RKTLIRLIFT NKKTTIEKLR CVRPSRPFRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTGRVLP PLARAPRAPS VPARPLPAKP 840 ALRQAQGTCK PNPPQKPLPA DPLARTTRLT HALARTFGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1	45	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO:	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein	TACAGAATTT CTGGCATGTT AA sequence	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
	45	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO:	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein	TACAGAATTT CTGGCATGTT AA sequence	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
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SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCY YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180 SHENTFNLAA KNVPPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240 DNAQLVSGVY FQSTTIGMAP IMSMCTADQS GGIVMHSDN PLGAAVTLAH ELGHNFGMNH 360 DNAQLVSGVY FQSTTIGMAP IMSMCTADQS GGIVMHSDN PLGAAVTLAH ELGHNFGMNH 360 DNAQLVSGVY FQSTTIGMAP IMSMCTADQS GGIVMHSDN PLGAAVTLAH ELGHNFGMNH 360 ACRDSSNSCD LPEFCTGASP HCPANVYHDD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 440 ACRDSSNSCD LPEFCTGASP HCPANVYHDD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMBDAKC GKICLNRQCO NISVFGWEC 660 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGSFVVKLK RKTLIELLFT NKKTIIEKLR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHAYIK . Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1		TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1	TACAGAATTT CTGGCATGTT AA sequence NP_003465	TATGGTGCAT AGCCCTTCCT	TACGTGGGCA CCAATTATAA	TTGTCTTTT GAGGATATGA	4980
YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180 SHRHTPNLAA KNVFPPPSQT WARRHRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240 LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300 DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360 DTLDRGCSCQ MAVEKGGCIM NASTGYPFPM VFSSCSKKDL ETSLEKGMGV CLFNLPEVRE 420 SFGGGKCGNR FVEESECDCD GEFBECNNRC CNATTCTLKP DAVCAHGLCC EDCOLKPAGT 480 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCGGAS RPVIGTNAVS 660 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCGGAS RPVIGTNAVS 660 AMQCRGRGVC NNRKNCHCER HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLLFT NKKTITIEKIR CVRPSRPPRG FQPCQAHLGH LGKGLMRXPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVV QQQSTQRVLP PLHRAPRAPS VPARPLPAXP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK . Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 COding sequence: 1351043 1 11 21 31 41 51		TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1 11	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21	TATGGTGCAT AGCCCTTCCT 31	TACGTGGGCA CCAATTATAA 41	TTGTCTTTT GAGGATATGA 51	4980 5040
YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG 180 SHRHTPNLAA KNVFPPPSQT WARRHRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240 LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300 DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360 DTLDRGCSCQ MAVEKGGCIM NASTGYPFPM VFSSCSKKDL ETSLEKGMGV CLFNLPEVRE 420 SFGGGKCGNR FVEESECDCD GEFBECNNRC CNATTCTLKP DAVCAHGLCC EDCOLKPAGT 480 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCGGAS RPVIGTNAVS 660 AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCGGAS RPVIGTNAVS 660 AMQCRGRGVC NNRKNCHCER HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLLFT NKKTITIEKIR CVRPSRPPRG FQPCQAHLGH LGKGLMRXPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVV QQQSTQRVLP PLHRAPRAPS VPARPLPAXP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK . Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 COding sequence: 1351043 1 11 21 31 41 51		TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG	TTGTCTTTT GAGGATATGA 51 DLWIPVKSFD	4980 5040
SHINTPNLAA KNVFPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR 240 LIEIANHUDK FYRPLNIRIV LVGVUVWIDM DKCSVSQDFF TSLHEFLDWR KMKLLPRKSH 300 DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PIGAAVTLAH ELGIMFGMNH 360 DTLDRGCSCQ MAVEKGGCIM NASTGYPFFM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE 420 SFGGGKGRR FVEEGEECDC GEPEECMRC CNATTCTLKP DAVCAHGLCC EDCQLKPAGT 480 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQVVDGY CYNGICQTHE QQCVTLWGPG 540 AKPARGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCQGGAS RPVIGTNAVS 600 IETNIPLQQG GRILCRGTHV YLGDDMPDFG LVLAGTKCAD GKICLNRQQ NISVFGVHEC 660 AMQCRGRGVC NNRKNCHCEA HWAPPFCDKF GFGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLEFT NKKTITLEKLR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1		TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG	TTGTCTTTT GAGGATATGA 51 DLWIPVKSFD	4980 5040
LIEIANHUDK FYRRLNIRIV LVGUEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300 DNAQLVSGYY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360 DTLDRGCSCQ MAVEKGGCIM NASTGYPFPM VPSSCSRKDL ETSLERGMGV CLFNLPEVRE 420 SFGGQKCGNR FVEEGEECDC GEPEECMNC CNATTCTLKP DAVCAHGLCC EDCQLKPAGT 480 ACRDSSNSCD LPECTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG 540 AKPAPGICFE RVNSAGDPYG NCGKVSKSSP AKCEMRDAKC GKIQCQGGAS RPVIGTNAVS 600 IETHIPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKIQCQGGAS RPVIGTNAVS 600 AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLFT NKKTTIEKLE CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPCSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAQGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK . Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCA GCAAAAAGGA AGAGTGGGA AGCGGCGAAG 600 GAGGAAGAGG GGAAAGGCA GCAAAAAGGA CAAAAGGATC CAGGTCTCC GACGGAGGT 120 GAGGAAGAGG GAAAAGGCA GCAAAAAGGA CCACCCCCCCGA GCGTCCCC GACGGAGGT 120 ACACGAGCTC CAGCGAGAAA GGCCGCCTGT CCCTGCGAA TACAGCGCG GGTCCCCAAG 240 TGGCCACCTT TGACCCGGC CGGGGGACCG ACGCCACCAA CCCCACCGAG ATCCACGCAC 240 ACACGAGCTC CAGCGAGAAA GGCCGCCTGT CCCTGCGAA TACAGCGGGG ATCCACGCAC 240 ACACGAGCTC CAGCGAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGGG ATCCACGCAC 240 GTTTGGTCAA CGCTGCGGAT GTGGGGTTGG GCGTGTTTGA ATGTTTCGAG AACACTCTT 360 GTTTGGTCAA CGCTGCGGAT GTGGGGTTGC CCTGCAGAA TACAGCGCGG GAAAACTCTT 360 ATGCCCAGGG CAAGTCATTC ATCAAAGACC CCTTGAAATG ATCAAGCCCG GAAAACTCTT 360 ATGCCCAGG CAAGTCATTC ATCAAAGACC CCTTGAAATG ATCAAGCCCAC GCTCTGGGG ACAGGTTCGC CGGGAATGCT CACGACCTG GGAAAATGGT TCCCAGTTGC 480 ACGGGGAATG CTACTCAAG CCGGAAGTGCC CGGCCATCAG GAAAATGGTG TCCCAGTGG CAACCTTGC GACCGGCAC GACCTCTGC GAAACTCTT GCGCGGCAC CCTGCACAC GCTCTGCGGC AACACCTTGC GACCGGGTGA AGCCGCCTGTC CAGGAGAAA ACCCCTACCGG GAAAATGGTG TCCCAGTGG AACACCTTT TCCAGTTGC GACCGGCAC GCCCCCACGC GGGAAAATGGTG TCCCAGTGG AACCTGTGG GACCTGTGG GACCTGTGG GACCTGTGG GACCTGTGG GACCTGTGC GACCTGTGG GACCTGTGC G		TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Frotein cession #: 1 11 ARALLLALAG RLQRESKELI	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR	TTGTCTTTT GAGGATATGA 51 DLWIPVKSFD NYTVILGHCY	4980 5040 60 120
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IETNIPLQQG GRILCRGTHV YLGDDMPDFG LVLAGTKCAD GRICLNRQQO NISVFGVHEC AMQCBGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLEFT NKRTILEKUR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51	50	TATATACTAT AGATGCCCAA ACCAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADOS NASTGYPFPM GEFEECMNRC	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG KOLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT	4980 5040 60 120 180 240 300 360 420 480
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AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL 720 LAAGFVVYLK RKTLIRLIET NKKTTIEKLR CVRPSRPPRG FQFCQAHLGH LGKGLMRKPP 780 DYPPRDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAG GAAAAGGCA GCAAAAAGGA AGAGTGGGA AGCGGCGAAG 60 GAGGAAGAG GAAAAGGCA AGAGGGGAC ACAAAGGATC CAGGTCTCCC GACGGAGGT 120 GAGGAAGAG GAAAAGGCA AGAGGGGAC ACAAAGGATC CAGGTCTCCC GACGGAGGT 120 ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACCAGCGAG ATCCAGCACT 300 GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCGAG AACAACTCTT 360 GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCGAG AACAACTCTT 360 ATGCCCAGGG CAAGTCATC ATCAAAGACC CCTTGAAATG TACAGGCGCAG GCTCTGGGGA ACCAGGTTCGC GAAAATTTG 420 ACAGGTTCGG CTGCATAAGC CCGGAAGTGC CCGCACCAC GCTCTGGGGA ACCAGCTTG GACGAGTTC ATGACTCTG GCGAAAATTTG TACAGGCACA GCCTCACGGG GAAAATTTG 420 ACAGGTTCGG CTGCATAAGC CCGGAAGTGC CCGCCACTCAG GCAAAATTTG 420 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCGCATCAG GCAAAATGGT TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACGACCTG GCGCGCTCC CCAGGAGAA ACCCCGGTGA 600 ACTTGCTGCT GACCTATCA GAGGACTTC TGCTGCCACA ACCCTACCTG GACCTCGTG 660 ACTTGCTGCT GACCTATCA GAGGACTTG TGCTGCACCA ACCCTACCTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGG GAGGAGTGC AGGAGGGCCA CCCCACCAG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGG GAGGAGTGC AGGAGGGCCAT CACCCCACAGC GTGCAGGTTC 720	50 55	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCD AKPAPGICFE	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAA 78 Protein cssion #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM PVEEGEECDC LPEFCTGASP RVMSAGDPYG	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWND MMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS	4980 5040 60 120 180 240 300 360 420 480 540 600
LAAGFVVILK RKTLIRLLFT NKKTITIEKIR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP 780 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAQGTCK PNPPQKPLPA DPLARTTRIT HALARTPGQW ETGLRAPLR PAPQYPHQVP 900 RSTHTAYIK . Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1	50 55	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGOKCGNR ACRDSSNSCD AKPAPGICFE	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAA 78 Protein cssion #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM PVEEGEECDC LPEFCTGASP RVMSAGDPYG	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWND MMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS	4980 5040 60 120 180 240 300 360 420 480 540 600
DSYPPKONPR RLLQCONVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALROAGSTCK PNPPQKPLPA DPLARTTRIT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCGA GCAAAAAGGA AGAGTGGGAG GAGGAGGGGA AGCGGCGAAG GAGGAGAGGG GAAAAGGAGA AGAGTGGGAG GAGGAGGGA AGCGGCGAAG GAGGAGAGGA	50 55	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV	TACAGAATTT CTGGCATGTT AA sequence vequence vequ	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSQDVDGY AKCEMRDAKC LVLAGTKCAD	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC	60 120 180 240 300 420 480 540 600 660
DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840 ALRQAGGTCK PNPPQKPLPA DPLARTTRIT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900 RSTHTAYIK Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCGA GCAAAAAGGA AGAGTGGGAG GAGGGGGAAG 60 GAGGAAGAGG GAAAAGGCGA AGAGGGGGG ACAAAGGATC CAGGTCTCCC GACGGGAGGT 120 TAATACCAAG AACCATGTGT GCCGAGCGG TGGGCCACCAA CCCACCCAG GGTCCCCAAG ACCACCACGA GAGGGGCT CCCAGCAGA ACCACGACGA GGTCCCCAAG GTTTGGTCT TGGCCACCTT TGACCCGGC CGGGGGACCG AGCCCACCAA CCCACCCAG GGTCCCCAAG GTTTGGTCA CGCTGCAGAAA GGCGGCTTTC CCTGCAGAA TACAGCGGAG ATCCAGCACT 300 GTTTGGTCAA CGCTGCGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGCAG AACAACCTCT 360 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GAAAATTTTG 420 ATGCCCAGGG CAAGTCATC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC 480 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GAAAATTTG 420 AGCGGGAATG CTCACTAAGC CACGACCTTG GAAATTTTA TAAGGCCCAC GCTCTGCGGC 480 ACAGGTTCGG CTGCATAAGC CACGACCTTG TGCGCGCACCAC ACCCTACCTG GACCTCGTGA ACTGCTGCTG GACCTTCTAAG CACGACCTTG TGCGCCCACGAC ACCCTACCTG GACCTCGTGA 600 ACTTGCTGCT GACCTCTGAG GACCTCGT TGCTGCACCA ACCCTACCTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	50 55	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Frotein 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM MAVEKGGCIM MAVEKGGCIM EVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA	TACAGAATTT CTGGCATGTT AA sequence value of the control of the con	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDI CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLLAGTKCAD GFGGSTDSGP	TACGTGGGCA CCAATTATAA 41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVNE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL	4980 5040 60 120 180 240 300 360 420 540 600 720
ALRQAQGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCA GCAAAAAGGA GAGGAGGGGA AGCGGCGAAG GAGGAGAGGA	50 55	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Frotein 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM MAVEKGGCIM MAVEKGGCIM EVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA	TACAGAATTT CTGGCATGTT AA sequence value of the control of the con	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDI CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLLAGTKCAD GFGGSTDSGP	TACGTGGGCA CCAATTATAA 41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVNE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL	4980 5040 60 120 180 240 300 360 420 540 600 720
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Seq ID NO: 79 DNA sequence Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51	50 55 60	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVPPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI	TACAGAATTT CTGGCATGTT AA sequence UP_003465 21 ALLAPCEARG INLERNEGLI LEGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKRTTIEKLR SRPLNGLNVP	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	A1 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH FLHRAPRAPS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAXD	4980 5040 60 120 180 240 300 420 480 540 660 720 780 840
Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCA GCAAAAAGGA AGAGTGGGA GAGGAGGGA AGCGGCAAG GAGAGAGGAG AGAGAGAG	50 55 60	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVPPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI	TACAGAATTT CTGGCATGTT AA sequence UP_003465 21 ALLAPCEARG INLERNEGLI LEGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKRTTIEKLR SRPLNGLNVP	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	A1 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH FLHRAPRAPS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAXD	4980 5040 60 120 180 240 300 420 480 540 660 720 780 840
Nucleic Acid Accession #: NM_003714 Coding sequence: 1351043 1 11 21 31 41 51 GAGGAGGAGG GAAAAGGCA GCAAAAAGGA AGAGTGGGA GAGGAGGGA AGCGGCAAG GAGAGAGGAG AGAGAGAG	50 55 60	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVPPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI	TACAGAATTT CTGGCATGTT AA sequence UP_003465 21 ALLAPCEARG INLERNEGLI LEGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKRTTIEKLR SRPLNGLNVP	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	A1 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH FLHRAPRAPS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAXD	4980 5040 60 120 180 240 300 420 480 540 660 720 780 840
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70 Coding sequence: 1351043 1 11 21 31 41 51	50 55 60	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVUK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQGG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: 1 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVPPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM FVEEGEECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNCY HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP	A1 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH FLHRAPRAPS	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAXD	4980 5040 60 120 180 240 300 420 480 540 660 720 780 840
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75 GAGGARGAG AGAGGAGGA AGAGGGAGAG ACAAAAGGATC CAGGTCTCCC GACGGAGGT 120 TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCACCTA CACGACCCG GCTTTGGTGT 180 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG 240 ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT 300 GTTTGGTCAA CGCTGGCGAT GTGGGGTTGG GCGTGTTTGA ATGTTTCGAG AACAACTCTT 360 ATGCCCAGGG CAAGTCATT CATCAAAAGACC CCTTGAAAAT TAAGGCCCAC GGAAAATTTG 420 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAAATGGT TCCCAGTTGC 480 ACAGGTTCGG CTGCATAAGC CAGCACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGTGA 600 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACCTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGAGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	50556065	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNIAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGKCGMA ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM FVEEGEECDG RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135.	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQVLP HALARTPGQW 714 31	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	4980 5040 60 120 180 240 300 420 480 540 660 720 780 840
75 GAGGARGAG AGAGGAGGA AGAGGGAGAG ACAAAAGGATC CAGGTCTCCC GACGGAGGT 120 TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCACCTA CACGACCCG GCTTTGGTGT 180 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG 240 ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT 300 GTTTGGTCAA CGCTGGCGAT GTGGGGTTGG GCGTGTTTGA ATGTTTCGAG AACAACTCTT 360 ATGCCCAGGG CAAGTCATT CATCAAAAGACC CCTTGAAAAT TAAGGCCCAC GGAAAATTTG 420 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAAATGGT TCCCAGTTGC 480 ACAGGTTCGG CTGCATAAGC CAGCACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGTGA 600 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACCTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGAGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	50556065	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHEPVINI YHGHVRGYSD SHHNTPNLAA LIEIANHUK DNAQLVSGVY DTLDRGCSCQ SFGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein eession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM PVEEGECCDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11	TACAGAATTT CTGGCATGTT AA SEQUENCE SP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDE NKRTTIEKLR SRPLNGLNVP DPLARTTRLT URENCE I #: NM_003 .1043 21	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QFQSTQRVLP HALARTPGQW 714 31	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRO TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKGN KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS INIVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 180 240 360 420 540 660 720 780 840 900
TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCAGTT CATGACCCTG GCTTTGGTGT 180 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG 240 ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCCGAGA ATCCAGCACT GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCGAG AACAACTCTT 360 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG 420 ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC 480 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAAATGGTC TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGTGA 660 TAGTGGAGAT GATCCATTTC AAGGACTTCC TGCTGCACCA ACCCTACCTG GACCTGCTGA ACTTGCTGCT GACCTGTGGG GAGAGGTGA ACGAGGCCAT CACCCACAGC GTGCAGGTTC 720	50556065	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHEPVINI YHGHVRGYSD SHHNTPNLAA LIEIANHUK DNAQLVSGVY DTLDRGCSCQ SFGQKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAQGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1	TAAAAAGGTT ATCCTTAGAT AAAAAAAAAA 78 Protein eession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM PVEEGECCDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11	TACAGAATTT CTGGCATGTT AA SEQUENCE SP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDE NKRTTIEKLR SRPLNGLNVP DPLARTTRLT URENCE I #: NM_003 .1043 21	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QFQSTQRVLP HALARTPGQW 714 31	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRO TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKGN KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS INIVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	60 120 180 240 360 420 540 660 720 780 840 900
TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACAA CCCACCGAG GGTCCCCAAG ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT GTTTGGTCAA CGCTGGCGAT GTGGGGGTGT GCGTGTTTGA ATGTTTCAGA AACACTCTT GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC ACAGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTCC CCAGGAGAAC ACCCGGTGA ACTTGCTGCT GACCATTTC AAGGACTTGC TGCTGCACGA ACCTACCTG GACCTCGTGA ACTTGCTGCT GACCTTGTGGG GAGAGAGTGA AGGAGGCCAT CACCCACAGG GTGCAGGTTC 720	50556065	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVUK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1 GAGGAGGAGG	TAAAAAGGTT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVPPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM PVEEGEECDE LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA . 79 DNA seq id Accessio uence: 135. 11 GAAAAGGCGA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ PLGAAVTLAH ETSLEKGMGV DAVCAHGLC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNGGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVRGN KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QCVTLWGFG RPVIGTNAVS NISVFGVHEC LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	4980 5040 60 120 180 240 300 360 420 480 660 720 780 840 900
TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACAA CCCACCGAG GGTCCCCAAG ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT GTTTGGTCAA CGCTGGCGGAT GTGGGGGTGT CGCTGTTTGA ATGTTTCGAG AACACTCTT GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG ATGCCCAGGG CAACTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC AGCGGGAATG CTACCTCAAG CACCACCTGT GCGCGGCTCC CCAGGAGAAC ACCCCGGTGA ACTTGCTGCT GACCATTTC AAGGACTTGC TGCTGCACGA ACCCTACCTG GACCTCGTGA ACTTGCTGCT GACCTTTGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQCTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLFT TRLLCCONVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11 GAAAAAGGCGA AGGAGGAGGAGA	TACAGAATTT CTGGCATGTT AA sequence inpossess 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLINVP DPLARTTRLT UGENCE i #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGAGG	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGBAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA GAGGAGGGGA CAGGTCTCCCC	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG KOLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	4980 5040 60 120 180 240 300 360 420 540 660 720 780 900
ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT 300 GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCAG AACAACTCTT 360 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG 420 ATGCCCAGGG CAAGTCATTC ATCAAAGACC CCTTGAAATG TAAGGCCCAC GCTCTGCGC 480 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC 540 AGCGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTCC CCAGGAGAAC ACCCGGTGA 660 TAGTGGAGAT GACCTATTC AAGGACTTGC TGCTGCACGA ACCCTACCTG GACCTCGTG 660 ACTTGCTGCT GACCTGTGGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA SEQUENCE NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETI LVGVEYWNDM IMSMCTADQS NASTGYPFPM MCGEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT UERCE n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGGGGGGGGGGGGGGGGGG	31 VSLWNEGRAD ASSFTETHYL SYULEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSKBU CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV CYMGICQTHE GKIQCQGGAS GKICLNRQCO IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVFE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP 51 AGCGGCGGAAG GACGGGAAGGT GCCTTTGGTGT	60 120 180 240 300 360 420 720 780 840 900
80 STITGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCGAG AACACTCTT 360 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG 420 ATGCCCAGGG CAAGTCATTC ATCAAAGACC CCTTGAAATG TAAGGCCCAC GCTCTGCGCC 480 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACGACTGT GCGCGGCTGC CCAGGAGAAC ACCCGGTGA 660 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACCGT GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA SEQUENCE NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETI LVGVEYWNDM IMSMCTADQS NASTGYPFPM MCGEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT UERCE n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGGGGGGGGGGGGGGGGGG	31 VSLWNEGRAD ASSFTETHYL SYULEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSKBU CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV CYMGICQTHE GKIQCQGGAS GKICLNRQCO IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVFE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP 51 AGCGGCGGAAG GACGGGAAGGT GCCTTTGGTGT	60 120 180 240 300 360 420 720 780 840 900
80 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTCT GCACAACGCT GGAAAATTTG 420 ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGGGC 480 ACAGGTTCGG CTGCATAAGC CGGAAAGTGCC CGGCCATCAG GGAAATGTG TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACGACCTGT GGCGGGTGC CCAGGAGAAC ACCCCGGGTGA 600 TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1 MAARPLPVSP SKNHPEVINI YHGHVRGYSD SHHNTPNIAA LIEIANHVDK DNAQLVSGVY DTLDRGGSCQ SFGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq 1 GAGGAGGAGG GAGGAGAGG GAGGAAGAGG TAATACCAAG TGGCCACCTT	TAAAAAGGTT ATCATAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM PVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV ANRENCHCEA RKTLIRLLFT RLLQCONVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11 GAAAAGGCGA AGGAGAGGAGGA AGCATGTGT TGACCCGGCG	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGAGCG GCCGGGGGACCGG	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSPTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACCAA	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ DAVCHGLCC CYNGICQTHE GKIQCQGGAS GKICLINRQC IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG CCCACCCGAG	51 DLWIPVKSFD NYTVILGRCY KLKSVRGSCG GKDLEKVRGN KNKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QCVTLWGFG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP	4980 5040 120 180 240 420 420 480 6600 6600 720 780 840 900
80 GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTCT GCACAACGCT GGAAAATTTG 420 ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGGGC 480 ACAGGTTCGG CTGCATAAGC CGGAAAGTGCC CGGCCATCAG GGAAATGTG TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACGACCTGT GGCGGGTGC CCAGGAGAAC ACCCCGGGTGA 600 TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCO AKPAFGICFE LETNIPLQG AMQCHGRGVC LAAGFVVLK DSYPPKDNPR ALRQAGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAAGAGG TAATACCAAGT TGGCCACCTI ACAGGAGCTC	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence inposed of the control of the c	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGTVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACGCCACCAA	41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG KOLLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKFAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGCGCGAAG GACGGGAGGT GGCTCCCCAAG ATCCAGCACT	4980 5040 60 120 180 240 480 660 720 780 840 900
ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC 480 ACAGGTTCGG CTGCATAAGC CGGAAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC 540 AGCGGCAATG CTACCTCAAG CACGACCTGT GGCGGGTGC CCAGGAAC ACCCTGAGTGA 660 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCO AKPAFGICFE LETNIPLQG AMQCHGRGVC LAAGFVVLK DSYPPKDNPR ALRQAGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAAGAGG TAATACCAAGT TGGCCACCTI ACAGGAGCTC	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence inposed of the control of the c	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPFRG QPQSTQVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACGCCACCAA	41	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG KOLLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKFAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGCGCGAAG GACGGGAGGT GGCTCCCCAAG ATCCAGCACT	4980 5040 60 120 180 240 480 660 720 780 840 900
ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC 540 AGCGGGAATG CTACCTCAAG CACCACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA 660 TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCTACCTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	5055606570	TATATACTAT AGATGCCAA ACCAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEYWNDM IMSMCTADQS NASTGYPFPM MCGEVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGAGCG CCGGGGGACCG CGGGGGACCG GGCCGCCTGTG	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDI CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTAA CCCTGCAGAA GGGTGTTTGA	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG CCCACCCGAG TACAGCGGAG ATGTTTCGAG	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVFE EDCOLKPACT QQCVTLWGPG RPVIGTNAVS INSVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP 51 AGCGGCGAAG GACCGGAGGT GCTTTGGTGT GGTCCCCAAG ATCCAGCACT AACAACTCTT	4980 5040 120 180 240 360 420 780 840 900 601 20 180 240 360
AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA 660 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	505560657075	TATATACTAT AGATGCCAA ACCAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGYEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDF NKRTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGACC GCCGAGCGGG CCGGGGGACCGG GGCCCTGTT GTGGGGTTTGCA	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPGSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT ACGCCACCAA GCCTGTTTGA CCCTGCAGAA GCGTGTTTGA	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRO TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGI CQTHE GKICCNGGAS GKICLNRQCO IRQADNQGLT FQPCQAHLGH FLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTTCC CCATCACCCGAG TACAGCGGAG ATGTTTCGAG GGCACACGCT	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKOR KNKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCOLKPAGT QQCVTLWGPG RPVIGTNAVS RPVIGTNAVS ISIUTILCL LGKGLMRKPP VPARPLPAKD PAPQYPHQVP 51 AGCGGCGAAG GACGGGAGGT GCTTTGGTGT GGGTCCCCAAG ATCCAGCACT AACAACTCTT GGGAAAATTTG	60 120 180 240 360 420 720 780 840 900
AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA 660 TAGTGGAGAT GATCCATTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	505560657075	TATATACTAT AGATGCCAA ACCAAAAAA Seq ID NO: Protein Acc I I I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE LIETNIPLQG AMQCHGRGVC LAAGFVVLK DSYPPKDNPR ALRQAGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAAGAGG TAATACCAAG TGGCAACTT ACAGGAGCTC GTTTGGTCAA GTGGAGATGC ATGCCCAGGG	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence inpossessessessessessessessessessessessesse	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDIN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACCCCGAGAA GCGTGTTGA TGACTTTTCT CCTTGAAATG	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTGA CCACCCGAG TACAGCGGAG ATGTTTCGAG GGCACACCCT TAAGGCCCAC	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVKE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGCGCGAAG GACGGGAGGT GGTCCCAAG ATCCAGCACT AACAACTCTT GGAAAATTTG GGCTCTGCGGC	4980 5040 60 120 180 240 480 660 720 780 840 900 60 120 180 240 300 360 440 900
TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	505560657075	TATATACTAT AGATGCCAA ACCAAAAAA Seq ID NO: Protein Acc I I I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE LIETNIPLQG AMQCHGRGVC LAAGFVVLK DSYPPKDNPR ALRQAGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAAGAGG TAATACCAAG TGGCAACTT ACAGGAGCTC GTTTGGTCAA GTGGAGATGC ATGCCCAGGG	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence inpossessessessessessessessessessessessesse	TATGGTGCAT AGCCCTTCCT 31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDIN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACTA ACCCCGAGAA GCGTGTTGA TGACTTTTCT CCTTGAAATG	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTGA CCACCCGAG TACAGCGGAG ATGTTTCGAG GGCACACCCT TAAGGCCCAC	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLFNLPEVKE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGCGCGAAG GACGGGAGGT GGTCCCAAG ATCCAGCACT AACAACTCTT GGAAAATTTG GGCTCTGCGGC	4980 5040 60 120 180 240 480 660 720 780 840 900 60 120 180 240 300 360 440 900
ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	505560657075	TATATACTAT AGATGCCCAA ACCAAAAAA Seq ID NO: Protein Acc I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ AKPAFGICFE IETNIPLQG AMQCHGRGVC LAAGFVYYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAAGAG TATACCAAG TGGCCACTT ACAGGAGTTCAA GTGAGATTCG ATGCCCACGG ACAGGTTCGGTCAA	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFM (HCPANVYLHD NCGKVSKSSF TYLGDDMPDFG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT uence n #: NM_003 .1043 21 GCAAAAAGGA AGAGGGAGCG GCCGGGGCCCGG GCCGGCCTGT GGGGGTTGCG GGGGTTTGCA ATCAAAGACG CCGGAAGTGCC	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCACCAA GCGTGTTTGA GCGTGTTTGA TGACTTTCTTGAAATG CCTTGAAATG CCGGCCATCAG	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTTTCCC CATGACCCTG CCCACCCGAG TACAGGCCAC GGAAATGGTT TAAGGGCCAC GGGAAATGGTG GGAAATGGTG	51 DLWIPVKSFD NYTVILGHCY KIKKVRGSCG GKDLEKVKQR KKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGTCCCAAG GACGGGGAGGT GCTTTGGTGT GGTCCCCAAG GATCCAGCACT AACAACTCTT GGAAAATTTG GGCTCTGCGGC	4980 5040 120 180 240 360 420 780 840 900 600 720 780 840 900 120 180 240 360 420 420 420 420 420 420 420 420 420 42
ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTC 720	505560657075	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc 1	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAA 78 Protein cession #: ! 11 ARALLLALAG RLQRESKELI SAVSLSTCSG KNVFPPPSQT FYRPLNIRIV FQGTTIGMAP MAVEKGGCIM FVEEGECDC LPEFCTGASP RVNSAGDPYG GRILCRGTHV NNRKNCHCEA RKTLIRLLFT RLLQCQNVDI PNPPQKPLPA 79 DNA seq id Accessio uence: 135. 11 GAAAAGGCGA AGGAGAGGG AACCATGTGT TGACCAGGGGG CCAGCAGAAA CGCTGGCGGT CCTGCTACAT CCTGCTACGGGG CTTGCTACAGGGGGA CCTGCTCAAGGGGGA CCTGCCTCAAGGGGGA CCTGCCTCAAGGGGGA CCTGCCTCAAGGGGGA CCTACCTCAAGGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGGA CCTACCTCAAGGGA CCTACCTCAAGGGA CCTACCTCAAGGCGA CCTACCTCAAGGCGA CCTACCTCAAGGA CCTACCTCAAGGCGA CCTACCTCAAGGCGA CCTACCTCAAGGCGA CCTACCTCAAGGA CCTACCTCAAGGCGA CCTACCTCAAGGCGA CCTACCTCAAGGA CCTACCTCAAGGCA CCTACCTCAAGGCA CCTACCTCAAGGA CCTACCTCAAGA CCTACCTCAAGGA CCTACCTCAAGA CCTACCTCAACA CCTACTCAACA CCTACT	TACAGAATTT CTGGCATGTT AA SEQUENCE SP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFPM GEPEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPPG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT UENCE 1 #: NM_003 .1043 21 GCAAAAAAGGAA AGAGGGAGCGGCGGGGGCCCGGT GGCGGGGGGCCCGGT GGGGGTTTGCA ATCAAAGACCG CCGGAAGTGCC CCGCACCTGT CCGCACCTGT	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSKDL CMATTCILKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGCAA CCCTGCAGAA GCGTGTTTGA TGGCTTTGA	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CCACCCGAG TACAGCGGAG GCACAACGCT TAAGGCCCAC GGAAATGGTG CCAGGAGAAC	51 DLWIPVKSFD MYTVILGHCY KLKSVRGSCG GKDLEKVKG KMKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDOQLKPAGT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAKP PAPQYPHQVP 51 GGGGGGGAAG GCCTGGGGG GACGGGAGGT GCCTTGGTGT GGTCCCCAAG ATCCAGCACT GGAAAATTTG GCTCTGCGGC ACCCAGGTGA	60 120 180 240 360 420 480 540 660 720 780 840 900
85 AGTGTGAGCA GAACTGGGGA AGCCTGTGCT CCATCTTGAG CTTCTGCACC TCGGCCATCC 780	505560657075	TATATACTAT AGATGCCAA ACCAAAAAAA Seq ID NO: Protein Acc I MAARPLPVSP SKNHPEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCQ SFGGGKCGNR ACRDSSNSCD AKPAPGICFE IETNIPLQQG AMQCHGRGVC LAAGFVVYLK Seq ID NO: Nucleic Ac Coding seq I GAGGAGGAGG GAGGAGAGG GAGGAGAGG GAGGAGAGG TAATACCAAG GTGGCACTT ACAGGACTC GTTTGGTCAA AGCGGGAATTCG ACAGGTTCGG ACAGGTTCGG ACAGGTTCGG ACAGGTTCGG ACAGGGTCGGAAAGAGGGTTCGT ATGCCCAGGGAAAGAGGTTCGG ACAGGTTCGG ACAGGTTCGG ACAGGGTCGGAAAGAGGGTTAGTGGAAATTCGAAATTCGAAGAGTTCGGAAATTCGAAGGTTCGG ACAGGTTCGGAATTCGGAGGGGAATTCGTAGAATTCGAAGGTTCGGAATTCGAAGGGGGAATTCGTAGAATTCGAAGGGGGAATTCGTAGAATTCGAAGGTTCGGAATTCGGAGGAGTTCGGAATTCGAAGGGGGAATTCGTAGAATTCGAAGGTTCGGAATTCGGAGGAGTTCGGAATTCGGAGGAGTTCGGAATTCGGAGGAGTTCGGAATTCGAAGTTCGGAGGAGTTCGGAATTCGAAGTGGGAGATTCGGAATTCGAAGTTCGGAAGTTCGGAATTCGAATTCGAAGTTCGGAAGTTCGGAATTCGAATTCGAAGTTCGAATTCGAATTCGAATTCGAAGTTCGAATTCGAATTCGAATTCGAAGTTCGAATTCAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAAT	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence ip 003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPFM GEFEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDPG HWAPPFCDKF NKKTTIEKT UCENCE n #: NM_003 .1043 21 GCAAAAAAGGA AGAGGGGACGG CGGGGGACGG CGGGGGACGG CGGGGGACGG CGGGGGACGG CGGGGGACGG CGGGGGACGG CGGGGACGGC CGGGGGACGG CGGGGGACGG CGGGGACGGC CGGGGACTGC CGGGAATTGCA ATCAAAGACC CACGACCTGT AAGGACTTGC	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA ASSFTETHYL DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG QPQSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTT TGAGCCACAA CCCTGCAGAA GCGTGTTTGA TGGCCATCAG GGGCGGCTGC TGCTGCACGA	TACGTGGGCA CCAATTATAA 41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTG TCCCCCACCGAG TACAGCGGAG ATGTTTCGAG GGAAATGGTG CCCACCAC CCCACGGGAAAC ACCCTACGTG ACCCTACGTG	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR KMKLLPRKSH ELGHNFGMNH CLPNLPEVRE EDCQLKPAGT QCCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP VPARPLPAXP PAPQYPHQVP 51 GACGGGGAGG GCTTTGGTG GGTTCCCAAG ATCCAGCACT AACAACTCTT GGAAAATTTG GGAAAATTG GGCTCCGGGTGA GCCCGGGTGA GCCCGGGTGA GCCCGGGTGA	60 120 180 240 360 420 480 540 660 720 780 840 900
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	50 55 60 65 70 75 80	TATATACTAT AGATGCCCAA ACCAAAAAAA Seq ID NO: Protein Acc I MAARPLPVSP SKNHEEVLNI YHGHVRGYSD SHHNTPNLAA LIEIANHVDK DNAQLVSGVY DTLDRGCSCO AKPAFGICFE LETNIPLQG AMQCHGRGVC LAAGFVVYLK DSYPPKDNPR ALRQAGGTCK RSTHTAYIK Seq ID NO: Nucleic Ac Coding seq I GAGGAAGAGG GAGGAAGAG GAGGAAGAG GAGGAAGAG GTTTGGTCAA GTGGGAATTCG ATGCCCACGG ACAGGTTCGG ACAGGTTCGGT ACTGCTGGTT	TAAAAAGGTT ATCCTTAGAT ATCCTTAGAT AAAAAAAAAA	TACAGAATTT CTGGCATGTT AA sequence NP_003465 21 ALLAPCEARG INLERNEGLI LRGLIVFENE WARRHKRETL LVGVEVWNDM IMSMCTADQS NASTGYPPM GEFEECMNRC HCPANVYLHD NCGKVSKSSF YLGDDMPDFG HWAPPFCDKF NKKTTIEKLR SRPLNGLNVP DPLARTTRLT UERICE 1 #: NM_003 .1043 21 GCAAAAAGGA AGAGGGGAGCGGC GCGGGGCCGGG GCCGGCCTGT GTGGGGTTGCG GGCTTTGCA ATCAAAGACG ATCAAAAGACG CCGGAACTGCC CCGAGCCTGT AAGGACTTGCC GGAGGACTGCT CGGAGGACTGCT CGGAGGACTGCT CGGAGGACTGCT CGGAGGACTGCT CGGAGGACTGCT CGGAGGACTGCT CGGAGGACTTGCCT CGGAGGACTTGCT CGGAGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTCT CGGAGACTTGCT CGGAGACTTGCT CGGAGACTTCT CGGAG	31 VSLWNEGRAD ASSFTETHYL SYVLEPMKSA KATKYVELVI DKCSVSQDPF GGIVMDHSDN VFSSCSRKDL CNATTCTLKP GHSCQDVDGY AKCEMRDAKC LVLAGTKCAD GFGGSTDSGP CVRPSRPPRG GPGSTQRVLP HALARTPGQW 714 31 AGAGTGGGAG ACAAAGGATC TGGGCCAGTA CCCTGCAGAA GCGTGTTTGA TGACTTTTCT CCTTGAAATG CGGCGGTGGC TGCTGCACGA AGGAGGCCAT AGGAGGCCAT AGGAGGCCAT AGGAGGCCAT AGGAGGCCAT AGGAGGCCAT	41 EVVSASVRSG QDGTDVSLAR TNRYKLFPAK VADNREFQRQ TSLHEFLDWR PLGAAVTLAH ETSLEKGMGV DAVCAHGLCC CYNGICQTHE GKIQCQGGAS GKICLNRQCQ IRQADNQGLT FQPCQAHLGH PLHRAPRAPS ETGLRLAPLR 41 GAGGAGGGGA CAGGTCTCCC CATGACCCTA CCACCCGAG ATGTTTCGAG GCACAACGCT TAAGGCCCAC GGAAATGGTG CCACGAGGCAC ACCCTACGTG CCACCCAGGCCACC CCAGGAGAAC CCCTACGTG CACCCACGGG	51 DLWIPVKSFD NYTVILGHCY KLKSVRGSCG GKDLEKVKQR RKKLLPRKSH ELGHNFGMNH CLFNLPEVRE EDCQLKPACT QQCVTLWGPG RPVIGTNAVS NISVFGVHEC IGILVTILCL LGKGLMRKPP PAPQYPHQVP 51 AGCGGCGAAG GACGGGAGGT GCTTTGGTGT GGTCCCAAG ATCCAGCACT AACAACTCTT GGAAAATTTG GGTCTGCGGC TCCCAGTTGC ACCCGGGTGA GGCCTGGAG GGTCCGGGTGA GGCCCGGGTGA	4980 5040 60 120 180 240 360 420 780 900 600 720 780 900 120 180 240 360 420 420 420 420 420 600 600 600 600 600 600 600 600 600 6

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	GGGCCCACCA	CCCCCAACCA	CCACATCACC	TOCCAGAGOC	CACCACTACC	GAGACTGGCC	900
	GOGCCCACCA	CGGGGAAGCA	GGACATCACC	TOCCHOMBCC	CAGCAGIAGG	GAGACTGGGG	
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_	TCGGGGGCCT	TGGGGCTCAG	GGACCTTCCG	GAAGCAGCGA	GTGGGAAGAC	GAACAGTCTG	1020
5	AGTATTCTGA						1080
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	GTCCATTTTC	TTATCTATGG	ACATTCCAAA	ACATTTACCA	TTAGAGAGGG	GGGATGTCAC	1140
	ACGCAGGATT	CTGTGGGGAC	TGTGGACTTC	ATCGAGGTGT	GTGTTCGCGG	AACGGACAGG	1200
	TCACATCCAC	NCCCCTCCCC	COURCECCE	TCAGGGGTGC	CTCCTCAATT	CTCCACTTAC	1260
4.0	ACGTACTCAA	GGGAGCGCGC	CCGCGTTATC	CTCGTACCTT	TGTCTTCTTT	CCATCTGTGG	1320
10	AGTCAGTGGG	TOTOGGCCCC	TOTATTATA	GGGAGGTGAA	CCACCGAGGG	GCAGGGCAAG	1380
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				GGTGCTGGGC			1440
	GCAGCAGCCT	CTGGTGCTGT	CTCCGCGGAA	GTCAGGGCGG	CTGGATTCCA	GGACAGGAGT	1500
				AGGAGAAGGG			1560
	AGGGGGTGCT	TGGTGCCAAA	CTGAAATTCA	GTTTCTTGTG	TGGGGCCTTG	CGGTTCAGAG	1620
15	CTCTTCCCCCA	GEGTEGAGEG	AGGAGTGTCA	TTTCTATGTG	TAATTTCTGA	GCCATTGTAC	1680
		22222222	CTCCCCC A CCC	GAGTGGCCCC	TIA THE A COMMUNE	TATTTIN A CC	1740
	ACTGCTTCAA	ATCTCGATTT	CACTTTTTTT	ATTTATCCAG	TTATATCTAC	ATATCTGTCA	1800
				TGGGTCATTA			1860
				GGCTGATTTT			1920
20	TTABABGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	GCCTGACATG	GACTCCTGCC	1980
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	TTTCCCTTAG	GATTTCGTTA	TCTCACCTTG	ACCCTCAGCC	AAGATTGGTA	AAGCTGCGTC	2100
				CTGGCTTCTC			2160
~ =	GAAAGAAGAG	AATGAAGACT	ACTTAGTAAT	TCCCATCAGG	AAATGCTGAC	CITTIACATA	2220
25	AAATCAAGGA	GACTGCTGAA	AATCTCTAAG	GGACAGGATT	TTCCAGATCC	TAATTGGAAA	2280
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					CAGAGAGAGA	GAGAGAGAGA	2340
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35	TSRKCPATRE	MVSQLORECY	LKHDLCAAAO	ENTRVIVEMI	HFKDLLLHEP	YVDLVNLLLT	180
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	CIATIACAGA	CCCATTAIAG			GDCLEGOT	man acres 600	
				CATCTCTTTC			240
	GCATCCTGGA	CAGGAAGAAG	ACATCCTCAG	CCCACCACCC	CTTCCCCTCC	AATGTGGACT	300
				ACTCTTCATT			360
50	GAGIGIIGGG	TCMCIGNIA	AGCAGIGCAG	ACICITOTI			
50				GAGACCTTGC			420
	AAAGATGTGA	AAGAAGACCT	TTAGCCACTC	AGTGTTATCA	AAAGCAATCA	CCAAAGAAGT	480
				ATCAGCAGTA			540
	TITIGCATCI	GGCATIGIGI	IGGGWCGICC	ATCAGCAGIA	CCGIACGGIC	ICITIACIGG	
	ACAAGTATTT	ACACCTTGTT	AACAGCAGTG	TACACCCGGT	GGAAAACTCC	TATCTAATGG	600
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<i>)</i>	CCTTAAACTT	TATTGGCTTC	TCCGGTCTTG	CCACTGCGGG	GCCCAAAAAC	TTTCAGAAGT	720
	AGGAATCCTG	TGGCATCTGC	TAATGGTGAT	TGGAAGAAAG	AGTAGAGGTG	ACAGTATCTA	780
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	AGAATCAAGA	GGATGGTTTT	CAAAGGAGGG	CGCACGGAGA	CGGAACTTGC	TCTGAAATAC	600
75		GAGGGTTGCC	TOCACCACA	AATCC	TGCCCCAGAT	CCTCATCATC	660
						GAAGGAAAGG	
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	GGCCTCTTCA	GCACCCTCAG	CAGCTCGGCC	ATCTGCTCCA	GCGCCACGCC	AGCTGGGAGC	900
80						CTGTGACTCG	
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	CAGCCCTGCC	AGAATGGAGG					
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	CAGCCCTGCC TGCCCGCTGG GTCGACCTCC	AGAATGGAGG CCTTTGGAGG TCTTCCTGCT	GGAGGCTAAC GGACAGCTCT	TGTGCCCTGA GCGGGCACCA	AGCTGAGCCT CTCTGGACGG	GGAATGCAGG CTTCCTGCGG	1080 1140
0.5	CAGCCCTGCC TGCCCGCTGG GTCGACCTCC GCCAAAGTCT	AGAATGGAGG CCTTTGGAGG TCTTCCTGCT TCGTGAAGCG	GGAGGCTAAC GGACAGCTCT GTTTGTGCGC	TGTGCCCTGA GCGGGCACCA GCCGTGCTGA	AGCTGAGCCT CTCTGGACGG GCGAGGACTC	GGAATGCAGG CTTCCTGCGG TCGGGCCCGA	1080 1140 1200
85	CAGCCCTGCC TGCCCGCTGG GTCGACCTCC GCCAAAGTCT	AGAATGGAGG CCTTTGGAGG TCTTCCTGCT TCGTGAAGCG	GGAGGCTAAC GGACAGCTCT GTTTGTGCGC	TGTGCCCTGA GCGGGCACCA GCCGTGCTGA	AGCTGAGCCT CTCTGGACGG GCGAGGACTC	GGAATGCAGG CTTCCTGCGG TCGGGCCCGA	1080 1140 1200
85	CAGCCCTGCC TGCCCGCTGG GTCGACCTCC GCCAAAGTCT	AGAATGGAGG CCTTTGGAGG TCTTCCTGCT TCGTGAAGCG	GGAGGCTAAC GGACAGCTCT GTTTGTGCGC	TGTGCCCTGA GCGGGCACCA GCCGTGCTGA	AGCTGAGCCT CTCTGGACGG GCGAGGACTC	GGAATGCAGG CTTCCTGCGG	1080 1140 1200

	GATGTGCCTG .	ACCTGGTCTG	GAGCCTCGAT	GGCATTCCCT	TCCGTGGTGG	CCCCACCCTG	1320
	ACGGGCAGTG	CCTTGCGGCA	GGCGGCAGAG	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	1380
	CAGGACCGGC	CACGTAGAGT	CCTCCTTTTG	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	1440
	CAGGACCGGC	CACGIAGAGI	6616611116	CICICICACI	TOTTOTOTO	ACCCACTGAG	1500
_	GCGGGCCCAG	CGCGTCACGC	AAGGGCGCGA	GAGCIGCICC	TGCTGGGTGT	AGGCAGIGAG	
5	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	1560
	GATCCTCAGG .	ATCTGTTCAA	CCAAATCCCT	GAGCTGCAGG	GGAAGCTGTG	CAGCCGGCAG	1620
	CGGCCAGGGT	CCCCCA CACA	DECCCTEGAC	CTCTCTTCA	TCTTCCACAC	CTCTGCCTCA	1680
							1740
	GTAGGGCCCG						
	GAGGTGAACC	CTGACGTGAC	ACAGGTCGGC	CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	1800
10	GCCTTCGGGC	TGGACACCAA	ACCCACCCGG	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	1860
10	000110000	0000000000	COURT COCCC	ACCGCCCTGC	TOCACATOTA	TCACAAAGTG	1920
	CCCTACCTAG	GIGGGGIGGG	CICAGCCGGC	ACCGCCCIGC	TOCACATOTA	TONCAMOTO	
	ATGACCGTCC	AGAGGGGTGC	CCGGCCTGGT	GTCCCCAAAG	CTGTGGTGGT	GCTCACAGGC	1980
	GGGAGAGGCG	CAGAGGATGC	AGCCGTTCCT	GCCCAGAAGC	TGAGGAACAA	TGGCATCTCT	2040
		TOCCOCCTCCC	CCCTCTCCTA	AGTGAGGGTC	TOCGGAGGCT	TGCAGGTCCC	2100
15	GICIIGGICG	IGGGCGIGGG	GCCIGICCIA	AGIGAGGGIC	20000000	CONTROL COC	
15	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC	GCCGACCTGC	GGTACCACCA	GGACGIGCIC	2160
	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	CCAGTCAACC	TCTGCAAACC	CAGCCCGTGC	2220
	ATTENATORGE	CCACCTCCCT	CCTGCAGAAT	GGGAGCTACC	GCTGCAAGTG	TCGGGATGGC	2280
	MIGHAIDAGG	000000000	CARCOCIONA	TGGAGCTCTT	COTOTOTATO	TOTORCOCAG	2340
	GGATGGATTC	TTGAGACGCC	CCTGAGGCAC	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	2400
20	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG	GGCACTGAAA	TGGTGCCTAC	CTTCTGGAAT	2460
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	MPNTSGTTRI	EIWLLOEPPG	HRALVAALLP	VSPSPELALA	PGYPPVPAAD	DRFTLPMIGG	60
	OMNGENIDLM	OT CUT CVERT.	VCKDDEEVNE	VHVSKETIGK	TSAASKMMWC	SAAVDIMFLL	120
	OLUGEYADTM	SEGVECTERE	VGKEFFEANE	ANARMITAN	CONTRACTOR D	CHOMOORIUS	
	DGSNSVGKGS	FERSKHFAIT	VCDGLDISPE	RVRVGAFQFS	SIBHPERFPD	SESTOUEVKA	180
30	RIKRMVFKGG	RTETELALKY	LLHRGLPGGR	NASVPQILII	VTDGKSQGDV	ALPSKQLKER	240
	CHAMILEVICIO	PODWPPT.VAT.	ASERBGOHUL.	LAEQVEDATN	GLESTLSSSA	ICSSATPAGS	300
	GVIVEAVGVR	FERMENDE	ADDITIOQUITE	2227 221001	CDT & DOOD BANK	CAT WE ST FICE	360
	PELVFMERLM	GISLIGPCDS	QPCQNGGTCV	PEGLDGYQCL	CPLMFGGEMM	CALALBUECA	
	VDLLFLLDSS	AGTTLDGFLR	AKVFVKREVR	AVLSEDSRAR	VGVATYSREL	LVAVPVGEYQ	420
	O'ISM'IUGIU	GIDPPGCPTI.	TGSAL POARE	RGFGSATRTG	ODRPRRVVVL	LTESHSEDEV	480
35 .	DAEDDAMODD	0111100212	ATTENDED	CONTRACTO	DOOD! PHOTO	PLOCKLCPPO	540
22 .	AGPARHARAR	EPPPPGACE	MAKWETTERTT	GSPKHVMVYS	DECORENCIE	EDQGRDCSRQ	
	RPGCRTQALD	LVFMLDTSAS	VGPENFAQMQ	SFVRSCALQF	EVNPDVTQVG	LVVYGSQVQT	600
	AFGLDTKPTR	AAMLRAISOA	PYLGGVGSAG	TALLHIYDKV	MTVQRGARPG	VPKAVVVLTG	660
	CDCAEDAAVD	NOVI DANKETO	UT VICUCIONI.	SEGLRRLAGP	PDST.THVAAV	ADLRYHODVI.	720
	GRGAEDAAVP	AUKDRINGIS	ADAAGEAD		MECONICENTE	Meecevarea	780
40	IEWLCGEAKQ	PVNLCKPSPC	MNEGSCVLQN	GSYRCKCRDG	WEGPHCENKE	WESCSVCVEQ	760
40	GWILETPLRH	MAPVOEGSSR	TPPSNYREGL	GTEMVPTFWN	VCAPGP		
	_	_					
	O TD NO	04 DVV					
	seq ID NO:	84 DNA seq	rence				
	Nucleic Act	id Accession	n #: Eos se	quence			
				quence			
45		uence: 12	424		41	51	
45				quence	41	51	
45	Coding sequ	uence: 12	424 21 	31 		1	
45	Coding sequ	uence: 12	424 21 			1	60
45	Coding sequents ATGCCCCCTT	uence: 12 11 TCCTGTTGCT	424 21 GGAGGCCGTC	31 TGTGTTTTCC	TGTTTTCCAG	AGTGCCCCCA	60 120
45	Coding sequents ATGCCCCCTT TCTCTCCCTC	lence: 12 11 TCCTGTTGCT TCCAGGAAGT	424 21 GGAGGCCGTC CCATGTAAGC	31 TGTGTTTTCC AAAGAAACCA	 TGTTTTCCAG TCGGGAAGAT	AGTGCCCCCA TTCAGCTGCC	120
	Coding sequence of the control of th	ience: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT	 TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC	120 180
45 50	Coding sequence of the control of th	111 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG	 TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT	120 180 240
	Coding sequence of the control of th	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAGAG	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT	120 180
	Coding sequence of the control of th	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAGAG	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT	120 180 240 300
	Coding sequence of the control of th	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCGAGAG CCTTGGATTC	224 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTCAACC	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG	120 180 240 300 360
	Coding sequence of the control of th	lence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAAGG CCTTGGATTC AAGAGGCCG	21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACGAGACG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTC CAACAGGAAG GAACTTGCTC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA	120 180 240 300 360 420
50	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAG CCTTGGATTC AAGGAGGTC AAGGAGGCC AAGGAGGCC	424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG	120 180 240 300 360 420 480
50	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAG CCTTGGATTC AAGGAGGTC AAGGAGGCC AAGGAGGCC	424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG	120 180 240 300 360 420
	Coding sequilar and control co	IEENCE: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTC AAGGAGGACCT AAGGAGGACC AAGGAGGACAGAAA GGGATGTGGAAA	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTC GGTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC	31 TGTGTTTTCC AAAGAAACCA GACACTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA	TGTTTTCCAG TCGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGGG TGTCACTGTG	120 180 240 300 360 420 480 540
50	Coding sequilibrium sequilibriu	Hence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCCGAGAG CCTTGGATTC AAGGAGGCG GAGGCAGAAA GGGATGTGGC GAGGCAGAAA GGGATGTGGC GGGTCAGGTT	424 21 GGAGGCCGTC CCATCTAAGC GGCTGCAGTG TGAAAGGTCC GGTTCAGAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CACCAGGAGG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGGAGCTGA	TGTTTTCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGGAGCCT	120 180 240 300 360 420 480 540 600
50	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGTGGC GGGTCAGGTT ACCTGCTGTT	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACCGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG	31 TGTGTTTTCC AAAGAACCA AGACATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGATC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG	TGTTTTCAG TCGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CASCGAGCCT CCTCTTCAGC	120 180 240 300 360 420 480 540 600 660
50	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGC GGTCAGGTT ACGTGCTGTT ACGTGCTGTT	424 21 GGAGGCCGTC CCATCTAAGC GGCTGCAGTG TGAAAGGTC GGTCAGAGTG ATTTTCAACC CACGGAGACC TGCTTCTGTG ACTGCCATCC TCCCAGGTGG CGGCTGAGCAG CTGCTCAGCG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGACATTCC CACCAGATCC CCCCAGATCC AAGCAGCTGA GAGGAGCTGA GAGGAGGTGG GTGGAGGATG GCCACGCCAG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAATACCT TCATCATCGT AGGAAAGGGG ATGCACTAGG CCACCAACGG	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCAGGGTCAC	120 180 240 300 360 420 480 540 600 660 720
50	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGC GGTCAGGTT ACGTGCTGTT ACGTGCTGTT	424 21 GGAGGCCGTC CCATCTAAGC GGCTGCAGTG TGAAAGGTC GGTCAGAGTG ATTTTCAACC CACGGAGACC TGCTTCTGTG ACTGCCATCC TCCCAGGTGG CGGCTGAGCAG CTGCTCAGCG	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGACATTCC CACCAGATCC CCCCAGATCC AAGCAGCTGA GAGGAGCTGA GAGGAGGTGG GTGGAGGATG GCCACGCCAG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAATACCT TCATCATCGT AGGAAAGGGG ATGCACTAGG CCACCAACGG	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCAGGGTCAC	120 180 240 300 360 420 480 540 600 660
50 55	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAAGCT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA AGGATGTGGC GAGCAGAAA AGGATGTGGC GGTCAGGTT ACCGGCCAT ACAGGACGCT ACAGGACGCT	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTTCAAGGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCAG CTGCTCCAGG	31 TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC AAGCAGCTGA GAGGAGCTGC GTGGAGGATG GCCACGCCAG CCGGAGTTCG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAATACCT TCATCATCGT TCATCATCGC ATGCACTGGC CCACCAACGG ACTGCAGGGT ACTGCAGGGT CTGCCAGGGT	AGTGCCCCA TTCAGCTGCC TTGGGTCTAAC CTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCGAGGCTCAC CCCATGCTGG	120 180 240 300 360 420 480 540 600 660 720 780
50	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGGAGCTT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGTGGC GGGTCAGGTT ACTGGCTGT ACTGGCCAT ACAGGACGCT GGCGGACCCT	424 21	31 TETGTTTTCC AAAGAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CACAGGAAG GAACTGGCTCA AGCAGCTGA GGGAGCTGC GTGGAGGATG GCCACCCCAG GCGCCCCAG GCGCACCCCAG GCGCACCCCAG GCGCACCCCAG	I TGTTTTCAG TCGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGGGAGCCT CCTCTTCAGC CCAGGCTCAC CCCATGCTGG CAGCTGGAAG	120 180 240 300 360 420 480 540 660 720 780 840
50 55	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT AGCAGGAGGC AAGGAGGCG AGGAGAGAAA GGATCAGGTT ACCTGCTGTT GCTCGGCCAT ACAGGACGC GGCGACCCT TACCCCCCC	424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGGAGTGG GCCACGCCAG GCGGAGTTCG GCTGCACACT TACAGGACCA	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCATGCTGC CAGCGTCAC CCCATGCTGA CACTGGAGG CACTGGAGG CACTGGAGG CACTGGAGG CCCCTGTGAC	120 180 240 300 420 480 540 600 660 720 840 900
50 55	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT AGCAGGAGGC AAGGAGGCG AGGAGAGAAA GGATCAGGTT ACCTGCTGTT GCTCGGCCAT ACAGGACGC GGCGACCCT TACCCCCCC	424 21	31 TGTGTTTTCC AAAGAAACCA GACATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGAGGAGTGG GCCACGCCAG GCGGAGTTCG GCTGCACACT TACAGGACCA	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CCATGCTGC CAGCGTCAC CCCATGCTGA CACTGGAGG CACTGGAGG CACTGGAGG CACTGGAGG CCCCTGTGAC	120 180 240 300 360 420 480 540 660 720 780 900 950
50 55	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCTGGGATC AAGGAGGGC GAGGAGAAA ACGATGTGGCC GGCTCAGGCAT ACGGCCAT ACAGGACGCT TAACCCACCC GCCAGAATGG	424 21	31 TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC GTGGAGGTGA GAGGAGCTGC GCGCGCCAG GCCACGCCAG CCGGAGTTCG GCTGCACACT TACAGGACCA GTTCCAGAAG GTTCCAGAAG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA CCTGCCCAGG GACTGGACGG GACTGGACGG	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CACCTGGAAG CCCCCTGTGAC CCTACCTGTAGC CCCCTGTGAC CCCCTGTGAC CCTACCTGTAC	120 180 240 300 360 420 480 540 660 720 780 900 950
50 55	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGTGGC GGTCTAGGTT ACGTGCTGT ACGGCCAT ACAGGACGCT TAACCCACCG GCCAGAAACG TGGCCTTTGGTTGGCTT TAACCCACCG TGACAGAATG	424 21 GGAGCCGTC CCATCTAAGC GGCTGCAGTG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCAG TGCTCCAGCTGG GGAGATGTCCAGC TGCTCCAGC TGCTCCAGC TGCAGCTGG AGGACACTTC TGCAGCTGC TGCAGCTGC TGCAGCTGC TGCAGCTGC AGGCACAGT	31 TETGTTTTCC AAAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC AGCAGCTGC GTGGAGGATG GCCACCCAG CGGGAGTTCG GCTGCACACCAG GCTGCACACCAG AGCACCAG AGCACCAG AGCACCAG AGCACCAG AGCACCAG AGCACCAG ACTGCACAACA AACTGTGCCC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TTGGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGCGAGCCT CCAGCTGGAAG CCCCTGTGAC CCAGTGCAC CCTAGCTGGAATGC CCTGGAATGC	120 180 240 300 360 420 480 540 660 720 780 840 900 1020
50 55 60	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTGGCCAGAAAA GGGATGTGGC GAGCAGAAA GGGATCAGGTT ACCTGCTGTT GCTCGGCCAT ACAGGACGT TAACCCACCC GCCAGAATGG TGGCCTTTGGTTGGCCTTTACCTCTCTT	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACCGAGACG TGCTTCTGTG ACTGCCATCC TCCCAGGTGG GGCTGAGCAG CTGCTCCAGC GGAGATGT TGCCACTGC AGGCACATGT AGGGGAGGT AGGGAAGGT GGTGCTGCTGC AGGCACATGT AGGGGAAGGT GCTGCAGC	31 TGTGTTTTCC AAAGAACCA AGCATCATGT AAGCACTTTG GGAGCATTCC CAACAGGAAG GAACTGGAC CCCAGATCC AAGCAGCTGA GGAGCTGC GTGGAGGATG GCCACCCCAG GCTGCACACT TACAGGACCA GTTCCAGAAG TACAGGACCA GTTCCAGAAG TTCCAGAAG TTCCAGAGAC TCTCCGGGCA	I TGTTTTCCAG TCGGGAAGAT TCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAG TCTGCACAGA CACTGATGGG TGTCACTGTG CAGGGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CAGCTGGAAG CCCTGTGAC CCTGAATGC CCGGAATGC CCGGAATGC CCGGCTTCCTG	120 180 240 360 420 480 540 600 720 780 840 900 900 1020 1080
50 55 60	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAAG GCATGGATTC AAGGAGGCG GAGGCAGAAA ACGATGGT ACCTGCTAT GCTCGCCAT TAACCCACCC TCCTCTCTCT TCTTCGTGAA	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTTCAAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCG TCCCAGGTGG GGTGAGCAG GGTGACAG TGCTCCAGC GGAGATGTC TGCGATGCT AGGGACATGT AGGGACATGT GCTGCACCG GGTGACAG GGGGAGGCT GGTGACAG GGGGAGGTTGTG GGGGTTGTG	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC GTGGAGGTGA GACTTGCTG GCCCCAGCCCAG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA CCTGCCCAGG GACTGGACGG TGAAGCTGAC TGAAGCTGAC TGAAGCTGAC TGAAGCTGAC TGAAGCTGAGA TGAAGCTGAGA	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TTGGTCTAAC CTGTGACGGT TAATCAAGAGG TCTGCACAGA CACTGATGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CCCCTGGAAGC CCCCTGTGAC CCTGGAATGC CCGGGTTGCC CGGGCTCCTG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140
50 55	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAAG GCATGGATTC AAGGAGGCG GAGGCAGAAA ACGATGGT ACCTGCTAT GCTCGCCAT TAACCCACCC TCCTCTCTCT TCTTCGTGAA	424 21 GGAGGCCGTC CCATGTAAGC GGCTGCAGTG TGAAAGGTCC GGTTCAAGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG ACTGCCATCG TCCCAGGTGG GGTGAGCAG GGTGACAG TGCTCCAGC GGAGATGTC TGCGATGCT AGGGACATGT AGGGACATGT GCTGCACCG GGTGACAG GGGGAGGCT GGTGACAG GGGGAGGTTGTG GGGGTTGTG	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC GTGGAGGTGA GACTTGCTG GCCCCAGCCCAG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA CCTGCCCAGG GACTGGACGG TGAAGCTGAC TGAAGCTGAC TGAAGCTGAC TGAAGCTGAC TGAAGCTGAGA TGAAGCTGAGA	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TTGGTCTAAC CTGTGACGGT TAATCAAGAGG TCTGCACAGA CACTGATGG TGTCACTGTG CAGCGAGCCT CCTCTTCAGC CGAGGCTCAC CCCATGCTGG CCCCTGGAAGC CCCCTGTGAC CCTGGAATGC CCGGGTTGCC CGGGCTCCTG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140
50 55 60	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCTT GCCCGAGAAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGGATGGCC GGTCAGGTT ACGTGCTGT ACGGCAT ACAGGACGCT GCCAGAATG GCCAGACCC TAACCCACCC GCCAGAATG TGGCCTTTGG TCCTCTTCCT TCTTCGTGAA	424 21	TETGTTTTCC ANAGANCCA ANAGANACCA GACATCATGT AAGCACTTGG GAGCATTCC CCCCAGATCC CCCCAGATCC AGCAGCTGC GTGGAGGATG GCCACCCAG CGGGAGTTCCAGACC TACAGGACAC ATCAGGACAC ATCAGGACAC TTCCAGAGA AACTGTCCCC CTGCTGGGCGTGC CCGGCCGTGC CCTGCTGGTGG	I TGTTTTCCAG TCGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TTGGCCGTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTGC CCAGTGCAC CCCATGCTGG CAGCTGGAAG CCCCTGTAAC CCTGGAATGC CCTGGAATGC CCTGGAATGC CCTTCCGGCC CGGGGGAGATAC	120 180 240 300 360 420 540 600 600 720 780 840 900 1020 1080 1140
50 55 60	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG CCTTGGATTG GCCCGAGAG GCATGGGT ACGGGTCAGGT ACTGGCTAT ACAGGACGC TACCACCC GCCAGAATGG TGGCCTTTGG TCCTTCCT TCTTCGTGAA TGGCCACAT TGGCCACAT TCGCCACAC TCGCCCACAC TCCTCCTTCCT TCTTCGTGAA TGGCCACAT TGGCCCACAT TCGCCACAC TCCTCCTTCCT TCTTCGTGAA TGGCCCACAT TCGCCACAT TCTCCTTCCT TCTTCGTGAA TGGCCACAT TCTGACCTGGT	424 21	TETGTTTTCC AAAGAACCA AGCATCATTG GAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GGCACCCAG GCCACCCAG CGGGAGTTCG GCTGCACACT TACAGGACCA TTCCAGAAG AACTGTTCACAGAC CGGGCCTGG CCTGCCGGCA CCGGCCTGGC CTGCCGGCAC CGGCCTGGC CTGCTGCTGG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGC TGGGTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CAGTGACTGTG CAGGGAGCCT CCTCTTCAGC CCAGGCTCAG CAGCTGGAAG CCCTGTGAC CTACCAGTGC CTGCAGGATGC CTGCAGGATGC CTGCAGGATGC CTGCAGGATGC CTGCAGGATGC CGGGGGAGTAC TGGGCCCACC	120 180 240 300 360 420 660 720 840 900 900 1020 1080 1140 1260
50 55 60	Coding sequilibrium sequilibriu	Hence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCAGGAGAA AGGAGGGCG GAGGCAGAA ACGAGGGCG GGCGACCT TAACCCACCC TCCTCTCTCT TCTTCGTGAA TGGCCACAT ACGCCACAT TGTCTGTGAA TGGCCACAT TGTCTGTGAA TGGCCACT TGTCTTCTT	424 21	TGTGTTTTCC ARAGAAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CTGGAGGAGG GACTTGGTG GGAGGAGTGC GTGGAGGATGC GCACCCAG GCACCCCAG GCACCCCAG CCGGGAGTTCG GCTCCAGAAG AACTGTGCCGGA CCGGCCTGCACCT TCCAGAAG AACTGTGCCG CTGCTGCGGGG CTGCTGCAGGA CGGGCCTTGC	I TGTTTTCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATAGG TGTCACTGTG CAGCGAGCCT CCCATGCTGG CAGCGTCAC CCCATGCTGG CCCCTGTGAC CCCTGTGAC CCTGGAATGC CGGGTCCCTG CGGCTCCCTG CGCCTCCGGC CGGCTCCCTG CTCCCGGCC CGCCTCCACC CTCCCACC	120 180 240 300 360 420 540 600 720 780 900 960 1020 1140 1200 1230
50556065	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT ACGTGCAGT TAACCACCC GCCAGAATGG TCGCCTTTCGT TCTTCGTGAA TGGCCACATA CTGACCTGGT GGCCACATA CTGACCTGGT GGCCACATA	424 21 GGAGGCCGTC CCATCTAAGC GGTCAGAGTG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCATCCAGC GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGAGATGTC TGCGCTCCAG TGCTCCAGC GGAGATGGTC TGCGCTCCAG CGGAGATGGTC TGCGCTCTGAGCAG CTGCACAGC AGGCACATGT AGGGAGAGCT GCTGGACAGC GCGGTTTGTG CAGCAGCGGAG AGTGAGCCTC AGGCAGCCCC GCAGAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCCC AGGCGCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCCC AGGCAGCCCCC AGCCCCCCCC	TGTGTTTTCC ARAGARACCA AGCARTAGT AGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CGAGCAGG GACTTGCTC AGCAGCTGA GAGCAGTGA GCACCCCAG GCGGAGCTCG CGGAGCTCG CTGCAGACG CTGCAGACG CTGCAGACG ACTGCAGACG ACTGCAGACG CTCTGCGGGCA CCGCCGTGC CTGCTGGTGG CTGCTTGCT	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ACTGCAAGGG ACTGCAAGGG GCCCTTCTA CCTGCCAGGG TGAAGCTGAC GACTGGACGG TGAAGCTGAC CCACTCTGGA CCGCTCTGGA CCGCTGCCAGG TGAAGCTGAC CCCTCTGGA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACGGG CACCGAGGCTCAC CCACTGATGGG CCACTGATGG CCACTGATGG CCCATGCTGG CCCATGCTGG CCCATGCTGG CCTGTGAC CCTGTGAC CCTGTGAC CCTGGAATGC CGGGGGTAC CCTCTGGGCC CGGGGGACA CCCCACGCCCACC CGCCACCACCACCACCACCACCACCACCACCACCACCACC	120 180 240 300 360 420 540 600 660 720 780 840 900 950 1020 1120 1260 1320 1380
50556065	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGT ACGTGCTGTT ACGTGCTGTT ACGTGCTGTT ACGTGCAGT TAACCACCC GCCAGAATGG TCGCCTTTCGT TCTTCGTGAA TGGCCACATA CTGACCTGGT GGCCACATA CTGACCTGGT GGCCACATA	424 21 GGAGGCCGTC CCATCTAAGC GGTCAGAGTG ATTTCAACC CACGGAGACG TGCTTCTGTG ACTGCATCCAGC GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGAGATGTC TGCGCTCCAG TGCTCCAGC GGAGATGGTC TGCGCTCCAG CGGAGATGGTC TGCGCTCTGAGCAG CTGCACAGC AGGCACATGT AGGGAGAGCT GCTGGACAGC GCGGTTTGTG CAGCAGCGGAG AGTGAGCCTC AGGCAGCCCC GCAGAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCC AGGCAGCCCCC AGGCGCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCC AGGCAGCCCCCC AGGCAGCCCCC AGCCCCCCCC	TGTGTTTTCC ARAGARACCA AGCARTAGT AGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CGAGCAGG GACTTGCTC AGCAGCTGA GAGCAGTGA GCACCCCAG GCGGAGCTCG CGGAGCTCG CTGCAGACG CTGCAGACG CTGCAGACG ACTGCAGACG ACTGCAGACG CTCTGCGGGCA CCGCCGTGC CTGCTGGTGG CTGCTTGCT	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ACTGCAAGGG ACTGCAAGGG GCCCTTCTA CCTGCCAGGG TGAAGCTGAC GACTGGACGG TGAAGCTGAC CCACTCTGGA CCGCTCTGGA CCGCTGCCAGG TGAAGCTGAC CCCTCTGGA	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACGGG CACCGAGGCTCAC CCACTGATGGG CCACTGATGG CCACTGATGG CCCATGCTGG CCCATGCTGG CCCATGCTGG CCTGTGAC CCTGTGAC CCTGTGAC CCTGGAATGC CGGGGGTAC CCTCTGGGCC CGGGGGACA CCCCACGCCCACC CGCCACCACCACCACCACCACCACCACCACCACCACCACC	120 180 240 300 360 420 540 600 660 720 780 840 900 950 1020 1120 1260 1320 1380
50 55 60	Coding sequilibrium sequilibriu	IERCE: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGCTCAGGAAGT GCCCGAGAG GCATGGATT ACAGGAGGTGGC GAGCAGAAA ACAGGACGT ACAGGACGT ACACCACCC GCCAGAATGG TGGCCTTTCCT TCTTCGTGAA TGGCCACATA CTGACCTGGT GGCCACATA CGGCCACTAGGCCCT TCCTTCCT TCTTCGTGAA TGGCCACTAG GGCCACTGG GCCACTGG GCCACTGG	424 21	TGTGTTTTCC AAAGAACCA AAGAATCATTG GAACATTTG GAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGCATCC AGCAGCTGA GCGCACCCAG GCTGCACACC TACAGGACCA TTCCAGAAG GATTCCAGAAG GTTCCAGAAG GTTCCAGAAG GTTCCAGAAG GACTGCACACT TCTGCGGCATCC CTGCTGGTGG GATGGCTTCC GAGGGTGGCT TTGCTCACTG	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC CTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGTGACTGG CAGCAGACCT CCTCTTCAGC CAGCTGGAAG CCCCTGTGAC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CTACCAGTGC CCCAGAATGC CCCAGGACA CCCAGGACA TGGCCCCACC CACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACCAGGACA CCACGGACA CCACCAGGACA CCACGGACA CCACGACA CCACAGGACA CCACGACA CCACAGCA CCACGACA CCACAGCA CCACAGCA CCACAGCA CCACAGCA CCACAGCA CCACACA CCACAGCA CCACACA CCACAGCA CCACACA CCACAGCA CCACAGCA CCACAGCA CCACAGCA CCACACA CCACAGCA CCACACA CCACACA CCACAGCA CCACACA CCACAC CCAC CCACAC CCACAC CCACAC CCACAC CCACAC CCACAC CCACAC CCACAC CCACA	120 180 240 300 360 480 540 660 720 780 900 900 1080 1140 1260 1320 1320 1440
50556065	Coding sequilibrium sequilibriu	Hence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCT AAGGAAGCT GCCCGAGAAG CCTGGGATC AAGGAGGCG GAGGAGAAA ACGAGGGCGACCT TAACCACC GCCGAAATGG TCCTCTTCT TCTTCGTGAA TCGCCATGG TCGCCATGGCCATG TCTCTCTCTCT TCTTCGTGAA TCGCCACATA CTGCCTTGG GGCACATA CTGCCTTGG GGCACATA CTGCCTTGCG GGCACATA CTGCCTTGCG GGCACATA CGGCCATAG CGGCACATA CGGCACATAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACAGAG CGGCACACAG CGGCACACAG CGGCACACAC CGCACACAC CCCACAC CCCCACAC CCCCACAC CCCACAC CCCACAC CCCACAC CCCACAC CCCCACAC CCCACAC CCCACAC CCCCACAC CCCACAC CCCACAC CCCACAC CCCCACAC CCCACAC CCCACAC CCC	424 21	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC GTGGAGGAG GACTTGGTG GCACCCCAG CGGGAGTTCG GCTGCACCA GTTCCAGAAG AACTGTGCCGGC TCTGCCGGGC CGGGCGTGC CTGCTGGTGC CTGCTGGGCACCTC CGGCGTGCC CTGCTGGTGC CTGCTGGTGC CGAGAGTGCC CGGGAGGTGCC CGGGAGGCTGCC ACAGGCAGCC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATAGG TGTCACTGTG CAGCGAGCCT CCTCTCAGC CCATGCTGG CCATGCTGG CCTTCAGC CCATGCTGG CCTTCAGC CTTCAGC CTCAGAATGC CTCTCAGC CTCCAGCACA CGAGGATACC CGACGACAC CGACGAC CCAC CGACGAC CGACGAC CGACGAC CGACGAC CGACGAC CGACGAC CGACGAC CGACAC CGACGAC CACAC CGACGAC CGACGAC CGACGAC CGACGAC CACAC CGACGAC CACAC CGACGAC CCAC CCACAC C	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1450
50556065	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAG GCTTGGATTC AAGGAGGCG GAGGCAGAAA AGGATGTGGT ACGTCAGCTT ACGTCAGCT ACGTCAGCT TAACCCACCC GCCAGAATGG TCGCCTTTCGT TCTTCGTGAA TCGCCACTAG CTGCCTTTCGT TCTTCGTGA TGGCCTTTGG GGCCACATA CTGACCTGGT GGCCACTAG GGCCACGTAG CAGCGCGTCAG CAGCGCTCAG CAGCCCTCAG CAGCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCAG CAGCCCCAG CAGCCCCCAG CAGCCCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCCAG CAGCCCCCCCC	424 21	TGTGTTTTCC ARAGARACCA ARGARATTGC GGAGCATTCC CCCCAGATCC CCCCAGATCC CTGGAGGATGC GGAGCATGC GGAGAGCTGC GCGGAGCTGC GCTGCACACC AACTCAGACC CTGCCAGACC CTGCCGGAGCTGC CTGCCGGGAGCTGC CTGCTGGTGGGGTTGG CGGAGCTGC CTGCTGGTGGCTGC CTGCTGGTGGCTGC CTGCTGGTGGCTGC CTGCTGGTGCTGCC CGAGAGCTGC CAGAGAGCTGC CCTGAGCTGCC CCTGAGCTGGC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA CCTGCCCAGG GACTGGACGG TGAAGCTGAC CCACTCTGGA CGGTGCCTGT CCTTCCAGGGACGG TGAAGCTGAC CGTTCCTGT CCTTCCTGT	AGTGCCCCA TTCAGCTGCC TTGGCTCAC TTGGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG CACTGATGG CAGCGAGCCT CCTCTTCAGC CCAGCGTCAC CCATGCTGG CCAGCTGAAG CCCTGTAGC CCTGCAGGCC CCTGCAGGCC CCTGGAATGC CGGGGGAGTAC CGGGGGAGTAC CGGCCCACC CGCCAGGCCAC CGAGGACAGCCGGCCACC CGACGGACA CGAGGACAGCGGACA CGAGGACAGCGGCCGGGCCCACC CGACCAGGACA CGAGGACAGCGGCCGGGGCCACC CGACCAGGACA CGAGGACAGCGGGCCACC CGACCAGCCACC CGACCACCCAC	120 180 240 300 360 420 540 600 780 900 950 1020 1140 1200 1320 1380 1440 1500
50556065	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTT GCCCGAGAG GCTTGGATTC AAGGAGGCG GAGGCAGAAA AGGATGTGGT ACGTCAGCTT ACGTCAGCT ACGTCAGCT TAACCCACCC GCCAGAATGG TCGCCTTTCGT TCTTCGTGAA TCGCCACTAG CTGCCTTTCGT TCTTCGTGA TGGCCTTTGG GGCCACATA CTGACCTGGT GGCCACTAG GGCCACGTAG CAGCGCGTCAG CAGCGCTCAG CAGCCCTCAG CAGCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCAG CAGCCCCAG CAGCCCCCAG CAGCCCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCCCAG CAGCCCCCAG CAGCCCCCCCC	424 21	TGTGTTTTCC ARAGARACCA AGCARTCATGT AGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CTGGAGGATGA GACTTGCTGAGGAGCTGA GAGCAGCTGA GCACCCAG CGGAGTTCG GCTGCACACC TTACAGGACC TTCGCGGGA ACTGTGCCGTGAGGAG CGGGCTGC TGCTGGTGG CGGAGCTGC CTGCTGGTGG CAGCAGCAG CAGCAGCAGC CTGCTGAGGCTGC CAGAGGCAGCC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA CCTGCCCAGG GACTGGACGG TGAAGCTGAC CCACTCTGGA CGGTGCCTGT CCTTCCAGGGACGG TGAAGCTGAC CGTTCCTGT CCTTCCTGT	AGTGCCCCA TTCAGCTGCC TTGGCTCAC TTGGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG CACTGATGG CAGCGAGCCT CCTCTTCAGC CCAGCGTCAC CCATGCTGG CCAGCTGAAG CCCTGTAGC CCTGCAGGCC CCTGCAGGCC CCTGGAATGC CGGGGGAGTAC CGGGGGAGTAC CGGCCCACC CGCCAGGCCAC CGAGGACAGCCGGCCACC CGACGGACA CGAGGACAGCGGACA CGAGGACAGCGGCCGGGCCCACC CGACCAGGACA CGAGGACAGCGGCCGGGGCCACC CGACCAGGACA CGAGGACAGCGGGCCACC CGACCAGCCACC CGACCACCCAC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1260 1320 1380 1450
50556065	Coding sequing	IERCE: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGCT TGGAGAGT GCCCGAGAG CCTTGGATTC AAGGAGGCG GAGCAGAAA GGATTGGCT ACGTGCTGT ACTGGCAT ACAGGACGT ACAGGACGCT TAACCCACCC GCCAGAATG TGGCCTTTGG TCCTCTTCCT TCTTCGTGAA CTGCACTTGG TCCTCTTCCT TCTTCGTGAA CTGCACTTGG TCCTCTTCCT TCTTCGTGAA CTGCACTTGG GGCACAGTAG CGGCACAGTAG CAGCGCTCAC CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCGTCA CAGCGCCGAC CAGCGCCACA CAGCGCCGCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCGCCCCACA CAGCCCCCCACA CAGCCCCCCCACA CAGCCCCCCACA CAGCCCCCCCACA CAGCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCACA CAGCCCCCCCC	424 21	TETGTTTTCC ANAGANCCA AGCATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC AGCAGCAGC GTGGAGGATG GCCACCCAG CGGGAGTTCC GCTGCACAC TACAGGACA AACTGTCCAGAC TTCCAGAAG AACTGTCCAGAC TTCTCGCGGCA CGGGCCTGTG CTGCTGGTGG GATGCCTTTTCCACTG CGAGAGCTGCC CGCTGACCTGC CGAGAGCTGCC CGCTGACCTGC CGAGAGCTGCC CCTGCTGACCTGC CGAGAGCTGCC CCTGCTGACCTGC CCTGCTGACCTGC CCTGCTGACCTGC CCTGACCTGCC CCTGACCTGCC CCTGACCTGCC CCTGACCTGCC CCTGACCTCCT	TGTTTTCCAG TCGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TCATCATCGT TCATCATCGC CCACCAACGG ACTGCACGGG ACTGCACGGG GCCCTTCTA CCTGCCCAGG TGAAGCTGAG TGAAGCTGAG TGAAGCTGAG TGAAGCTGAG TGAGCAGGG TGAAGCTGAG CCACTCTGGA CGGTGCCTGT CCTTCCGTGGG AGTCACACTC TCCGGAAGCG TCGGGAAGCG TCCTGCTGGG TCGGGAAGCG TCCTGCTGGG TCGGGAAGCG TCCTGCTGGG TCGGGAAGCG TCCTGCTGGG TCGGGAAGCG TCCTGCTGGG TCGGGAAGCT TCTGTTTGGGA	AGTGCCCCA TTCAGCTGCC TTGGCTCTAAC TTGTGACGGT CACTCCTCAT AATCAAGAGG TCTGCACAGA CACTGATGGG CACTGATGGG CAGCGAGCCT CCTCTTCAGC CCAGTGCTAC CCCATGCTGG CAGCTGGAAG CCCCTGTGAC CCTGCAGCC CCTGCAGCC CCACCAGGACA CCCCAGTGCTCCTC CTCCGGCC CGGGGAGTAC CCCCAGTGC CCACCAGCAC CCACCAGGACA CCACCAGGACA CCACGAGACA CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGATCAC CGAGGACAC CGAGGATCAC CGAGGATCAC CGAGGACCAC CACCAGCCC CACCACCC CACCACCC CACCACCC CACCACCC CACCAC	120 180 240 300 360 420 480 540 660 720 780 900 900 1080 1140 1260 1320 1320 1340 1500 1500
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCT AAGGAAGCT GCCCGAGAAG CCTGGGATGC GAGGAGAGAA ACGAGGGCG GAGGAGAAA ACAGAGGCCAT ACAGCAGAC GCCGAACCT TAACCACC GCCAGAATGG TCCTCTTCT TCTTCGTGAA TCGCCATG GGCACATA CTGCTCTTGCT GGCCTTGGC GGCACATA CTGCCTGGC GGCACATA CTGCCTGCG GGCACATA CTGCCTGGC GGCACATA CTGCTCTTCC GGCACATA CTGCCTGCG GGCACATA CTGCTCTTCC GGCACATA CTGCCTTGCG GGCACATA CGGCACTTGC CGGCACATA CGGCCTTGC CGGCACATA CGGCCTTGC CGCAGAATTT	424 21	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC GAGCAGCAGC GGAGCATCC GCTGCACCA GCTCCAGAAC GTTCCAGAAG AACTGTGCCG CTGCTGCAGGA CGGCCCTGC CGGCCTGC CGGCCTGCC CTGCTGCAGCC CCGAGCTGC CCGACCTCCTC CGGCCCTGC CCGAGCTGC CCGAGCTGC CCGACCTCCTC CGACCTCCTC CGACCTCCTC CCAGAGCTGC CCAGACCTCCTC CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTCT CCAGACCTCCTTC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATAGG TGTCACTGTG CAGCGAGCCT CCTCTCAGC CCATGCTGG CCCATGCTGG CCTGGAATGC CTTCAGC CGCGTCCTC CGCGTCCTC CGCGTCCCTG CTCCGGGC CACCAGGACA CGCGTCAC CGCGTCCAC CGCGTCCAC CGCGTCCAC CGCGTCCAC CGCGTCCCTG CTCCGGGC CGCGTCAC CGCGTCAC CGCGTCAC CGCGTCAC CGCGTCAC CGCGCTCCAC CGCGCTCCAC CGCGCTCCAC CGCGCTCAC CGCGCTCAC CGCGCTCAC CGCGCTCCAC CGCGCCACC CGCCTCCAC CGCCTCCAC CGCCTCCAC CGCTCTCCCC CGCTCCCCC	120 180 240 300 360 420 540 660 720 780 900 960 1020 1320 1380 1440 1560 1560 1680
50556065	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCTC AAGGAGGCT GCCCGAGAAG GCGTCAGGATTC AAGGAGGCG GAGGCAGAAA ACGACCT GCTCTGGTT TCTCGGCCAT ACACCACCC GCCAGAATG TCTCTTCGT TCTTCGTGAA TCGCCACATA CTGACCTGGC GGCCACATA CTGACCTGGC GGCCACATA CTGACCTGGC GGCCACTAG CGCCACTAG CGCCTCAG CGCACATA CGGCACATA CGGCAGAATT ACCCTGACCT CCGAGAATT ACCCTGACGT CCCGAGAATT	424 21	TGTGTTTTCC ARAGAACC ARAGAACTTG GGAGCATTCC CCCCAGATCC CAACAGCAGC GAACTTGC GGAGCATCC CTGGAGGATCC GCGGAGTCC GCGCACCCAG GCTGCCAACC GTTCCAGAAG AACTGTGCC TACAGACCT TACAGACCT TACAGACCT TACAGACCT CTGCCGGCC CTGCCGTGC GACGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CCTGAGCTGC CCTGAGCTGC GACCCTGCC CCTGAGCTGC CCTGAGCTGC GACCTTCGCC GGAGCTTCC CCTGAGCTGC CCTGAGCTGC GACCTTCGCC GGAGCTTCC CCTGAGCTGCC CCTGAGCTTCC CAGAGCTTTC CAGAGCTTTCC CAGACCTTTCC CAGACCTTTCC CAGACCTTTCC CAGCCTTCC CAGCCTTCC CAGCCTTCC CACCCTCCTCCT CACCCTCCTCC CACCCTCC CACCCTC CACCCT CACCCTC CACCCTC CACCCT CACCC CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCT CACCCT CACCC CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCC CACC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GCTCCTTCTAG CCACTGGCCAGG GACTGGACTG	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG TCTGCACGGT CACCGTGTGC CAGCGGAGCCT CCTCTCAGC CCATGCTGG CCATGCTGG CCCCTGGAAGC CCTGGAATGC CGGGGGAGTAC CGGGGAGTAC CGGCTGCAGGCC CGCCTGGACA CGGGGAGAGAC CGGGGAGAGAC CGACGGCCCCCGGCC CGCCTGGACA CGACGTGCAGC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACCAC CGCCCCCCCC	120 180 240 300 360 420 540 600 720 780 900 950 1020 1140 1250 1380 1440 1560 1560 1620 1620 1740
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCTC AAGGAGGCT GCCCGAGAAG GCGTCAGGATTC AAGGAGGCG GAGGCAGAAA ACGACCT GCTCTGGTT TCTCGGCCAT ACACCACCC GCCAGAATG TCTCTTCGT TCTTCGTGAA TCGCCACATA CTGACCTGGC GGCCACATA CTGACCTGGC GGCCACATA CTGACCTGGC GGCCACTAG CGCCACTAG CGCCTCAG CGCACATA CGGCACATA CGGCAGAATT ACCCTGACCT CCGAGAATT ACCCTGACGT CCCGAGAATT	424 21	TGTGTTTTCC ARAGAACC ARAGAACTTG GGAGCATTCC CCCCAGATCC CAACAGCAGC GAACTTGC GGAGCATCC CTGGAGGATCC GCGGAGTCC GCGCACCCAG GCTGCCAACC GTTCCAGAAG AACTGTGCC TACAGACCT TACAGACCT TACAGACCT TACAGACCT CTGCCGGCC CTGCCGTGC GACGCTGC CAGAGCTGC CAGAGCTGC CAGAGCTGC CCTGAGCTGC CCTGAGCTGC GACCCTGCC CCTGAGCTGC CCTGAGCTGC GACCTTCGCC GGAGCTTCC CCTGAGCTGC CCTGAGCTGC GACCTTCGCC GGAGCTTCC CCTGAGCTGCC CCTGAGCTTCC CAGAGCTTTC CAGAGCTTTCC CAGACCTTTCC CAGACCTTTCC CAGACCTTTCC CAGCCTTCC CAGCCTTCC CAGCCTTCC CACCCTCCTCCT CACCCTCCTCC CACCCTCC CACCCTC CACCCT CACCCTC CACCCTC CACCCT CACCC CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCT CACCCT CACCC CACCCT CACCCT CACCCT CACCCT CACCCT CACCCT CACCC CACC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GCTCCTTCTAG CCACTGGCCAGG GACTGGACTG	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG TCTGCACGGT CACCGTGTGC CAGCGGAGCCT CCTCTCAGC CCATGCTGG CCATGCTGG CCCCTGGAAGC CCTGGAATGC CGGGGGAGTAC CGGGGAGTAC CGGCTGCAGGCC CGCCTGGACA CGGGGAGAGAC CGGGGAGAGAC CGACGGCCCCCGGCC CGCCTGGACA CGACGTGCAGC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACAC CGACGACCAC CGCCCCCCCC	120 180 240 300 360 420 540 600 720 780 900 950 1020 1140 1250 1380 1440 1560 1560 1620 1620 1740
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGCAGGAGCT TGGAGAGCT GCCCGAGAG GCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGT ACGTGCTGT ACGTGCTGT ACGTGCTGT TACCCACCC TAACCACCC TCACCTGCT TCTTCGTTAC TCTTCGTTAC TCTTCGTTAC CGCCACATA CTGACCTTGGT CGCCACATA CTGACCTGGT GGCCACATA CTGACCTGGT CAGGATCT CAGGACGT CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CGCCACATA CTGACCTGGT CAGCGCGTAC CGCCACATA CTGACCTGGT CAGCGCGTAC CGCCACATA CTGACCTGGT CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGTAC CAGCGCGAC CCCGAGAATTI ACCCTGACCGAC CCCTGACCGAC CGCCACACCCTACCGGCCGAC CCCGAGAATTI ACCCTGACCGAC	424 21 GGAGCCGTC GGAGGCCGTC CCATTAAGC CCATTAAGC GGTCAGAGTG ATTTCAACC GGTCAGAGTG ACTTCTCTG ACTGCATCC GGCTCAGGTGG GGCTGAGCAG GGCTGAGCAG GGAGATGGTC TGCCAGCTGG AGGCACATGT AGGGAGAGCT GCTGACAGC CTGCACAGC AGGCACAGC CTGCACAGC CTGCACACC CTGCACAGC CTCCACACC CTCCACC CT	TETGTTTTCC ARAGARACCA ARAGRARCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC GTGGAGGATG GCACCCAG GCACCACCAG GCTGCACCAG GCTGCACCAG GCTGCACCAG GCTGCACCAG ACTGCACCAG GCTGCACCAG GCTGCACCAC TCTCCCGGCA ACTGCACCAG CCTGCTGCTGC CCTGCTGCTGC CCTGCTGCTGC CCTGAGAGCACCA CCGAGCCTTCC CCAGAGCTTCC CCGCGCTGCC CCCCGCCCCC CCCCCCCCCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGCAAG TGAAATACCT TGAAGCAAG TGAAATACCT TCATCATGGC AGGCAAGGGA ATGCACTGGC GTCCCAGGGT CTGGCCAGG GACTGGAGGA TGAAGCTGA CCACTCTGGA CCACTCTGGA CCACTCTGGA CCGTCCTGG AGTCACAGG TCGGAGGA CCGTCCTGG AGTCACACT TCCTGCTGGG CCAAGCATGT AGGGAAGCT TCATGTTGGA TGAGAAGCTGG TGAGAAGCTG TCATGTTGGA TGAGAAGCTG TGAGAAGCTG TGAGAAGCTG TGAGAAGCTG TGTTTGGAGAGC TGTTTGGAGAGCT TGTTTGGAGAGCT TGTTTGGAGAGCT TGTTTGGAGACT TGTTTGGGAG	AGTGCCCCA TTCAGCTGCC TTGGTCTAAC TTGTGACGGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACGGG CACCGAGGCTCAC CCATGCTGG CAGCGAGCCT CCATGCTGG CCCATGCTGG CCCATGCTGG CCTGTGAATGC CCTGTGAATGC CCTGTGAATGC CCTGTGAATGC CGGGGGACAC CCACCAGGCTAC CGGGGACACAGCAGCACAGCA	120 180 240 300 360 420 480 540 660 720 780 900 900 920 1140 1260 1320 1380 1440 1500 1680 1740 1680 1740
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGCAGGAGCT TGCAGGAGCT GCCCGAGAG CCTTGGATTG GCCCGAGAG GGGCAGAAA GGGATGTGGC GAGCAGAAA ACAGGACGCT TACCCACCC GCCAGAATGG TGGCCTTTGGTT TCTTCGTGAA TGGCCACTT TCTTCGTGAA TGGCCACTT CGTGGACCT TCTTCGTGAA TGGCCACTTGG CAGGCCTTGG TCCTCTTCCT TCTTCGTGAA TGGCCACATA CGGCCAGAATGG CAGGCCTTAG CAGGCCTTGG CAGCCCTCAG CGGCCAGAATGG CAGCCCTCAG CGGCCAGAATTT ACCCTGACGT CGTGCCGGAC CCGAGAATTT ACCCTGACGT GGCTGACAC TAGGTGGGGCACAC	424 21	TGTGTTTTCC AAAGAACCA AACAGAAG GACATTGT GGAGCATTCC CCACAGATCC CAACAGGAAG GAACTGGTCC AAGCAGCTGA GGCACCCAG GTGGAGGATC GCTGCACACT TACAGGACCA TTCCAGAAC AACTGTACC TCTGCGGCA TCTGCTGCTGC GATGCTGTGC CTGCTGTGG ACTGTGTGC CTGCTGTGG CACACTTTCTCACTG CAGAGCTTCC CAGAGCTGC CACAGCTGCC CACAGCTGCC CACAGCTGCC CACAGCTGCC CACAGCTGCC CACAGCTGCC CACAGCTGCC CACAGCTTCC CACAGCTTTCC CACAGCTTTCC CACAGCTTTCC CACAGCTTTCC CACAGCTTTCC CACAGCTTTCC CACAGCCTTCC CACAGCCTCCC CCGGCCGGCC CCGGCTGGCC CCGGCCGCCC CCGGCCGCCC CCGGCCGCCCC CCGACCCCCCC CCACACCCCCCC CCACACCCCCCC CACACCCCCC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGG TGTCACTGTG CAGCGTCAC CCCATGCTGG CAGCGTCAC CCCATGCTGG CAGCTGCAAG CCCTGTGAC CCCTGTGAC CCCTGTGAC CCCAGGCCCAC CCAGGATGC CGGGGAAGTAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGAGGATGAC CGACTGCAC CGAGGATGAC CGACTTCCTG CTCCGGGCC CGCGGAAGAC CGAGGATGAC CGACTTCCTGC CTCCAGGACA CGAGGATGAC CGACTTCCCAC CGACGATCAC CGAGGATGAC CGACTCCAC CGACGACCAC CGACGACCAC CGACGACCAC CGACGACCAC CACTGCCAC CCACGGACAC CCACTGCCAC CCACGGACAC CCACTGCCAC CCACGGACAC CCACTGCCAC CCACGGACAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCACTGCCAC CCATTAGCCAC CCATTGCCAC	120 180 240 300 360 420 540 660 720 780 900 1080 1140 1260 1320 1380 1440 1500 1680 1740 1860 1860
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT GCCCGAGAAG GCGTCAGGATT ACGGCAGAA AGGATGGCT GCTGGTTGGTT GCTCGCCAT ACGGCAGAA TCGCCACCA TGGCCTTGGTT TCTTCGTGAA TGGCCACAT TGGCCCGACA TGGCCGCAC TAGGTGGCG TAGGTGGCG TAGGTGGCG TAGGTGGCG TCCAGAGAGGC TAGGTGGCG TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGGAGGGC TCCAGAGGGGC TCCAGGAGGGC TCCAGAGGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGAGGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGCC TCCAGGAGGGC TCCAGGAGGCC TCCAGAGGCC TCCAGAGGGCC TCCAGGAGGCC TCCAGAGGCC TCCAGAGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGCC TCCAGAGC TCCAGGCC TCCAGCC TCCAGAGCC TCCAGCC TCCAGAGC TCCAGCC TCCAGCC TCCAGACC TCCAGCC TCCACC TCCAGCC TCCACC TCCACC TCCACC TCCACC TCCACC TCCACC TCCACC TCCACC	424 21	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC CGGAGCATCC GGAGCATCC GCGCAGCCCA GCACCCCA GCCCCAGACC CCGGAGCTCC CTCCCGGCAC CTCCCGCGCC CTCCCCGCCCC CTCCCCCCC CCGGAGCTGC CTGCTGCTGC CAGACCTGC CTGCTGCTGCC CCGGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCGGCCTTCCCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCTGCCCCC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GCCCTTCCAG GACTGCCAGG CCACTCCAG CCACTCCGG GACTGGACGG TGAAGCTGGG CCACTCTGG TGAGGTGAGG	AGTGCCCCA TTCAGCTGCC TTGGTCCCCA TTGGTCACGT TCAGCTCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG TCTCACTGTG CACGCTCAC CCCATGCTGG CCAGGGCTCAC CCCATGCTGG CCCCTGGAATGC CCTCTGGACG CCCCTGGAATGC CGGCTCCCGC CGGCTCCCG CGGCTCCCG CGCCTCCTGG	120 180 240 300 360 420 540 660 720 780 900 960 1020 1380 1140 1320 1380 1440 1560 1680 1740 1800 1800 1800 1800
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT GCCCGAGAAG GCGTCAGGATT ACGGCAGAA AGGATGGCT GCTGGTTGGTT GCTCGCCAT ACGGCAGAA TCGCCACCA TGGACCT TCTCGTGAA TGGCCTTGGT TCTTCGTGAA TGGCCACATA CGGCACATA CCCAGAGATT ACCCTGACGT CCCGAGAATT CCCTGACGT CCTAGCGGCACA CTAGGTGGCG TAGGTGGCG TAGGTGGCG TAGGTGGCG TAGGTGGCG TAGGTGGCG TCCAGAGAGGC TAGGTGGCG TCCAGAGGGGC TAGGTGGCG TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGAGGGGC TCCAGGAGGGC TCCAGAGGGGC TCCAGAGGGCC TCCAGAGGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGGAGGGC TCCAGAGGGCC TCCAGGAGGGCC TCCAGGAGGGC TCCAGGAGGCC TCCAGGAGGGC TCCAGGAGGCC TCCAGAGGCC TCCAGAGCC TCCAGAGGCC TCCAGACC TCCAGAGGCC TCCAGACC TCCAGACGC TCCAGACC TCCAGCC TCCAGCC TCCAGCC TCCAGCC TCCAGCC TCCAGCC TCCAGC TCCAGCC TCCACC	424 21	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC CGGAGCATCC GGAGCATCC GCGCAGCCCA GCACCCCA GCCCCAGACC CCGGAGCTCC CTCCCGGCAC CTCCCGCGCC CTCCCCGCCCC CTCCCCCCC CCGGAGCTGC CTGCTGCTGC CAGACCTGC CTGCTGCTGCC CCGGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCTGAGCTGC CCGGCCTTCCCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCCTGCCCCC CGGCTGCCCCC	I TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GCCCTTCCAG GACTGCCAGG CCACTCCAG CCACTCCGG GACTGGACGG TGAAGCTGGG CCACTCTGG TGAGGTGAGG	AGTGCCCCA TTCAGCTGCC TTGGTCCCCA TTGGTCACGT TCAGCTCTCAT AATCAAGAGG TCTGCACAGG TCTGCACAGG TCTCACTGTG CACGCTCAC CCCATGCTGG CCAGGGCTCAC CCCATGCTGG CCCCTGGAATGC CCTCTGGACG CCCCTGGAATGC CGGCTCCCGC CGGCTCCCG CGGCTCCCG CGCCTCCTGG	120 180 240 300 360 420 540 660 720 780 900 960 1020 1380 1140 1320 1380 1440 1560 1680 1740 1800 1800 1800 1800
50 55 60 65 70 75	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGCAGGAGCT TGGAGAGCT GCCCGAGAG GCCTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGT ACGTGCTGTT ACGTGCTGT TCTCGTGAT GCTGGCAT TAACCACCC GCCAGAATG TCCTCTTCGT TCTTCGTGA TGGCCTTTGG TCCTCTTCGT CGCCACACC CGCCAGAATG GGCCACATA CTGACCTGGT GGCCTTGGG CGCCACATA CTGACCTGGT CGGCAGATG CGGCACATA CTGACCTGGT CGCCTAGGC CGGCAGACC CGGCAGAATT AGGTCGGAC CCGAGAATT ACCCTGACT CGGTGCCGAC CCGAGAATT TCCTGACGT CGCTGACGAC CCGAGAATT TCCCTGACGT CGCTGACACC CTAGGTGGGGT TCCAGAGGGC TCCAGAGGGC TCCAGAGGGC TCCAGAGGGC TCCAGAGGGC CCGAGAATT TCCAGAGGGC CTAGGTGGGGGT TCCAGAGGGC GCGCAGAGGGC TCCAGAGGGC CCGAGAGGGC TCCAGAGGGC CCGAGAGGC CCGAGAGGC CCGAGAGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCGAGAGGC CCCGAGAGGC CCCGAGAGGC CCCGAGAGGC CCGAGAGGGC CCCGAGAGGGG CCCGAGAGGGC CCCGAGAGGGC CCCGAGAGGGC CCCGAGAGGC CCCGAGAGC CCCGAGACC CCCGAGAGC CCCGAGAC CCCGAGAGC CCCGAGAGC CCCGAGAC CCCGAGAGC CCCGAGAGC CCCGAGAGC CCCGAGAGC CCCGAGAGC CCCGAGAC CCCGAGAC CCCGAGAC CCCGAGAC CCCGAGAC CCCGAGAC CCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCGAGAC CCCCCCCC	424 21	TGTGTTTTCC ARAGARACCA AGCARTAGT AGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CTGCAGAGG GAACTTGCTC GGAGGATGC GTGGAGGATGC GTGGAGGATGC GTGCAGACG GTCCAGAAG ACTGTCAGAGG ACTGTGCCCAGAAG ACTGTGCCCAGAAG ACTGTGCCCAGAAG ACTGTGCCCAGAGG CGGAGGTTGG CGAGGCGTGC CTGCTGGTGG GACGTGGT CCGGGTGG CCGGGTGC CCTGGTGG CGGGTGCCCAGAGGCTGCC CGGGTGCCCAGAGGCTGCC CGGGGTGCCCAGAGGCTGCC CGGGGTGCCCAGAGCTGCC CGGGGTGCCCAGAGCTGCCC CGGGGTGCCCAGAGCTGCCC CGGGGTGCCCAGACCCCCC CCTGGCCCAGACCCCCC CCTGGCCCAGA	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT TCATCATCGT AGGAAAGGGG ATGCACTGGC GTCCCTTCTA GGAAGCTGAG GACTGCAGG TGAAGCTGAG CCACTCTGGA CCGTCCTGGC AGTCACTGG TGAAGCTGAG CGGTCCTGT TCCTGCTGGG AGTCACACT TCCTGCTGGG TGAGAAGCT TCATGTTGGG TGAGAAGCT TCATGTTGGG TGAGAAGCT TCATGTTGGG TGAGAAGCT TCATGTTGGG TGTGAGAAGCT TGTGTGCGGG TGTGTGCGGG TGTGTGCGGG TGTGTGCGGG TGTGTGGGGG TGTGTGCGGGG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGG	AGTGCCCCA TTCAGCTGCC TTGGTCCAT TTCAGCTGCC TTGGTCACGT TCACTCCTCAT AATCAAGAGG TCTGCACAGG TCTGCACGGG CACGGAGCCT CCTCTTCAGC CCATGCTGG CCAGGCTCAC CCATGCTGG CCACTGATGC CCACTGATGC CCACTGCTGAC CCACTGAATGC CCACTGCTGAC CCACTGCTGAC CCACTGCTGAC CCACTGCTGCC CGGGGGAGTAC CGGCTCCACC CGACGAGACA CGAGGATGAC CGACGGCCACC CACCAGGACA CGACGACCACC CGCCCACC CCACCAGGACA CCACTGCTGC CGTCCACC CGCCCACC CCACCAGGACA CCACGGTGCAC CCACCGTGCAC CCACCACCAC CCACCACCAC CCACTGCAC CCACCACCAC CCACTGCAC CCACTCCAC CCACTGCAC CCACCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTCCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCACTGCAC CCAC	120 180 240 300 420 480 540 660 720 780 900 900 900 120 120 1250 1260 1320 1440 1560 1620 1680 1740 1860 1980
5055606570	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGTGGTGCTC AAGGAGGTTGGCT GCCCGAGAG GCTTGGATTG GCCCGAGAG GGGCAGAAA GGGATGTGGC TACCAGCC GGGTCAGGTT ACAGGACGT ACAGCACC TAACCACCC GCCAGAATGG TGGCCTTTGGTT TCTTCGTGAA TGGCCACTTGGT TCTTCGTGAA TGGCCACTTGG CAGCACTTGGT CAGCACTTGGT TCTTCGTGAA TGGCCACTTGGT CAGCACTTGGT TCTTCGTGAA TGGCCACTTGG CAGCACTTGGT CAGCACTTGGT CAGCACTTGGT CAGCACTTGGT CAGCACTTGGT CAGCACTCA TGGCCTGACGT CAGCACTCA TGGTGACGT TCCTGACGT TCCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCAGAGGGC TCCAGAGGGC TCCAGAGGCC TCCAGAGGC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGGCC TCCAGAGCC TCCAGAGGCC TCCAGAGCC TCCAGAGC TCCAG	424 21 21 GGAGCCGTC CCATCTAAGC GGTCAGAGTG TGAAAGGTCC GGTCAGAGTG ATTTTCAACC CACCGAGACG TGCTTCTGTG ACTGCTCCAGC GGAGATG TGCTCCAGC GGAGATGT TGCGGTGCTC TGCGGTGCT TGCGGTGCT TGCGGTGCT TGCGGTGCT TGCGGTGCT TGCGGTGCT TGCGGTGCT TGCAGCAGGT GCTGAGCAGC TGCAGCAGGT CAGCAGGT CAGCAGGT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCAGCT TGCAGCACC TGCAGCACC TGCAGCCGCCT TGCAGCCGCT TGCAGCCGCT TGCAGCCGCT TGCAGCCGCT TGCAGCCGCT TGGAGCCCTT TGGAGCCTT TGGAGCCCTT TGGAGCCTT TGGAGCCTT TGGAGCCT TGGACCCTT TGGAGCCT TGGACCT TGGAGCCT TGGAGCCT TGGAGCCT TGGACCAC TGGACCAC TGGACCAC TGGACCAC TGGACCAC TGCACCAC TGCAC TGCACCAC TGCAC TGCA	TGTGTTTTCC AAAGAAACCA AAGAATCATTG GAACACTTTG GGAGCATTCC CAACAGGAAG GAACTTGCTC CCCCAGATCC AAGCAGCTGA GAGCATCA GAGCAGCTGA GCACCCAG GCTGCACACT TACAGGACAC TACAGGACAC TACAGGACAC TCTGCCGGCA TCTGCCGGCATCC CTGCTGGTGG GACCTCCTCC CAGAGCTTTC CAGAGCTTTC CAGAGCTTCC CCCCCCCCC CCCCCCCCCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGCC TTGAGCTGCC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGG CAGCGAGCCTAC CCCATGCTGG CAGCGTGCAG CCCATGCTGG CAGCTGCAG CCCTGTGAC CCTGGAATGC CTTCAGCC CGGGTTCCTG CGGGTTCCTG CGGGGAGTAC CGAGGATAGC CGAGGATGAG CGACTGCAG CGAGGATGAG CGACTGCAG CGACTGCAG CGACTGCAG CGACTGCAG CGACTTCCCAG CCACGGACA CGACTGCAG CCACTGCAG CCATTAGCCAG CCATTAGCCAG CCATTGACAAA CGATGCACAC CGATTCCAGG CCATTGACAAA CGATGCACAC	120 180 240 300 360 420 540 660 720 780 900 960 1080 1140 1260 1320 1380 1560 1680 1740 1860 1920 1920 1920
50 55 60 65 70 75	Coding sequilibrium sequilibriu	IERCE: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT GCCCGAGAAG GCAGGATGT ACGGCCAT ACGGCCAT ACGGCCAT ACGGCCAT ACCTGCTTG TCTCTCTCT TCTTCGTGAA TGGCCACAT TGCCACCAT GCCAGAATGG TCCTCTTCT TCTTCGTGAA TGGCCATAG TGGCCATAG CGGCAGATGG CAGCGTCAG CGGACCTT CTTCTCTGTAA TGGCCACATA TGGCCACATA TGGCCACATA TGGCCACATA TGTCCTGGC CAGGAGACGT CAGCGCTCAG TGGCCTCGGC CCGAGAATTT ACCTGACGT CCGAGAATTT ACCTGACGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGGACACGT TCCGGGGGGGGG TCCGGACACGT TCCGGGGGGGGGG	424 21 GGAGGCCGTC CCATGTAAGC GGTCACAGTG TGAAAGGTCC GGTCAGAGTG TGCTCAGGC GGTGAGACG GGTGAGACG TGCTCAGC GGTGAGACG GGTGAGACG GGAGATGT TGCCAGC AGGCACAGC AGGCACAGC CGGAGACG CGGAGGCG CGAAGCCGC CGAACCAATC CAAACCCACC CGGCCTCAGC CGGGCTCAGC CGGGCTCAGC CGGGCTCAGC CGGGCCCC CGGCCCCC CGGCCCCCCC CGGCCCCCC	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC GAGCAGCTGC GGAGGAGTTCG GCCCCAGACCC GCTGCACCCCAG CCGCAGATCC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGCC CTCCCAGCC CCTGAGCTGC CCTGCCCCAG CCTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTGAGCTGC CTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTAAGTGACC CTAAGTGACC CTACCCCACC CCTAAGCTGCC CTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCCGCC CCTAAGCTGCC CCTAAGCCGACC CCTAAGCCGACC CCTAAGCCGACC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA GGAAGGGG GACTGGACGG TGAAGCTGGC CCACTCTGGA TGAGCGAGGG TGAGCGAGGG TGAGCGAGGG CCACTCTGGA TGAGCTGGA CGGTGCCTGT TCCTGCTGG TCGGGAGCGC TCATGTTGGA TGGGAGCGC TTCTGTGGG TGGGAGCGC TGTATGGACGG TGAGGAAGCT TGTGTGGGGG TGGGGAGCGC TGTTGGGGGGG TGTGTGGGGGG TGTGTGGGGGG TGTGTGGGGGG	AGTGCCCCA TTCAGCTGCC TTGGTCCCC TTGGTCCCC TGGGTCTAAC CTGTGACGGT TAATCAAGAGG TCTGCACAGG TCTGCACAGG TCTCACTGTG CACGCTCAT CCTCTTCAGC CCATGCTGG CCACTGCTGG CCACTGCTGG CTACCAGGCCC CGCCTCCCGG CGCCTCCCTG CTCCCGGCC CGCCTCCCGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CCACCAGGACAA CGTGCACCC CCACAGGACAC CGCTCTCAGC CCACTCTGCC CCACTCCCAG CCACTCTCCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCATTAGCCAG CCATTAGCCAG CCATTGCCAG CCATTGCAGCAC CCATTGCAGCAC CCATTGCAGCAC CCATTGCAGCAGC CCTTTGCAGG CCATTGCAGC CCATTGCAGG CCATTGCAGCAC CCATTGCAGG CCATTGCAGG CCATTGCAGG CCATTGCAGG CCACGACGTG CCACGACGTC CCACGACGTC CCACGACGTC CCACCACCAC CCACCACCAC CCACCACCAC CCACCA	120 180 240 300 360 420 540 660 720 780 960 1020 1380 1440 1350 1560 1560 1680 1740 1800 1920 1980 2040 2100
50 55 60 65 70 75	Coding sequilibrium sequilibriu	IERCE: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT GCCCGAGAAG GCAGGATGT ACGGCCAT ACGGCCAT ACGGCCAT ACGGCCAT ACCTGCTTG TCTCTCTCT TCTTCGTGAA TGGCCACAT TGCCACCAT GCCAGAATGG TCCTCTTCT TCTTCGTGAA TGGCCATAG TGGCCATAG CGGCAGATGG CAGCGTCAG CGGACCTT CTTCTCTGTAA TGGCCACATA TGGCCACATA TGGCCACATA TGGCCACATA TGTCCTGGC CAGGAGACGT CAGCGCTCAG TGGCCTCGGC CCGAGAATTT ACCTGACGT CCGAGAATTT ACCTGACGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGAGAGGGGG TCCGGACACGT TCCGGGGGGGGG TCCGGACACGT TCCGGGGGGGGGG	424 21 GGAGGCCGTC CCATGTAAGC GGTCACAGTG TGAAAGGTCC GGTCAGAGTG TGCTCAGGC GGTGAGACG GGTGAGACG TGCTCAGC GGTGAGACG GGTGAGACG GGAGATGT TGCCAGC AGGCACAGC AGGCACAGC CGGAGACG CGGAGGCG CGAAGCCGC CGAACCAATC CAAACCCACC CGGCCTCAGC CGGGCTCAGC CGGGCTCAGC CGGGCTCAGC CGGGCCCC CGGCCCCC CGGCCCCCCC CGGCCCCCC	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC GAGCAGCTGC GGAGGAGTTCG GCCCCAGACCC GCTGCACCCCAG CCGCAGATCC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGACC CTCCCAGCC CTCCCAGCC CCTGAGCTGC CCTGCCCCAG CCTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTGAGCTGC CTGCCCCAG CCTGAGCTGC CCTGCCCCAG CCTAAGTGACC CTAAGTGACC CTACCCCACC CCTAAGCTGCC CTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCTGCC CCTAAGCCGCC CCTAAGCTGCC CCTAAGCCGACC CCTAAGCCGACC CCTAAGCCGACC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ATGCACTGGC CCACCAACGG GTCCCTTCTA GGAAGGGG GACTGGACGG TGAAGCTGGC CCACTCTGGA TGAGCGAGGG TGAGCGAGGG TGAGCGAGGG CCACTCTGGA TGAGCTGGA CGGTGCCTGT TCCTGCTGG TCGGGAGCGC TCATGTTGGA TGGGAGCGC TTCTGTGGG TGGGAGCGC TGTATGGACGG TGAGGAAGCT TGTGTGGGGG TGGGGAGCGC TGTTGGGGGGG TGTGTGGGGGG TGTGTGGGGGG TGTGTGGGGGG	AGTGCCCCA TTCAGCTGCC TTGGTCCCC TTGGTCCCC TGGGTCTAAC CTGTGACGGT TAATCAAGAGG TCTGCACAGG TCTGCACAGG TCTCACTGTG CACGCTCAT CCTCTTCAGC CCATGCTGG CCACTGCTGG CCACTGCTGG CTACCAGGCCC CGCCTCCCGG CGCCTCCCTG CTCCCGGCC CGCCTCCCGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CGCCTCCAGC CCACCAGGACAA CGTGCACCC CCACAGGACAC CGCTCTCAGC CCACTCTGCC CCACTCCCAG CCACTCTCCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCACTCTCCAG CCATTAGCCAG CCATTAGCCAG CCATTGCCAG CCATTGCAGCAC CCATTGCAGCAC CCATTGCAGCAC CCATTGCAGCAGC CCTTTGCAGG CCATTGCAGC CCATTGCAGG CCATTGCAGCAC CCATTGCAGG CCATTGCAGG CCATTGCAGG CCATTGCAGG CCACGACGTG CCACGACGTC CCACGACGTC CCACGACGTC CCACCACCAC CCACCACCAC CCACCACCAC CCACCA	120 180 240 300 360 420 540 660 720 780 960 1020 1380 1440 1350 1560 1560 1680 1740 1800 1920 1980 2040 2100
50 55 60 65 70 75	Coding sequilibrium sequilibriu	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGTGGTGCTC AAGGAGGCT GCCCGAGAG GCGTTGGATTC AAGGAGGCG GAGGCAGAAA GGATGTGGT ACGTGCTGTT ACGTGCTGTT ACAGGACGCT TAACCCACCC GCCAGAATGG TCCTCTTCCT TCTTCGTGAA TGGCCATAG CGGCACATA CTGACCTGGT GGCCATAG GGCCACATA CTGACTGGT GGCCAGAATGG TCCTCTCCT TCTTCGTGAA TGGCCACATA CTGACTGGT GGCCACATA CTGACTGGT GGCCACATA CTGACTGGT GGCCACATAG CTGACTGGC GGCCACATAG CTGACTGGC CCGAGAATTI ACCCTGACGT GGCTGACGAC CCGAGAATTI CCCTGACGC CCCGAGAGCG CCCGAGAGCG CCCGAGAGGCG CCCGAGAGGGC CCCGAGAGGGCG CCCGAGAGGGCG CCCGAGAGGGCG CCCGAGAGGGCG CCCGAGAGGGCG CCCGAGAGGGCG CCCGGACGGCG CCCGGACGGCG CCCGGACGCG CCCGGACGGCG CCCGGACGGCG CCCGGACGGCG CCCGGACGGCG CCCGGACGGCG CCCGGACGGGGGGGG	224 21 GGAGGCCGTC CCATCTAAGC GGTCGCAGTG TGAAAGGTCC GGTTCAGGTG ATTTTCAACC CACGGAGACG TGCTTCTGTG GGCTGCAGGG GGCTGAGCAG GGAGATGGT TGCACCTGC TGCCAGGCG AGGACATGT AGGGAGAGCT AGGGAGAGCT GCTGGACAGC GCGGTTTGTG AGGGAGAGCT CGCAGGGGC CTGCACGCC CGACAGGCCC CGACAGGCCC CGACAGGGCC CGACAGGGCC CGACCAGGCC CGACCAGGCC CGACCAGGCC CGACCAGGCC CGACCAGGCC CGACCAGGCC CGACCAGGCC CGACCGCC CGACGCCC CGACCCC CGACCC CGCC CGACCC CGACC CGACCC CGACCC CGACCC CGACCC CGACCC CGACCC CGACCC CGACCC CGACCC CGCC CGACCC CGACC CGACCC CGACCC CGACCC CGACC CGCC CGACCC CGACCC CGCC CGACCC CGACCC CGCC CGACCC CGACCC CGCC	TGTGTTTTCC ARAGARACCA AGCARTAGT AGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CGAGCAGG GACTTGCTG GGAGGATGC GTGCAGCAGG GCACCCCAG GCTGCAGCAGC CTACAGGAGG CGGGAGTTCG GCTGCAGAGG ACTGTGCAGAGG ACTGTGCAGAGG CGGGGGTGC CTGCTGGTGG GAGCGTGGC CCTGAGCTGG CCTGAGCTGG CCTGAGCTGG CCTGGTGG CGGGCTGCG CCTGGTGG CGGCTGCCCAGAGG CGGCCTGCCCAGAGC CCTGCCCAGAG CCTGCCCAGAGC CCTAGCCCCAGG CCTAGCTGGC CCTAGCTGGC CCTGCCCAGAGC CCTAGCCCCAGG CCTAGCCCAGG CCTAGCCCCAGG CCTAGCCCAGG CCTAGCCCAGG CCTAGCCCAGG CCAGCCCAGG CCAGCCCAGG CCAGCCCAGG CCAGCCCAGG CCAGCCCAGGCC CCTGCCCAGG CCAGCCCAGGCCCCCC CCTGCCCAGGCCCCCC CCTGCCCAGGCCCCCC CCTGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCC CCAGCCCAGGCCCCCCCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT TGAAGGCAAG TGAAATACCT TCATCATCGT TGAAGGCAAG TGAAATACCT TCATCATCGT AGGAAAGGGG ACTGCACAGG GCCCACTCTGG GACTGGACGG CCACTCTGGA CGGTGCCTGT CCTGCCAGG CCACTCTGGC AGGAAGCATGT CCTTCCATGG CCACTCTGGC AGTCACACT TCCTGCTGGG CCACTCTGGC AGTCACACT TCCTGCTGGG CCACTCTGGC AGTCACACT TCCTGCTGGG CCACTCTGGA AGCTGAGAAGCT TGGAGAAGCT TGGTGCGGG TGGTGCCGGG AGTCACCT AGCTGAGGAG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGG TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCTGCGGGAC TGCGGGGACC TGCGGGACC TGCCGGGACC TGCCGGACC TGCCGGACC TGCCGGCACC TCCCGCACC TCCCGCACC TCCCCCCC TCCCCCCC TCCCCCCCC TCCCCCCCC	AGTGCCCCA TTCAGCTGCC TTGGTCCCC TTGGTCCCC TTGGTCACGT TCACTCCTCAT AATCAAGAGG TCTGCACGAG TCTGCACGAG CACTGATGG CAGCGAGCCT CCATGCTGG CAGCGAGCCT CCATGCTGG CCATGCTGG CCATGCTGG CCACTGTAGC CCACTGATGC CCACTGAATGC CCACTGAATGC CGGGCTTCACG CGGGGAATGC CGGCCTCCACC CGCCTGCAGC CGACGACTAGC CGACGACTAGC CGACGACTAGC CGACGACCAC CGACCACCCCACC	120 180 240 300 420 480 540 660 720 780 1020 1080 1140 1260 1320 1380 1440 1560 1620 1680 1740 1860 1980 2040 2160
50 55 60 65 70 75	Coding sequing	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TGCAGGAGGT TGTGGTGCT AGGAGGAGT GCCCGAGAG GGAGCAGAAA GGAATGGC GGGCAGGAA ACGGCAGGCA ACGGCAGAGG TCCTCGGATC TACCCACCC GCCAGAATG TCCTCTTCCT TCTTCGTGAA TGGCCATTGG TGCCTTTGG TCCTCTTCCT TCTTCGTGAA CGGCACATGG GGCCACATGG TGCCTTGG TCCTCTTCCT TCTTCGTGAA CGGCCACAGATGG GGCCACAGATGG GGCCACAGATGG TCCTCTCCT TCTCGTGAA TGGCCTGGC TAGCTGGC TCGGCAGAGGC GGCCAGAGGC TCGGGAGAGC TCGGGAGGC TCGGGAGGC TCGTGGGCC TCGGGAGGC TCGTGGGCC TCGGGCGCAGGC TCGTGGGCC TCGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGTGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGGCC TCGGCC TCGGGCC TCGGGCC TCGGCC TCGCC TCGGCC TCGCC TCGGCC TCGCC TCGCC TCGCC TCGCC TCGCC TCGCC TCGCC TCCC TCC TCC TCC TCCC TCC	424 21 21 GGAGCCGTC GGAGGCGTC GGTCAGAGTG ATTTCAACC CACGAGACG TGCTTCTGTG ACTGCTCCAGGC GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGAGAGGCGGAGAGGCGCGCA CAGGAGAGGCGCGCA CAGCAGAGCGCGCC GGAGAGGCGCGCC CAACCAAC	TGTGTTTTCC AAAGAACCA AAGCAATCATGT AAGCACTTGGGAGCATTCC CCCCAGATCC CACCAGATCC CACCAGATCC CCCCAGATCC CCCCAGATCC CGCCAGATCC CGCCAGATCC GGAGGTTCC GGAGGTTCC GCTGCACACT TACAGGACA AACTGTCCCC CTGCTCGTGG GATGCCATCC CGAGAGCTGC CGCCTGCCCAGAC CGGCCTGCC CGCCTGCCCAGAC CGGCCTGCCC CGCCCGCCCC CGGCCTGCCCCC CGGCCCCCCC CGGCCCCCCC CGCCCCCCCC	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGAGCTGC TGGGTCTAAC CTGTGACGGT TATCAAGAGG TCTGCACAGA CACTGATGG TGTCACTGTG CAGCGTCAC CCCATGCTGG CAGCGTCAC CCCATGCTGG CAGCTGCAAG CCCTGTGAC CCCATGCTGG CAGCGTTCCTG CTCTCGGCC CGAGGATGC CGAGGATGC CGAGGATGC CGACTTCCTG CTCCAGGCCAC CGAGGATGAC CGACTTCCCAC CGACGATGAC CGACTTCCAG CTCCAGGACA CGAGGATGAC CGACTTCCAG CTCCAGGACA CGAGGATGAC CGACTGCAC CGAGGATGAC CGAGGATGAC CGACTTCCAG CCACGGACAC CGAGGATGAC CACCAGCCAC CCAGGACATC CACCAGGACATC CACCAGGACATC CACCAGGACATC CGATGCACAC CGAGGACATC CGACGACGTC CACCAGGACATC CGCTTCCAGGACATC CGCTTCCAGGACATC CACCAGCCCCC CACCAGGACATC CACCAGCCCCC CACCAGGACATC CACCACCCCCC CACCACCCCCCC CACCACCCCCCCC	120 180 240 300 360 420 540 660 720 780 900 1080 1140 1250 1320 1380 1560 1680 1740 1890 1920 1920 2100 2100 2220
50 55 60 65 70 75 80	Coding sequilar and control co	Jence: 12 11 TCCTGTTGCT TCCAGGAAGT TCCAGGAAGT TGGGTGCT AAGGAGGCT GCCCGAGAAG GGATGTGGC GAGGCAGAAT ACGGCCT GGCGCACCT TAACCACCC GCCAGAAGC TGCCTTTGGT TCTTCGTGAA TGGCCATAG TGGCCTTTGG TCTTCTCTGTA TGGCCACTAG GGCAGACCT TAACCACCC GCCAGAATGG TCCTCTTCC TCTTCTGTGAA TGGCCACTAG CGGCAGACT GGCCACTAG CGCCAGAATGG CCCGAGACT CTCTTCT TCTTCGTGAA TGGCCACTAG CGGCAGAGG CCCGAGAATT ACCCTGCC CCGAGAATT CTGCTGGCC CCGAGAATT CTGTGGGC TCCTGACCGT CCTGACCGT CCTGACCGT CCTGCGCC CCGAGAATT CCCTGACGG CCGAGAGGG CCCGAGAGGG CCCGAGAGGG CCCGAGAGGG CCCGAGAGGG CCCGAGGGG CCCGAGGGG CCCGAGGGG CCCGGACCC CGGCCCCCCC CGGCCCCCCC CGGCCCCCCC CGGCCCCCC	424 21 21 GGAGGCCGTC CCATGTAAGC GGTCACAGTG TGAAAGGTCC GGTCAGAGTG ACTGCCAGC GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGCTGAGCAG GGAGATGGT AGGCACAG AGGCACAG CGGAGACG CGGAGGCGC CGAAGCCGC CGGAGCGC CGACACAGCC CGGACGCGC CGACCAGC CGGCCGCC CGACCAGCC CGGCCCCGCC CGGCCCCGCC CGGCCCCGCCC CGGCCCCGCCC CGGCCCCGCCCCCC	TGTGTTTTCC ARAGAACCA GACATCATGT AAGCACTTG GGAGCATTCC CCCCAGATCC CCCCAGATCC CCCCAGATCC GAGCAGTCG GAGCATTCG GCACCCCAG GCACCCCAG GCCCACAGCCCAG GCCCCAGATCC GCTGCACCCC GCTGCACCCC GTTCCAGAAG AACTGTGCC CTGCTGGTGG CAGAGCTGC CTGCTGGTGG CAGAGCTGC CCTGAGCTGC CCTGCCCAGG CCTAGCTGC CCTGCCCAGG CCTAGCTGC CCTGCCCAGT CCTAGCTGC CCAGCCAGTCC CAGCCAGTCC CAGCCAGTC CAGCCAGTC CAGCCAGTC CAGCCAGTC CAGCCAGTC CAGCCAGTC CA	TGTTTTCCAG TCGGGAAGAT TTCTGTTAGA CCATCACAGT AGTTCAGTTC	AGTGCCCCA TTCAGCTGCC TTGGTCCCC TTGGTCCCC TTGGTCACGT TATCAAGAGG TCTGCACAGA CACTGATAGG TCTCACCTGTG CACGCTCAC CCCATGCTGG CCACTGCTGC CCCATGCTGG CCCCTGTGAC CCCCTGTGAC CCCCTGTGAC CTACCAGGCCC CGCCTCCCTG CTCCGGGCC CGCCTCCCTG CTCCGGGCC CGCCTCCAC CGCCTCCAC CGCCTCAC CGCCTCCAC CGCCTCCAC CGCCTCCAC CGCCTCCAC CGCCTCCAC CGCCTCCAC CCACAGGACA CGCTCTCAC CCACAGGCCC CCACAGGCCC CCACAGGCCC CCACAGGCCC CCACAGGCCCC CCACAGGCCC CCACAGGCCCC CCACAGGCCCC CCACAGGCCCC CCACAGGCCCC CCACAGGCCCC CCACAGCCCC CCACAGCCCC CCCTCCAGGCCCC CCCTCCAGGCCCC CCACAGCCCC CCACAGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGGCCCC CCTCCAGCCCC CCTCCCAGCCCC CCTCCCAGCCCC CCTCCCAGCCCC CCTCCCCCCC CCTCCCAGCCCCC CCTCCCCCCC CCTCCCAGCCCCC CCTCCCCCCC CCTCCCCCCCC CCTCCCCCCCC	120 180 240 360 420 540 660 720 780 960 1020 1320 1380 1440 1560 1560 1560 1560 1580 1740 1880 1740 1890 2040 2160 2220
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		CCAGCAACTA CCCCAGGTCC	CAGAGAAGGC TTAG	CTGGGCACTG	AAATGGTGCC	TACCTTCTGG	2400
_	Seq ID NO:	85 Protein	sequence				
5	Protein Acc	ession #: E	os sequence	1			
	1	11	21	31	41	51	
	MODELLIEN	CURLESPUDD	SLPLQEVHVS	 VETICKISAA	SKMMWCSAAV	DIMPLIDGEN	60
			LDISPERVRV				120
10			GLPGGRNASV				180
	FAVGVRFPRW	EELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SOPCONGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360 420
15	RAKVEVKREV	RAVLSEDSKA	RVGVATYSRE GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLIGUES	480
13			SDPQDLFNQI				540
	SVGPENFAQM	QSFVRSCALQ	FEVNPDVTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISO	600
	APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAV	PAQKLRNNGI	660
20			PRDSLIHVAA				720
20		NGSYRCKCRD LGTEMVPTFW	GWEGPHCENR NVCAPGP	EMESCEACAS	QGWILETPLR	RMAPVQEG55	780
		86 DNA sequ	ence 1 #: Eos sec	nience			
25		ence: 892		•			
	1	11	21	31	41	51	
			- COCCOCTOTO	 managenera	COCCCCCCC	CCGNGCCCTG	60
			CCCGGGTCTG ATATCAACAT				120
30	TGTTTTCCTG	TTTTCCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATTT	CAGCTGCCAG	CAAAATGATG	TGGTGCTCGG	CTGCAGTGGA	240
			GGTCTAACAG				300
			GTGACGGTCT				360 420
35	AGCATTCCAG	ANGGERAGER	CTCCTCATCT	GGAATTCCCC	GGAGGGGGGA	CGGAGACGGA	480
55	ACAGGAAGIG	AAATACCTTC	TGCACAGAGG	GTTGCCTGGA	GGCAGAAATG	CITCIGIGCC	540
	CCAGATCCTC	ATCATCGTCA	CTGATGGGAA	GTCCCAGGGG	GATGTGGCAC	TGCCATCCAA	600
	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAGGTTTC	CCAGGTGGGA	660
40	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTTGG	CTGAGCAGGT	720
40			TCTTCAGCAC AGGCTCACCC				780 840.
	GGAGTTCGCT	GGCAATGCCC	CATGCTGGAG	AGGATCGCGG	CGGACCCTTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
45	TCCAGAAGGA	CTGGACGGCT	ACCAGTGCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG GCTTCCTGCG	GGTCGACCTC	CTCTTCCTGC	TGGACAGCTC	1140 1200
	GCCCGTGCTG	ACTOTOGACO	CTCGGGCCCG	ACTCCCTGTC	GCCACATACA	GCAGGGAGCT	1260
	GCTGGTGGCG	GTGCCTGTGG	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
50	TGGCATTCCC	TTCCGTGGTG	GCCCCACCCT	GACGGGCAGT	GCCTTGCGGC	AGGCGGCAGA	1380
	GCGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACACTCCG	AGGATGAGGT TAGGCAGTGA	TGCGGGCCCA	GCGCGTCACG	AGGAGATCAC	1500 1560
	AGAGCTGCTC	ANGCATGTGA	TGGTCTACTC	GGCCGTGCGG	GATCTGTTCA	ACCAAATCCC	1620
55	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
			CCTCTGCCTC				1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCGG	1800
			AGGTGCAGAC				1860 1920
60			TTAGCCAGGC			CCCGGCCTGG	1980
00	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
			ATGGCATCTC				2100
	AAGTGAGGGT	CTGCGGAGGC	TTGCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
65						AAGCCAAGCA	2220 2280
03						TCCTGCAGAA AGAACCGATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCTA	CCTTCTGGAA	TGTCTGTGCC	2460
70	CCAGGTCCTT	AGAATGTCTG	CITCCCGCCG	TGGCCAGGAC	CACTATTCTC	ACTGAGGGAG	2520
70	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCACCCAC	2580
						TACCTGCTGT GGGTCCTGAA	2640 2700
						AGAATGTTGT	2760
			GAGGCCTTTA				. = -
75							
		87 Protein					
			Eos sequenc		41	51	
	1	11 1	21	31 	41	j.	
80	MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
	MVPKGGRTET	ELALKYLLHR	GLPGGRNASV	POILIIVIDG	KSQGDVALPS	KOLKERGVTV	180
	FAVGVRFPRW	EBLHALASER	RGQHVLLAEC	VEDATNGLES	TLSSSAICSS	ATPDCRVEAH	240 300
85						YRTTCPGPCD SAGTTLDGFL	360
55	201 COMOGIC		· Jurini Com				

5	LTGSALRQAA EAVRAELEEI SVGPENFAQM APYLGGVGSA SVLVVGVGPV	ERGFGSATRT TGSPKHVMVY QSFVRSCALQ GTALLHIYDK LSEGLRRLAG	RVGVATYSRE GQDRPRRVVV SDPQDLFNQI FEVNPDVTQV VMTVQRGARP PRDSLIHVAA GWEGPHCENR	LLTESHSEDE PELQGKLCSR GLVVYGSQVQ GVPKAVVVLT YADLRYHQDV	VAGPARHARA QRPGCRTQAL TAFGLDTKPT GGRGAEDAAV	RELLLLGVGS DLVFMLDTSA RAAMLRAISQ PAQKLRNNGI	420 480 540 600 660 720
10	Nucleic Aci	88 DNA sequ d Accession mence: 113	#: NM_0198	394		•	
	1	11	21 	31 	41 	51 	
15	ATGTTACAGG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TCGATGTCAA	ACCCCTGCGC	60 120
13			GACCTTCAGA CATTGTGGTT				180
			TCTCCACTTC				240 300
			GGACGAGGAG CAAGGACCGA				360
20			TTTCGACAAC				420 480
			CAAACCCACT CACAGAAAAC				540
	GGGCCCTGTC	TCTCAGGCTC	CCTGGTCTCC	CTGCACTGTC	TTGCCTGTGG	GAAGAGCCTG	600
25			TGGGGAGGAG GCACGTCTGT				660 720
	CTCACGGCAG	CCCACTGCTT	CAGGAAACAT	ACCGATGTGT	TCAACTGGAA	GGTGCGGGCA	780
	GGCTCAGACA	AACTGGGCAG	CTTCCCATCC	CTGGCTGTGG	CCAAGATCAT	CATCATTGAA	840 900
			GCCCATCTGT				960
30			TGGATGGGGC				1020 1080
			AGTCCAGGTC CGAGAAGATG				1140
	GACACCTGCC	AGGGTGACAG	TGGTGGGCCC	CTGATGTACC	AATCTGACCA	GTGGCATGTG	1200
35			CTATGGCTGC				1260
	Seq ID NO:	89 Protein	sequence:				
40	1	11	21	31	41	51	
40	MIADPDSDOP	LNSLDVKPLR	 KPRIPMETFR	 KVGIPIIIAL	 LSLASIIIVV	VLIKVILDKY	60
	YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKOR	STLQVLDSAT	120
			RQMGYSSKPT KTPRVVGGEE				180 240
45	LTAAHCFRKH	TDVFNWKVRA	GSDKLGSFPS	LAVAKIIIIE	FNPMYPKDND	IALMKLQFPL	300
	TFSGTVRPIC	LPFFDEELTP	ATPLWIIGWG DTCQGDSGGP	FTKQNGGKMS	VGIVSWGYGC	GGPSTPGVYT	360 420
	KVSAYLNWIY						
50	Sea ID NO:	90 DNA sequ	ience				
	Nucleic Ac:	id Accession	n #: NM_002	776.1			
	Coding sequ	uence: 82! 11	912 21	31	41	51	
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55	ACCAGCGGCA	GACCACAGGC	AGGGCAGAGG CATGAGAGCT	CACGTCTGGG	ACCTCTCCCT	CGCCTCTGGC	60 120
	GCCCGGGCTC	TGGCGAAGCT	GCTGCCGCTG	CTGATGGCGC	AACTCTGGGC	CGCAGAGGCG	180
	GCGCTGCTCC	CCCAAAACGA	CACGCGCTTG GGTCTCGCTC	GACCCCGAAG	CCTATGGCGC	CCCGTGCGCG	240 300
60	GTCCTGGTGG	ACCAGAGTTG	GGTGCTGACG	GCCGCGCACT	GCGGAAACAA	GCCACTGTGG	360
			CCTGCTGCTT				420 480
	GATGAGCACG	ATCTCATGTT	GTACCACCAG GCTAAAGCTG	GCCAGGCCCG	TAGTGCCGGG	GCCCCGCGTC	540
65	CGGGCCCTGC	AGCTTCCCTA	CCGCTGTGCT	CAGCCCGGAG	ACCAGTGCCA	GGTTGCTGGC	600
05	TGGGGCACCA ACTATCCTGA	GCCCTAAAGA	GAGAGTGAAG GTGTGAGGTC	TACAACAAGG	GCCTGACCTG	CAACAACATG	660 720
	ATATGTGCTG	GACTGGACCG	GGGCCAGGAC	CCTTGCCAGA	GTGACTCTGG	AGGCCCCCTG	780
	GTCTGTGACG CAGCATCCAG	AGACCCTCCA	AGGCATCCTC	AAATACATGT	CCTGGATCAA	TAAAGTCATA	840 900
70	CGCTCCAACT	GATCCAGATG	CTACGCTCCA	GCTGATCCAG	ATGTTATGCT	CCTGCTGATC	960
						CCTCTCACCT	1020 1080
	CATTCCCCCA	CCTATCCCCA	TTCTCTGCCT	GTACTGAAGC	TGAAATGCAG	GAAGTGGTGG	1140
75						AGAGCAGTTA GGGCAAGCCA	1200 1260
15	AGTGCCCTCT	CTGAACCTCA	GTTTCCTCAT	CTGCAAAATG	GGAACAATGA	CGTGCCTACC	1320
	TCTTAGACAT	GTTGTGAGGA	GACTATGATA	TAACATGTGT	ATGTAAATCT	TCATGTGATT	1380
	GTCATGTAAG AAAAAAAAAA		GIGGGIGGTG	AGTTCTGACT	AAAGGTTACC	TGTTGTCGTG	1440
80-							
	Seq ID NO:	91 Protein	sequence NP_002767.1				
	1	11	21	31	41	51	
85	MPAPHT.HI.CA	ASGAPAT.AKT	 LPLLMAOLW#	AEAALLPONE	 TRLDPEAYGA	 PCARGSQPWQ	60
00	. aca munda	- AUGISTALIA					

5	YHQGSGPILP RVKYNKGLTC	CAGVLVDQSW RRTDEHDLML SSITILSPKE GSAQHPAVYT	LKLARPVVPG CEVFYPGVVT	PRVRALQLPY NNMICAGLDR	RCAQPGDQCQ	VAGWGTTAAR	120 180 240
	Nucleic Aci Coding sequ	92 DNA sequence: 182-6	1 #: NM_0320 558				
10	1	11	21	31	41	51	
10	GCCCTTAGAG AGAAGCGCTA	AGCTCCAGAA TCTTGGTTGC GTAAGGTCTC AGAAGCATGC	CAAACAGATT TGAGATCCTT	TGCAGATCAA GCACTAGCTA	GGAGAACCCA CATCCTCAGG	GGAGTTTCAA GTAGGAGGAA	60 120 180 240
15	CCTGGGTGAT TTGCTATGGT TTACGGAAAC AGAGTACATA	ATCATCATGA TACTTCAGGA GGAGCCCACC AGTGGCTATC CAGTGGCAGT	GACCCAGCTG AGCTGAGGAA TGGCATCTAT AGAGAAGCCA	TGCTCCTGGA CTGGTCTGAT CCTGAGTTTA GCCGATATGG	TGGTTTTACC GCCGAGCTCG AAGGAAGCCA ATTGGCCTGC	ACAAGTCCAA AGTGTCAGTC GCACCATAGC ACGACCCACA	300 360 420 480 540
20	CAAGTCCATG TTGGAGCAGC CAAGAATCAA GCTAAATCTG	GGTGGGAACA AACGAATGCA GATTCTGCTA CTCATTATTT CTTTTTTAGG	AGCACTGTGC ACAAGCGCCA ACTCCTGCAC CAGAGGGGAA	TGAGATGAGC ACACTTCCTG AGCCCCGTCC ACCTAGCAAA	TCCAATAACA TGCAAGTACC TCTTCCTTTC CTAAGAGTGA	ACTTTTTAAC GACCATAGAG TGCTAGCCTG TAAGGGCCCT	600 660 720 780 840
25	CTAGCTCTAA GTCTCTGGCT CTTTGGCCAT AGACCCCTTC	ATGTTTGCCC GTCTCGAGCA AAGAAGTAAA AGCTTCTACA CTGCTTGTTT	CGCCATCCCT GTCTAGAAGA GATTTGAAGA CCCTTCTGCC	TTCCACAGTA GTGCATCTCC CAGAAGGAAG CTCTCTCCAT	TCCTTCTTCC AGCCTATGAA AAACTCAGGA TGCCTGCACC	CTCCTCCCCT ACAGCTGGGT GTAAGCTTCT CCACCCCAGC	900 960 1020 1080 1140
30	TAGGTTGATG Seq ID NO:	TGGGCCATAC 93 Protein	ATTCCTTTAA sequence				
	Protein Acc	ession #: 1 11	VP_114433.1 21	31	41	51	
35	î	î	î	Ĩ.	ì	Ĩ	
	YGNGAHLASI	LLSCLAKTGV LSLKEASTIA EMSSNNNFLT	EYISGYQRSQ	PIWIGLHDPQ			60 120
40							
	Nucleic Ac:	94 DNA sequid Accession	1 #: XM_051	360			
	couring sequ	uence: 140					
45	1	lence: 140	186 21 1	31 1	41 i	51 	
45	1 GAGCTAGCGC CGGCGCGGGG		21 CCCAGCGCGG GCTGAGCGCG	 TGCTATCGGA GCCAGGGTCT	 CAGAGCCTGG GAACCCAGAT	CGAGCGCAAG TTCCCAGACT	60 120 180
	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC	120 180 240
45 50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG	21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCCGC ATGGGAGCTG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGÇCA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA	120 180 240 300
	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT	21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGC ATGGGAGCTG ACTCTGACCT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG	120 180 240
	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCC ACCATGTGCA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCTC TGACCAGAGC TATCGGCCAG	21 CCCAGCGCGG GCTGAGCGCG ACGCCCCGGG CCTGGCCGC ACTCTGACCT ACTCTGACCT CCTGAGTTGC GGCAAGACAC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC	CAGAGCCTGG CAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTA GACCAAGACC ACGGTCTATT	120 180 240 300 360 420 480
50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGACG TGCTGACCAT CTGGGTGCCC ACCATGTGCA CCATCTCACAT	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CAGCTGGCTC TGACCAGAGGC TATCGGCCAG CTCAGAGGGA	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG ACTGGCCCGG ACTGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGACAC GGCAAGCTGG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGA ACCCTGGA TGCTGCTCAC TCATTAAAGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTTT	120 180 240 300 360 420 480 540
	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TCTGGGTGCCC ACCATCTGCA CCATCCACAT TGCGAACCCG	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCT TGACCAGAGC TATCGGCCAG CTCAGAGGGA CTCAGAGGGA GCACATCCTG GGGCAATTTC	21 CCCAGGGGG GCTGAGGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC ACTGACATTA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA ACCCTGGAA TGCTGCTCAC TCATTAAAGA TGCTGCTCAC TCATTAAAGA TGTATGGAAGCT TGTATGGAAG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCCG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGCTGATGAA	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTA ACAGTGCTATT CCGATTGTTT AGTGCCCTCT GGTATTCAGC	120 180 240 300 360 420 480
50	1 GAGCTAGCGC CGGCCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT CTGGATGCCA CCATGTGCA CCATGCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCTC CACTGCCAGG CAGCTGGCTC TGACCAGAGC CTCAGAGGGA CTCAGAGGGA GCACATCCTG GGGCAATTTC CTATGGTCTG	21 CCCAGGGGG GCTGAGCGG ACGCCGGG ACTGGCCGG ATGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGACAC GGCAAGCTG ATTGACAACG ACCATCATTT AAGTACATTG	I TGCTATCGGA GCCAGGGTCT AGCTCGCGG GAGGCGTGAC CTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGATGAA AGGAGGCGCT	CGAGCGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACT CCGATTGTTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGCC CTTGAGTTGC	120 180 240 300 360 420 480 540 600 660 720
50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTTCCGGG AGAGGGAGCA TGCTGACCAT CTGGGTGCCA ACCATGTGCA ACCATCTACAT TGCGAACCCG GCCCTTTCCA ATGGAACCTTA ATGGAACGAA	11 TCAAGCAGAG AGCCAGCGGG CCGCTGCGCT CACTGCCTC TGACCAGAGC CAGCTGGCTC TGACCAGAGGA CTCAGAGGGA GCACATCCTG GGGCAATTCTG AAAGCTCTCC	21 CCCAGCGCGG GCTGAGCGCG ACGCCCGGG CCTGGCCCGG ACTGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGCAG GGCAAGCAG ATTGACAACG ACGATCATTT AAGTACATTT AGGTACATTTT AGGTACATTTT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTCGCAGGCA ACCCTGGA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAGG GGGTTGGTAA TGAACAAGAC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGCTGATGAA AGGAGGGGT CCTTCACCCA	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCTCT GGTATTCAGC CTTGAGTTCAGC GGTGGCATGG GGTGGCATGG	120 180 240 300 360 420 480 540 600 660 720 780
50	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT TACGTCGGGG AGAGGGAGCA TGCTGACCAT TCGGGTGCCC ACCATCTACACAT TGCGAACCCG GCCCTTTCCA CGGATCCTA ATGGACAGAA CAGAAGGAGG	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CACCAGAGC TATCGGCCAG CTCAGAGGGA GCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTTT	21 CCCAGGGGG GCTGAGGGGG GCTGAGGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGCAGA ACTAGACAACG ACCATCATTT AAGTACATTG TGGACATTTTC GAAAGGAGCT	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTCGGAGGCC AACCCTGGA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCT CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGATGCTGGG GGCTGATGAA AGGAGGGGCTCATCACCCA TGGAGTTATT	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGCTAT CCGATTGTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GGTGGCATGG GTTCCATGCCATG	120 180 240 300 360 420 480 540 600 660 720
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGAGGGAGCA TGCTGACCAT TGCGATCCACAT TGCGAACCCG GCCTTTCCA ATGGACAGAA CAGAAGGAGA ATGGACAGAA CAGAAGGAGAA AGAAGAGTGA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCTC CACTGCCTC TGACCAGAGC CTATCGCCAG GCACATCCTG GGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTTT ATCAGGCACA ACGTCTGGTC	21 CCCAGGGGG GCTGAGCGG ACGCCCGGG ACGCCCGGG ACTGAGTGG ACTCTGACTG ACTCTGACTG ACTCAGACAC GGCAAGACAC GGCAAGACAC GTAACATTT AAGTACATTT TGGACATTTC GAAAGGAGCT GTCATCATTT CAGTATTTGA	I TGCTATCGGA GCCCAGGGCTCT AGCTCGCGGC GAGGCGCAGGCA TGCTCCCTGG AACCCTGGAA TGCTATTAAAGA GAGGAGAGCT TGTATGAAGA GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTTCACCGGTT ACGCGGTTCACCGGTTCACCGGTTCACGGGTCCC	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGAGGAG GCATGCTGACCA TGGAGTTATT TGACACCTAT CGATGGCAGGG CGATGATGAC CCTTCACCCA TGGAGTTATT CGATGGCAGGG	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC CCGATTGTTT AGTGCCTCT GGTATTCATG CTTCATGTCG GTTGCTTGC GTTGCTTGC GTTGCTTGC ACAGCCAGA ATCCTTTCTG	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT TACGTCGGGG AGAGGGAGCA TGCTGACCAT TCGGGTGCC ACCATCTACA TGCGAACCAC GGCCTTTCCA ATGGACAGA ATGGACAGA TCGACCCCAA AAGAAGGAG TCGACCCCAA AAGAAGTGA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CAGCTGGCTC TGACCAGAGC TATCGGCCAG GCAATTCC GGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGCACA GGCAAGCACA ACCATCATTT AAGTACATTG TGAAAGAGGCT GTCATCCATTT CAGTATTTGA TCTCGAAATC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTCGGAGGCA ACCCTGGA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC TGGATGACACAT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGCTGATGAA AGGAGCGGT TCCTTCACCCA TGGAGTTATT TGACACCTAT TGACACCTAT CGATGGAGAG GGCCAGAGAG GGCCAGAGAG GGCCAGAAAG	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAAGACCA TACAAGACCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCCTCT GGTATTCAGC CTTGAGTTCG GTTGAGTTGG GTTCATGTCA AGATCCAAGA ATCCTTTCTG GCGATGACCCA	120 180 240 300 360 420 480 540 660 720 780 640 900 960 1020
50 55 60	1 GAGCTAGCGC CGGCCGGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TGCGATCCCA CCATCTCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTTA ATGGACAGAA CAGAAGGAGG TCGACCCCAA AAGAGAGTGA TTGCAGTGAA ATTGCGGAAG	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCTC CACTGCCAGG CACTGCACAC CTACAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTATCTTC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGTT CAAACACTTC TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTT TCCATCATCTTC TCCATCTTC TCCATCATCTTC TCCATCATCTTC TCCATCATCTTC TCCATCTTC TCCATCATCTTC TCCATCTTTC TCCATCATCTTTC TCCATCATCTTTC TCCATCATCTTTC TCCATCATCTTTC TCCA	21 CCCAGGGGG GCTGAGCGG ACGCCCGGG ACGCCCGGG ACTGAGCTG ACTCTGACTG CCTGAGTTGC GGCAAGCTG ACTATACAACG ACCATCATTT TGGACATTT GAAAGAGGT GTCATCCATT CAGTATTTGA TCTCGAAATC CTGCACATG TCAGTGGACAC	I TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTGCGAGGCA TGCTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG TGATCACAC CTGACCACCGGTT ACGCGGTGCC TGGATGACA ACCATATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGCC CCACGACGAG GCATGCTGATGA AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCAGAG GGCCAGGAG GCCAGGAGAG ATTGCAGGA ATATCATGGA ATATCATGGA	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC TCCAGTGGCTT CCGATTGTTT AGTGCCCATT CGTATTTCTC GGTGTTATTCCGTTTCATTCCTTCATTCCTCAGGTCTATTCTCCAGTTCTCATTCCTCTTCATTCCTCTCCAGAGACCATTCTAACTGCCATGCTTCAACTCCAAGA ATCCTTTCTCACTCCAACACTTCTAACTGCCATCAACACTCCAACGACCT	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TCTGGGTGCC ACCATCTACA TGCGAACCCG ATGCACCACA ATGGACAGA ATGGACCCCAA AAGAAGGAG TCGACCCCAA AAGAAGTGA TTGCACTGAA AATTGGAAGAA ATTGGAAGAA ATTGGAAAGAAC TTGAACGAAA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CAGCTGGCTC TGACCAGAGC TATCGGCCAG GCAATTCC GCAATCCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACATTC TCCATCATCT CCAGTCATCC CCAGTTTC CCAGTTC CCAGTTTC CCAGTTTC CCCGGTTATC CCCGGTTATC	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG GCTGGCCGG ATGGGAGCTG ACTCTGACCT CCTGAGTTGC GGCAAGCAG ACCATCATTT AAGTACATTG TGAACATTG TGAACATTG TCAGTATTCAATTTC AGTATTTGA TCTCGAAATC CTGACCTTG TCAGTGAATG ACTTGAATTTTAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTTAATTGAATTTTAATTGAATTTTAATTGAATTTTAATTGAATTTTAATTGAATTTTAATTGAA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTCGGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TGTATGGAAG GGGTTGGTAA TGAACAAGAC GGGGCCACCG CTGACCGGTT ACGCGGTGCC TGGATGACAT ACGCAGTGCC ACCATATTGAA ACAATATGA ACAATATTGA ACAATATTGA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCACATCC CCCTGGCCAT CCCTTCTGCG CCACGACGAG GCATGCTGGG GGCTGATGAA AGGAGCGGT TCGTCACCCA TGGAGTTATT TGACACCTAT TGACACCTAT TGACACCTAG GGCCAGGAAG GCCTTGGAGT ATATCATGGA ATGACATAT	CGAGGGCAAG TTCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCTCT GGTATTCAG CTTCAGTCAG GATCATGT GGTATTCAG GTTCATGT GGTATTCAG GTTCATGTC GTTCATGTC GTTCATGTC GTTCATGC GTTCATGTC TTCAACTG CATCGAGGCT TTCTAACTG CATCGAGGCT TTCCAAGTTT TTCAATGTTT	120 180 240 300 360 420 660 660 660 720 780 840 900 900 1020 1080 1140 1200
50 55 60	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGAGGGAGCA TGCTGACCAT TCTGGATGCC ACCATCTACACAT TGCGAACCCC ACGATCCTA ATGGACAGA TCGAACGAG TCGACCCCAA AAGAGAGGAG TTGACCCCAA AAGAGAGGAG TTGACTGAA TTGCAGTGAA TTGCAGTGAA CTGCTGCC CTTTTCTCCAG	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGGCCT CACTGCCAGG CAGCTGGCTC TGACCAGGCT TATCGGCCAG CTCAGAGGG CTCAGAGGGA CTCAGAGGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC TCCATCATCT TCCATCATCT TCAGTCAGGTT TCAGTCGGTT TCAGTCGGTT TGAGTGGGTT TCAGTCGGTT TGAGTGGGTT	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC ACCATCATTT AAGTACATTG CGAAAGGGGGT GTCATCCATT CAGTATTGA TCTGCACTTG TCAGTATTGAAATC CTGCACCTTG TCAGTGGAAATC CTGCACCTTG TCAGTGGAAA AAATTGTTCC CAAAGAGGTGG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTCGGAGGCA ACCCTGGA TGCTGCTCAC TCATTAAGA GAGGAGAGCT TGTATGGAGC GGGTTGGTA TGAACAAGAC GGGCCACCG CTGACCGGTT ACGCGTGCC TGGATGACAA GACTACAACAA ACCATATTGA AGACAAGACA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGCCACATCC CCCTGGCCAT CTCTTCTGGC CCACGACGAG GCATGCTGAGAG GCATGCTGATGAA AGGAGCGCT TCGACTCACCAA TGGAGTTATT TGACACCTAT TGACACCTAT TGACACCTAG GGCCAGGAG GCCTGGAGT ATATCATGGA ATATCATGGA ATGGCGAATAT GGGCGAATAT GTGGTTCGAT	CGAGCGCAAG TTCCAGACT CAGCGACCAG CTACAAGACCA TTCAAGGCCC TTCAAGACCA ACAGTGGCTG GACCAAGACC ACGGTCTATT CCGATTGTT AGTGCCCTCT GGTATTCAGC CTTGAGTTGC GTTCATGTCA AGATCCAAGA ATCCTTCTG GGGATGACCA TTTCTAACTG CATCGAGGCT TTCAACTG CATCGAGGTT TTCAATGTTT CATGAGTTTC CATGAGGTT CATGAGAGACT	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1200 1260
50 55 60	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGAGGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAG GCCTTTCCA CGGATCCTTA ATGGACAGAA AAGAGGAG TCGACCCAA AAGAGGAG TTGCAGTGAA AATTGGAAG AATTGGAAG TGAAGGAAG TTGCAGTGAA CTGCTGCTGC TGCTGCTGC	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCAGG CAGCTGGCTC TGACCAGAGC TATCGGCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCATCTTC AAAGCTCTC TATCATCTT TATCAGGCACA ACGTCTGGTC TGATGAAGT TCAATCATCT CCAGGTATTC TCCATCATCT TCCATCATCT TCCATCATCT TCCATCATCT TTAAAGGTGGGG	21 CCCAGGGGG GCTGAGCGG ACGCCCGGG ACGCCCGGG ACGCCGCG ATGGAGCTG ACTCTGAGTTG ACTCTGAGTTG ACTATATAACAT GGCAAGACAC GGCAAGACAC TGGACATTT CAGACATTC CAGTATTTGAACAT CTGCACATT CTGACTTC CTGCACATT CTGACTCCATT CTGACATC CTGCACATT CTGACATT CTGACACT CTGACACT CTGACACT CTCACACT CTCACAC CTCACACT CT	I TGCTATCGGA GCCCGGCCGCCGCGCGCGCGCGCCGCCGCGCACGCCGCCG	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGCC CCACGACGAG GCATGCTGATGA AGGAGGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCAGAG GCCAGGAGAG GCCAGGAGAG TGGCAGATAT TGGCAATAT TGAGACTAT TGAGACTAT TGAGAGTCAGG ATATCATGGA TGGCGAATAT GAAAGCTCAC	CGAGGGCAAG TTCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCTCT GGTATTCAG CTTCAGTCAG GATCATGT GGTATTCAG GTTCATGT GGTATTCAG GTTCATGTC GTTCATGTC GTTCATGTC GTTCATGC GTTCATGTC TTCAACTG CATCGAGGCT TTCTAACTG CATCGAGGCT TTCCAAGTTT TTCAATGTTT	120 180 240 300 360 420 660 660 660 720 780 840 900 900 1020 1080 1140 1200
50556065	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT TACGTCGGGG AGAGGGAGCA TGCTGACCAT TCTGGATGCA CCATCCACAT TGCGAACCCG GCCCTTTCCA CGGATCCTA ATGGACAGA TCGACCCCAA AAGACAGGG TCGACCCCAA AAGACAGGGA TTGCAGTGAA CTGCTGCC CTTTGTCCAG TATCTCAGAC TATCTCAGAC TATCTCAGAC	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CAGCTGGCTC TATCGGCCAG CTCAGAGGG CTCAGAGGGA CTCAGAGGCAATTTC CTATGGTCTG AAAGCTCTGC TGATCAGAGG CCAATCATCT TCAGAGGCACA CCTCTGGTC TGATGAAGGT CCAACACTT TCCATCATCT TCAGTCAGTT TAAAGGTGGGT TAAAGGTGGGT TCAATTGGT TAAAGGTGGGT TCAATTGGT TAAAAGGTGGGT TCCAATTGGT TCAATTGGT TAAAAGGTGGGT TCAATTGGT TCAATTGAT CCAATTGGT TCAATTGGT TCAATT	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGCAG ACTACATT AAGTACATTG TGACATTT CAGTATTC CAAAAGGAGCT GTCATCCATT CAGTATTGA AATTTTGACATTC CTGCACCTTG TCAGTGAAATC CTGCACCTTG TCAGTGGAAAT AAATTTTTCC CAAGAGCGTGG GAGAAAATTT ATACAGGCA CAGGATTATA	I TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTCGGAGGCA ACCCTGGA ACCCTGGA TGCTGCTCAC TCATTAAGA TGACAGAGCT TGTATGGAGG GGGTCGCACCG CTGACCGGTT ACGCGTGCCACCG TTGACCAGT ACCATATTGA ACCATATTGA ACCATATTGA ACCATATTGA AGCAGACCC AGACCTCTGG CTGACAGGAC AGTGGACGGA AGTGACAGAGCA AGTGACAGAGCA AGTGACAGAGCA AGTGACACTTGGA AGCACTCTTG GCTTGCATGGA GGTTTGCTTG	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCG GGCCACATCC CCCTGGCCAT CCCTTCTGCC CCACGACGAG GCATGCTGGG GGCTGATGAA AGGAGCGGT TCGTCCCAC TGGAGTTATT TGACACCTAT TGACACCGAT TGGATTAC TGGACTCAC CTACGACCGG	CAGGCGCAAG TTCCAGACCA TTCAAGGCCA TTCAAGGCCA TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTCTATT AGTGCCCTCT GGTATTCAGC CTTCAAGTCCA GATCCAAGA ACACTGAGTCTAT AGTGCCTCT GGTATTCAG TTCATGTC GGTAGCATGG GTTCATGTCA TTCATGTC TTCAATGTC TTCTAACTG CGATGACCA TTCTAACTG CGATGACCA TTCAAGATTT CATGATAAAG CCAGGAAAAA CCTCAGCACCG GGCAGAGCCT	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1260 1260 1380 1440
50 55 60	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGACGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAT TGCGAACCAG CCATCCACAT TGCAACCAG ATGCAACCAG ATGCAACAGAA ATGCAAGAA AAGAAGGAG TGAACCCCAA AAGAAGGAA TGCAGTGAA CTGTGCTGCAC TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA TATCCAGCA AGGTTGTCTA	11 TCAAGCAGAG AGCCAGCGGG CGGCTGCGCT CACTGCCAGG CACTGCCAGG CACTGCCAG CTGACCAGGC TATCGGCCAG CTCAGAGGGA CTCAGAGGGA CTCAGAGGCAATTCC CTATGGTCTG AAAGCTCTCC TGATGAGGT TGATGAGGT TCAACACTTC TCCATCATCT TCCATCATCT TCAGTCTGGT TTAAAGGTGGG TCCCATTGAT TCAAAAAAGC CCCTTTTACGGC CCGTTTTCGGCC CCGTTTTCGCGCC CCGTTTTCCGCC CCGTTTCCCCC CCGTTTCCCC CCGTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTCCCC CCGTTTCCC CCGTTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTTCCCC CCGTTCCCC CCCCC CCCCC CCCCC CCCC CCCC CCCC CCCC	21 CCCAGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG ATGGGACTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGCTG ACTATTT AAGTACATT AAGTACATT CAGTATTTC GAAATTT CAGTATTTC TCGAAATT CTGCACTTG TCAGCGGCACTTG CAAGACGGGG AAATTTTTCA	I TGCTATCGGA GCCAGGGTCT AGCTCGCGG GAGGCATGCA ACCCTGGA ACCCTGGA GGGTAGACA GGGTAGACA GGGTAGACA ACCATATGA AGCAGAGCA ACCATATGA AGCAGAGCA ACCATATGA AGGACACAG CAGACCTCG CTACATGGA GGGTTGCTTAGATA ACCATATGA AGCATACAG AGCATACTGA AGTGACAGAGCA AGTGACAGAG CAGACCTCTG CTACATGGA GGTTTGCTTG GGAAGCCTTTG GGAAGCCTTTG CTACATTGGA GGTTTTCTTG GGAAGCCTTTTG GGAAGCCTTTTG GGAAGCCTTTT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGCC CCACGACGAG GCATGCTGAGA AGGAGGCGCT CCTTCACCCA TGGAGTTAAT CGATGGCAGAG GCCAGGAGAG GCCAGGAGAG TGGCAGAAG TGGCAGATAG ATATCATGGA TGGGCAATAT TGGCGAATAT TGGGCAATAT TGGGCTACGAC TGGAGTTCGAC GGAGTTCGAC GGAGTTCGAC GGAGTTCGAC GGAGTTCGAC GGAGTTCAC GGAGTTCAC GGAGTTCAC GGAGTTCAC GGAGTTCAC GGAGTTCAC GGAGTTCAC GGAGCCCAAA	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGGCCA ACAGTGGCTG GACCAAGACC TCGAGTCTATT AGTGCCTTT AGTGCCTTT AGTGCCTGT GGTATTCATGC GTGGCATGG TTCCATGTC GTGATCAAGAC ACACTCAAGAC ATCCTTCTG GCGATGACCA TTCCTAATGT CATCGAGGCT TTCAATGTT TATGATAATG CATCGAGGCT TCCAATGTT TCAATGTTT CATGATAAAG CCAGGAAAAA CTCAGCACG GGCAGACCCT CTCACAGTCA	120 180 240 300 360 420 540 660 720 780 900 900 900 1020 1080 1140 1200 1320 1320 1340 1500
50556065	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGCTACCACT ACGTCCGGG AGCATCCACAT TGCGATGCCA CCATGTGCA CCATGTCCACAT TGCGAACCAG ATGGAACCAG ATGGAACAGAA ATTGGAAGAA AATTGGAAGAA AATTGGAAGAA ATTGGAGAAC CTGATCCCAA AAGAAGAAAC TTGCAGTGAA AATTGGAACAC TTAGCAGAC TATGCAGAC TATGCAGAC TATGCAATCG AGGTTGTCTAA CCGGAGCTA CCGAGCTA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCTC CACTGCCAGG CACTGCCTC TCACCAGAGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGGA CTCATCTC CTATTTTTT ATCAGGCACA ACGTCTGGTC TCATAGACAT CCAGTCATC CCATCATC CCAGTCATC CCAGTCTC CCATTGAT CAAAAAAGGT CCAATTGAT CAAAAAAAGGT CCATTGAT CCAATTGAT CAAAAAAAGGT CCATTGAT CAAAAAAAGGT CCATTGAT CAAAAAAAGGT CCATTGAT CAAAAAAAGGT CCATTGAT CAAAAAAAGGT CCATTGAT CAAAAAAAGGT CAATGTAGAGG CCATTGAT CAATGTAGAC CCATTGAT CAATGTAGAC CCATTGAT CAATGAGAC CCATTGAT	21 CCCAGGGGG GCTGAGCGG ACGCCCGGG ACGCCCGGG ACGCAGCCC ACGAGACC ACTCAGATGC ACTCAGATGC GGCAAGACAC GGCAAGACAC GGCAAGACAC TGGACATTT CAGACATTT CAGACATTC CAGTATTTGA TCTCCAATT CTCACATT TCAGTATTGA AAATTGTCC CAGAATATT ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA ATACAGGCCA CAGGATTATA ATACAGGCCA AGACCATTC CAGCACTTC CAGCATTCT CAGCACTTC CAGCATTCT ATACAGCCATTC AGCACCATTC	I TGCTATCGGA GCCCAGGGCC AGCTCCCCGG AACCCTGGAA TGCTATAAAGA TGCACAGGCA CGGGCACACG CTACATATGAA AGACAGACCACAGACCACAG CTACATATGAA AGACAGACCACGGTT ACACAGACCACGCTCACATGAACAGACCACGGCTCACAATGAACAACCACCCTCGCACAGGCCACGGCTTACAATGAA AGACACTCTGCACAATGAA CAGACCTCTG CTACAATGGA GGTTTCCTTCG AGACCTGT TGAACCTGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGATTATT TGACACCTAT TGACACCTAT CCGTTGGAGT ATATCATGGA TGGGTCGAT TGAAGCTCAC TGGAGTTAT TGAAGCTCAC TGGAGTTAAC TGAGTTCAACACGA GGAGTTAAC TGAACCCAA GGAGTTAAC TGGAGTTAAC TGGAGTTAAC TGGACCAAA GGAGCCAAA GGAGCCAAA	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACGGTCTATT AGTGCCCTCT GGTATTCTCA GGTGGCTTG GTTCATGTCC GGTGGCATGG TTCATGTCC GCTGAGACCA ACATCCTTCTG GCGATGACCA TTCTCAAGTCT TCAATGTTT CATGAGACCA TTCTAATGTT CATGAGACCA TTCTAATGTT CATGATAAAG CCAGGAAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA CAGTCATGAC CAGTCATCATGAC CAGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1260 1260 1380 1440
50556065	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGCTGACCAT TCTGGATGCC ACCATCTGCA CCATCCACAT TGCGACCCCACAT TGCGACCCCACAT ATGGACAGAG TCGACTCCACAT ATGGACAGAG TCGACTCCACAT AAGAGAGGAG TCGACTCCACAT AAGAGAAGGAAG TGAAAGGAAG TGTACTGCAGC TATCTCAGAC TATCTCAGAC	11 TCAAGCAGAG AGCCAGCGG CCGCTTGCCC CCGCTGCCCC CACTGCCAGG CACTGCCAG CACTGCCAG CTACAGAGG TATCAGAGGG GCACATCCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAGGT TCATGATTC TCATCATCT TCATCATCT TCATCATCT TCATCATCT TCATCTGT TAAAGGTGGGT TCAATCTGATC TCAATCATCT TCAATCATCT TCAATCATCT TCAATCATCT TCAATCATCT TCAATCATCT TCAATCTGGT TCAAAAGGTGGG TCCCATTGAT CAAAAAAAGGC CCGTGTACGG CAATCTCAGAC TACCCTGGTC TCCCTGCAGA	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGACAT TGACATT AAGTACATTT AAGTACATT CAGTATTTGA AATTTTGA AATTTTGA AATTTTTCC CAAGAGGGGT GTCACCTTG TCAGTGGAAT TCTCAGTGGAAT ATTACAGGCCA CAGGATTATA TTCCTCTGTG AGCACCATTC ATTGCCAGTGA ATTGCCAGTGA ATTGCCAGTGA ATTCCTCTGTG ATTGCCAGTGA	I TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGGCA GCTTCCCTGG AACCCTGGAA TGCATCACAC TCATTAAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAAGAC CTGACCAGTT ACGCGTTGCACAC TGATTAGACA ACCATATTGA AGACCAGGT CACATATTGA AGACCAGGT CTACAATGGA CAGACCTCTG CTACATTGCA CTGAATTGACTCCCAACCAGGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CCCTGGCAT CCCTGGCAT ACGACGAG GCATGCTGGG GCATGCTGGG GCATGCTGGA TGGAGTTATT TGACACCTAT CGATGCAGAG CCCTTGGAGT ATATCATGGA TGGGATTAT GTGGTTCGAT GAAGCTCAC CTACGACCGG GAGGCCCAAA GGATAATGTA CATGTACCAG CAAAGTGCAC	CGAGGGCAAG TTCCCAGACT CAGCGACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAGACACC CGATTGTTT AGTGCCCTCT GGTATTCAGC GTTGAGTTCA GGTACTCAGA ATCCTTCAG GCGATGACCA TTCCTAACTG CATGAGTCA ACATCAAGA ATCCTTCAG CCAGGAAAAA ATCCTTCAG CCAGGAAAAA CTCAGGACCT TTCAATGTT TCAATGTT CATGATAAAG CCAGGAAAAA CTCAGCACCG GGCAGACCCT CTCACAGTCA CAGTCATGGA GCAGAAGAGT GCAGAAGAGT	120 180 240 300 360 420 540 660 720 780 960 900 900 91020 1080 1140 1260 1380 1440 1500 1560 1660
5055606570	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGACGGAGCA TGCTGACCAT TGCGAACCAT TGCGAACCAT TGCGAACCAC CCATCTCACAT TGCGAACCAC ATGCAACCAC ATGCAACACAC ATGCAACACAC ATGCAACACAC ATGCAACACAC AAGAGAGGA TTGCAGTGAA AATTGGAAAG TGAAAGGAAA AATTGGAAGA TTGCAGTGAC TATTCAACAC TATTCAACAC TATTCAACAC TATTCAACAC TATTCAACAC AACTTGAACAC AACCTGAGAC TCAGGTGCT TGTACCTGCA	11 TCAAGCAGAG AGCCAGCGG CCGCTGCGCT CACTGCCAGG CACTGCCAG CACTGCCAG CACACCAGG CTCAGAGGC TATCGGCAG CTCAGAGGCAATCCT CAAACACTCTC TCAACACACT TCAATGATCTC TCAATGAGCAC ACGTCTGGTC TCAATGAGGT TCAACACTTC TCCATCATCT TCAATCATCT TCAATCATCT CCAGGTATTC TCAATCATCT CAACACTTC TCCATTGAT CAAAAAAGGT CCCTTTTAGT CAAAAAAGGT CCCTTGTTC CCGTGTACGG CAATGTGAAC TACCCTTGGTC TCCCTGCAGA CCTCCTGCAGA CCTCCGGGGAG CCATCGGGGAG CCACCTGGTC TCCCTGCAGA CCTCCGGGGAG CCACTGGGGAG CCCTCCTGCAGA CCTCCGGGGAG CCCCTCCAGAGA CCATCGGGGAG CCACTGGGGAG CCCCTCCAGAA CCTCCGGGGAG CCCCTCCAGAA CCTCCGGGGAG CCCCTCCAGAGA CCATCGGGGAG CCCCTCCAGGAG CCCCTCCAGAG CCCCTCCAGAG CCCCTCCAGAG CCCCTCCAGAG CCCCTCCAGAG CCCCTCCAGAG CCCCTCCAGGAG CCCCTCCAGGAG CCCCTCCAGAG CCCCCTCCCAGAA CCCCTCCAGAG CCCCTCCCCCCAGAC CCCCTCCCAGAC CCCCCCCCCAGAC CCCCCCCCCC	21 CCCAGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG ATGGGACTG ACTCTGACTT CCTGAGTTGC GGCAAGACAC GGCAAGACAC GGCAAGACAC GGCAAGACATTC GAAAGAGT TCGAAATTC CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTATTTGAACTT CAGTACTTGAACTT CAGTACTTGAACTT ATACAGGCCA GAGAAAATTT ATACAGGCCA CAGGACTGGA ACCCATTCATTGCCAGTA ATTCCTCTGTG AGCACCATTC ATTGCCAGTA ATCCTGCGCCC GAGATAGACG GAGATAGACCG GAGATAGACCC GAGATAGACCG GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACC GAGATAGACCC GAGATAGACCC GAGATAGACCC GAGATAGACC	I TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCATGAC CTGCGAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGAAG TGAACAAGAC CGGGCCACCG CTGACCAGT AACAGAGCA AGCAGGAGACCTCTG CTACAATGAA GGTTTGCTAG GGTTTGCTAG AGCAGGAC AGTTAGTAGACA TGATTAGACA AGTTAGACAGCCTCTG CTACAATGGA GGTTTGCTTG TGAACTTGGA CGGAACCCTGT CGAACCAGGT CCAACCAGGT GCAACCAGGT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGCC CCACGACGAG GCATGCTGATGA AGGAGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCAGAG GCCAGGAGA TGGCGAATAT GTGGTCGAT GAAAGCTCAC TGGAGTTAAC GAGGCCCAAA GGATAATGTA CATGTACCAC GAGGCCCAAA GGATAATGTA CATGTACCAC GAGGCCCAAA GGATAATGTA CATGTACCAC GGAGGCCGAAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG GCAGGCGGAGAG	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCATC CGTTATTCAGGCATG GTTCATGTG GTTCATGTG GTGCATGG TTCATGTAG ATCCTTCAGGACA ATCCTTCTG GGGATGACCA ATCCTTCTG GGGATGACCA TTCTAATGTT CATGATGTT CATGATAAAG CCAGGAAAAA CTCAGCACCG GGCAGACCT CTCACAGTCA CAGTCATGA GCAGAAGAGT CTCACAGTCA CAGTCATGA GCAGAACCA GTTGGGCTTC	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1200 1320 1380 1440 1500 1560 1680 1740
50556065	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCGGGG AGAGGGAGCA TGCTGACCAT TCTGGGTGCC ACCATGTGCA CCATCTCACAT TGCGAACCCG AGAGCGAACCACAT ATGGCACCCAA AATGACAGA AAGAAGGAG TCGACCCCAA AAGAAGGAAG TTGCACTCAGAC CTTTTCCAG CTTTTCCAG TATCTCAGAC TATCTCAGAC AGGTTGTCTA CCACTGGAGCTA CCACTGGAGA TCCAGGTGCT TGTACCTGGAG TGTACCTGGAG TGTACCTGAGA TCCAGGTGCT TGTACCTGGAGA TCAGCCGGAACT TGTACCTGGAGA TCAGCCGGAAC TGTACCTGGAGA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CACTGCCAG CTGCAGAGC TATCGGCCAG CTCAGAGGGA GCACATCCTG GGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC TCCAGTATTC TGAGTGGGTT TAAAGGTGGGT TCCAGTTACAG CCCTGTTACAG CATGTTACAG CATGTCAGAC CATCTCGCAGAA CATCGCGGAG CATCATAGTG CATCAGGAG CATCATAGTG	21 CCCAGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG ACGCCCGGG ACGCCCGGG ATGGGAGCTG ACTCTGACCT CCTGAGTGC GGCAAGCAC ACCATCATTT AAGTACATTG TGACATTT CAGTATTTC ACTACTTT CAGTATTTC CTGACCTTG TCACCTTG TCAGTGAAT TCTCGAAAT TCCTGAAAT TTCCTTCTGTG AGCACTTG AGCACTTG AGCACTTC ATTGCCAGTA TCCTGCGCCC GGGATAGAC ATGGGGGGAGA ATTGCCAGTGA ATGCCCCC GGGATAGAC ATGGGGGGAGA	TGCTATCGGA GCCTGGGGC GAGGCGTGAC CTGGGAGGCA GCTTCCCTGG ACCCTGGAA TGCTGCTCAC TGATATAAGA GAGGAGAGCT TGTATGGAAG GGGTTGGTAA TGAACAGGAC GTGACAGTT ACGCGGTT ACGCGGTT ACGCGGTT ACGCAGTC GGATGACAG AGTGGACACT CTACAATGGA GGTTGCTTG CTACAATGGA GGTTTGCTTG GGAACCTCTG CTACAATGGA CGTTTGCTTG CTACAATGGA CGTTTGCTTG CTACAATGGA CGTTTGCTTG CCAACCAGGT TGAATCACA CCTGATTACTC CCAACCAGGT TGACCTGGACACT TGACCTGGACACT TGACTGGACACA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGGC CCACGACGAG GCATGCTGGG GGATTATT TGACACCTAT TGACACCTAT TGATGCAGGG GCCAGAAG TGGTTCGAC TGGATTATT TATATCATTGAA TGGCGAATAT TGAACCTAT CGATGGATTCGAC TGGATTCGAC TGGATTCGAC TGAACTTCGAC TGGATTCGAC TGAACTTCAC TGAACTTCAC CAAACTCCAC CAAACTCCCC	CGAGGGGAAG TTCCCAGACT CAGCGACCA CTACAGACCC ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC ACAGTCTTT AGTGCCTCT GGTATTCAGC CTTCAGTTCAG	120 180 240 300 360 420 540 660 720 780 960 900 900 91020 1080 1140 1260 1380 1440 1500 1560 1660
5055606570	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGACGGAGCA TGCTGACCAT CTGGATGCC CCATCCACAT TGCGAACCCG CCATCTACACT TGCGAACCCG ATGCACACAT TGCAACACG ATGCACACAT ATGCACGAA AAGACAGGAA AAGACAGGAA AATTGCAATCA AACTTGAACAC TGACCGAACTAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACACCTGAAA ACATCTGCAAA ACATCTGCAAA ACATCTGCAAAACACACACACACACACACACACACACACA	TCAAGCAGAG AGCCAGCGG CGCTGCGC CACTGCCAGG CACTGCCAGG CACTGCCAGG CACTGCCAGG CTACAGAGC CTACAGAGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGAATTTC CTATGGTCTG AAAGCTCTCC CCATTATTTTT TCAAGCACAC TCATCATCT TCATCATCT TCAATCATCT CCATCATCT TCAATCATCT TCAATCATCATCT TCCTTTTACGAGAC CATCATTGATC TTCTTTTGAC ACACTTTGACA	21 CCCAGGGGG GCTGAGCGG GCTGAGCGG ACGCCCGGG ATGGGAGCTG ACTCTGAGTTG CGGAAGACAC GGCAAGCTG ACTATTTAAAGTACATT AAGTACATTT CAGTATTTG GTACATTTCAATT CAGTATTTGACATT TCAGAATT CAGTATTTGA AATTCTCAATT ATACAGGCG GAGAAAATT ATACAGGCTG GAGAAATT TCCTGTAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCCAGT ATTGCGGGCG ATGGGGGAGA ATTCGCAGCG ATGGGGGAGAG ATTCGATACC GGGACGAGGCG GCCCCGGGGAGGCGCG ATTCGATACC GGCACCAGGCG GGGACGAGGC GGGACGAGGCG GGCACCAGGC GGCACCAGAGC GGCACCAGAGC GCCCAGGCC GGCACCAGCC GCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCAGCC ACCCCACC ACCCCCACC ACCCCACC ACCCCA	I TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCGTGAC CTGGGAGGCA TGCTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGGT TGTATGAAG TGAACAAGAC CGGGCCACCG CTGACCGGTT ACCCGGTT ACCCGGTT ACCCGGTT ACCCGGTCACATGAA AGTCGACGAC CTGACCTGG CTACATTGA AGTTTGACA CTGACATTGA AGTTTGACA TGAAACCTCTG CTACATTGA GGTTTGCTTG CGAACCCTCTG CTACACTGGA CTGACCTGGA CTGACCTGGA CTGACCTGGA TGGACCACTGGA TGGACCACTGGA TGGAGCACA TGGAGCACAA TTGGAGCACAA TTGGAGCACAA TTGGAGCCACATT	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CCCTTGCCC CCACGACGAG GCATGCTGAGA AGGAGCGCT CCTTCACCCA TGGAGTTATT TGACACCTAT CGATGCAGAG GCCAGGAGAG GCCAGGAGAG TGGCAGATAT GTGGTTCGAT GAAAGCTCAC TGGAGTTAAC CTACGACCGA GGATAATGTACCAC GAGGCCCAAA GGATAATGTA CATGTACCAC GAGGCCCAAA GGATAATGTA CATGTACAC CACAGAGGA ATGCTACCC CATCAAGTTT GGGACACCAC	CGAGGGGAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC CTACAGGCCA ACAGTGGCTT CGGATTGTTT AGTGCCTCT GGTATTCATGTC GGTGGCATGG GTTCATGTCA ATCCTTTCTG GGGATGACCA ATCCTTCAGTTC CATCGAGCCT TCCAATGTT CATGATAAG CCAGGAAAAA CTCAGCACG GCAGACCCT CTCACAGTCA CAGTCATGGA GCAGAACCA GGTAGACCA GTTCGTCAGCCC CAGTCATGGA GCAGAACCA GTTCGGGATAACCA CTCACAGTCA CAGTCATGGA GCAGAACCA GTTCGGGAT CTCACAGTCA CGGCAAACCA CTTCGGGAT CTCCCAGGTCA CGCTCTCGCGAT CTCCCAGTCA CGCTCTCGGAT CTTCCGGAT CTTCCGGAT CTTCTGGGAT CTTCTGGGAT CTTCTGGGAT CTTCTGGGAT CTTGGGCTC	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1260 1320 1340 1500 1560 1620 1620 1680 1740 1860 1920
5055606570	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCAT TCTGGGTGCC ACCATGTGCA CCATCTCCA CGGATCCTTA ATGGACAGA ATGGACAGA ATGGACAGA ATGGACAGA ATTGCGAACGC CTTTCCA CGGATCCTA ATTGCAGAC TGACCCCAA AAGGAGGA ATTGCAGAC CTTTGTCCAG CTTTGTCCAG CTTTGTCCAG TATCTCAGAC AACCTGGAGCTA CCACTGGAG TCCAGGTGCT TGTACCTGCA ACATCGCAA ACATCGCAA ACATCGCAA ACATCGCAA ACATCGCAA ACATCGCAA ACATCGCAA CTAAGGCAGAA ACATCGCAA ACATCCCCAA ACATCCCCAA ACATCACCAA ACATCACAA ACATCACCAA ACATCACCAA ACATCACCAA ACATCACCAA ACATCACCAA ACATCACAA ACATCACCAA ACATCACCAA ACATCACAA ACATCACCAA ACATCACCAA ACATCACAA ACATCA	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAG CACTGCCAG CACTGCCAG CTCAGAGGGA TATCGGCCAG GCAATTCC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC TCCATCATCT TGAGTGGGTT TAAAGGTGGGT TAAAGGTGGGT TCCATTGAT CCAGTACATC CCGGGTATCC TCCATCATCT TCAGTCGGTC TCATCATCT TCAGTCGGTC TCAGTGAAGGT TCCCTGCAGA CATCCTGCAGG CATCCTGCAGG CATCGGGGAG CATCATAGTG CATCATCTGAT TTCCTTGAGA CATCAGTGGAAC TTCCTTGAGAG TTCCTTTGAC ACACTTTGAC ACACTTTGAC TCCCTGCAGAG TCACTTTGAC TCCCTGCAGAG TTCCTTTTGAC TCCCTGCAGAG TCACTTTGAC TCCCTGCAGAG TCACTTTGAC TCCCTGCAGAG TCACTTTCAC	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACCT CCTGAGTGC GGCAAGCAC ACGCAAGCAC ACGCAAGCAC ACGATATT AAGTACATTG GAAAGAGGCT GTCATCCATT CAGTATTGA TCTCGAATTC CAGGAGATT TCAGTGGAG AAATTGTTCC CAGGAAAATT TTCCTCTGTG ATTGCCAGT ATTCCTGTGGCCC ATTGCGCCC ATTGGGGGAGA TTCGTGGGCGGG ATTGGATACC CGGAATACC CGGAATACC CGGAATACC CGGAATACC CTGGCCCGTG CCCGCGCGCGGGACC CTGGCCCGTG	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TGTATGAAGA GAGGAGAGCT TGTATGAAGA CGGGCCACCGGT ACCCGGTT ACGCGGTT ACGCGGTCACCGGTT ACGCGGTCCCGGTT ACGCGGTCCCGGTT ACACAGACCTCTG CTACATGAA GGTTGCACGGT CTACATGAA CGAGCCTCTG CTACATGGA CGGCCTCTG CTACACCGGT TGAACCTGGA CTGATCCTTG GGAGCCTGT TGAACCTGGA CTGATCCTGGA CTGATCCTGGA CTGATCCTGGA CTGATTACTC CCAACCAGGT TGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA TTGGAGGACAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGGC CCACGACGAG GCATGCTGGG GGATGCTGGG GGCTGATGAA AGGAGGGCTATATT TGACACCTAT CGATTGACAGA GCCAGGAGAG TGGCCAGAAG TGGAGTTAAT TGAAGCTCAG TGGAGTTCAT TGAAGCTCAG TGGAGTTCAT CATCATCAGG GCCGCAAA GGATAATGTA CATGTACCAG CAAAGTTGCAG ATGCTACCAG ATGCTACCCC CATCAAGTTTT GGGACAGCAG AAGGGGAGGGT AAGGGAGGG	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGTTT AGTGCCTCT GGTATTCAGC CTTGAGTTCAG GGTGGCATGG GTTCATGTCA AGATCCAAGA ATCCTTTCTG GCGATGACCA TTCTAATGTTC CATGGAGGCT TTCAATGTTT CATGATAAAG CTCAGGACCA CCAGGAAAAA CTCAGCACCG GGCAGAGCCT CTCACAGTCA CAGTCATGGA GCAGAAGACCA GCTGGCATCA CTCACAGTCA CTCACAGTCA CTCACAGTCA CGCTCAGGAAAC CTCAGGAAAC CTCACAGTCA CGCTCAGGAACCT CTCACAGTCA CGTGGGCTT CTCAGGAACCT CTCACAGTCA CGTGGGAAACC GCTCTGGGAT CTGGGGACCT TACAGAAACC GCTCTGGGAT CTGGTGGGTC TTAGGTGGGTC TTAGGTGGGTC	120 180 240 300 360 420 600 660 720 780 900 900 910 1020 1140 1200 1260 1320 1440 1500 1560 1740 1800 1740 1800 1900
505560657075	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGAGGGAGCA TGCTGACCAT TCTGGTGCC ACCATCTGCA CCATCCACAT TGCGACCCC ACGATCCTA ATGGACAGA ACGAAGGAGG TCGACCCCA AAGAGAGGGG TCGACCCCA AAGAGAAGGAAG AATTGCAGAC TATCTCAGAC TATCTCAGC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCAGACAC TCAGCTGCC TGTACCTGCAC TGTACCTGCAC TGTACCTGCAC TGACCCGGAA TCAGCGGAA TCAGCGGAA TCAGCGGAA TTAAGGCAGC AGTACCCGAA TTAAGGCAGC AGTACCCGAA ACCTCACAAC TTAAGGCAGC AGTACCCACATCCACAT TCACATACCAT	11 TCAAGCAGAG AGCCAGCGGG CCGCTTGCCC CACTGCCAG CACTGCCAG CACCAGCAGGCTGCCT TATCGGCCAG CTCAGAGGG CTCAGAGGGA CTCAGAGGC ACATCCTG GAGCAATTTC ATCAGGCACA ACATCTGGT TGATCAGGGA CCTCTGGT TCAGAGGT TCAGAGGT TCAGAGGT TCAGAGGT TCAGAGGT TCAGAGGT TCAATCAGT TCAATCAGGT TCAATCAGGT TCAATCAGGT TCAATCAGGT TCACTTGGT TCAATCAGGT TCACTTGGT TCAATCAGGT TCACTTGGT TCACTGGT TCACTGGT TCACTGGT TCCCTGCAGA CATCGGGAG CATCATAGTG TTTCTTTGAC ACACTTTCGAG TCACTTTCCAC CAGGGACCTC CAGGGACCTC CCGGGGACCTC CCAGGGACCTC CCAGGGACCTC CCAGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCACGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCACGGGGACCTC CCAGGGGACCTC CCACGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCACGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCACGGGACCTC CCACGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCAGGGGACCTC CCACGGGACCTC CCACGGGACCTC CCACGGCACCTC CCACGGGACCTC CCACGGCACCTC CCACGCACCTC CCACGGCACCTC CCACGCACCTC CCACCTC CCACCT	21 CCCAGGGGG GCTGAGGGG GCTGAGGGG GCTGAGGGG ACGCCCGGG ACGCCCGGG ATGGGAGCTG ACTCTGACTT CCTGAGTTGC GCAAGACAC GCAAGACAC GCAAGACAC GTGACATT AAGTACATTG CAGTATTGAAACG GTCATCATT CAGTATTGAAATC CTGCACCTTG CAAGAATC CTGCACCTTG AAGACGTGG GAGAAAATT ATACAGGCA AATTGTCCTGTGG AGGACATTAT TCCTCTGTG AGGACATTAT TCCTCTGTG AGGACATTAT TCCTGCGCCG GAGATACAC ATTGCCAGTA TCCTGCGCCG GGGACGAGGC CTGGCCGGTGC CTGGCCGGTGC CTGGCCGGTGC TCCATCCATC	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGCATGGCA GCTTCCCTGG AACCCTGGAA TGCATCACA TCATTAAAGA GAGGAGAGCT TGTATGGAA GGGTTGGTAA TGAACAAGAC CTGACCAGTT ACGCGTTGCACA ACCATATTAGA AGACAGACA ACCATATTAGA AGACCAGT GATTACTC CTACAATGGA GGGTTGCTGT GGAAGCCTCTG CTACAATGGA CGGACCTCTG CTACAATGGA GGTTTGCTTG GGAAGCCTCTT TGAACTTGGA CTGATTACTC CCAACCAGGT TGAACTAGCA TTGAGCACAG TTGAGCACA TTGAG	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGCCACATCC CCCTGGCAT CCCCTGGCAT CCACGACGAG GCATGCTGGG GGATTGTGGG GGCTATGAG AGGAGGCGCT CCTTCACCCA TGGACTATT TGACACCTAT CGATGCAGAG GCATGATGAG TGGAGTTATT TGACACCTAT GGATGATGAG TGGAGTTCAG GAAGCTCAC CTACCACCGG GAGGCCAAA GGATAATGTA CAAGTGGCA CAAGTGCCA CACAGCGGCGCAG ATGCTACCCAC CACAAGTTTT GGGGCAAGCT CATCAAGTTTT GGGGCAAGCT CATCAAGTTTT GGGGACACCAG AAGGGGAGGG AAGGGGAGGT TCGCTGCCTC	CGAGGGCAAG TTCCCAGACT CAGCACCAG CTACAGACCC TTCAAGGCCA ACAGTGGCTG GACCAGACCC TCGAGTTGTTT AGTGCCCTCT GGTATTCAGC GTTGAGTTCG GTTCATGCATGCATGCATGCATGCATGCATGCATGCATGC	120 180 240 300 360 420 600 660 720 780 900 900 910 1020 1140 1200 1260 1320 1440 1500 1560 1740 1800 1740 1800 1900
5055606570	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGGG AGAGGGAGCA TGCTGACCACT TGCGGTGCC ACCATGTGCA CCATCCACAT TGCGACCCGA ATGGACACG ATGGACACG ATGGACAGA ATGGACAGA ATGGACAGA ATGGACAGA ATGGACAGA ATTGGAAGA ATTGCAGAGA ATTGCAGTGCA TATCTCAGAC TATCTCAGAC TATCTCAGC TATCTCAGC TATCTCAGC TATCTCAGC TATCTCAGC TATCTCAGC ACCTTGCACT TGTACCTGCA TGTACCTGCA TGTACCTGCA TGTACCTGCA TGTACCTGCA TGTACCTGCA TGTACCTGCA ACATCTGCACC AGTACCCGATACCACC AGTACCCGATACCAT CCACATACAT CCACGGATACAT CCACGCATACAT CCACGGATACAT CCACGCATACAT CCACGGATACAT CCACGATACAT CCACGGATACAT CCACGATACAT CCACGATACAT CCACGATACAT CCACGATACAT CCACGATACAT CCACGATACAT CCACGATACAT CCACTACT CCACTACT	TCARGCAGAG AGCCAGCGGG CCGCTTGCCC CCGCTGCGCT CACTGCCAGG CAGCTGGCT CACTGCCAG CTGACAGGGCA CTCAGAGGGA GCACATCCTG GGCAATTTC CTATGGTCTG AAAGCTCTCC CTATTTTTT ATCAGGCACA ACGTCTGGTC TGATGAAGGT CAAACACTTC TCCATCATCT CCGGGTATTC TGAGTGGGT TAAAGGTGGGT TAAAGGTGGGT TCCATCATGT CCAGTGTATC CAAAAAAGGC CCGTGTACGG CAATGTGAG CAATGTGAG CATCATGT TCCTTGCAGA ACACTTTGCAG ACACTTTGAC CACACTTGAC CATCTTGAC CACACTTGAC CATCTTGAC CACACTTGAC CACTTGAC CACACTTGAC CACACTTGAC CACACTTCACAC CAGGGACCTC CAGGGACCTC CTGGTGATAC TTGTTTTGAC TTGTGCCGGGAG	21 CCCAGGGGGG GCTGAGGGGG GCTGAGGGGG GCTGAGGGGG ACGCCCGGG ATGGGAGCTG ACTCTGACCT CCTGAGTGC GGCAAGCAC ACCATCATTT AAGTACATTG GAAAGAGAC TCGACATTT CAGTATTTGA TCTCGAAATC CTGACCTTG TCAGCGGGAAAATT TCCTCTGTG AGGACATTC ATTGCACATT ATTCCTCTGTG AGGACATTC ATTGCAGGGAGA TTCCTGCGCC CGGAGAAACT CGGACAGAC ATGGGGGAGA CTGGCCGTG CCTGGCCGTG CCTGGCCGTG CCTGGCCGTG CCTGGCCGTG CCTGGCCGTG CCTGCCCTC AAGGACGTAC AGGACGTTG AAGGACGTTG CAAGACGTTG CAAGACGTTG AAGGACGTTG AAGGACGTAACCT AAGGACGTACCA	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC GAGGCAGGCA GCTTCCCTGG AACCCTGGAA TGCTGCTCAC TGCAGAGAGCT TGTATGAAGA GGGAGAGCT TGTATGAAGA CGGGCCACCGGT ACCCGGTT ACGCGGTGACACCGGT ACCCGGTT ACGCGGTCCCTGGATGACAT GATTAGACA AGTCGACGGT TGAACAGGCA ACTGGATGACAT TGAGAGCCTCTG CTACAATGGA GGTTTCGTTG CGAACACGGT TGAACCTGGA CTGATTACTC CCAACCAGGT TGAGCCTGT TGAACTTGGA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGGGGGCCAA TTGAGCATATCTC TGGGGCTATAAA CTTTTGACCAA	CAGAGCCTGG GAACCCAGAT GCCTGGCGGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CTCTTCTGCC CCACGACGAG GCATGCTGGG GGATTATT TGACACCTAT CGATTGACCAG GGCCAGAAG TGGCAGATAT TGAACCTTAT CGATGGCAGAT TGAACCTAT CGATGATTAT CATGTCACCAG GGCCAGAAG GGAGTTAAC TGAACTGTAC TGAACTGTAC CAACTGGC CAACAGTGCC ATGTACCAG CAACTGGC AAGTGCCAG ATGCTACCAG CAACTGGC AAGTGCCAG ATGCTACCAC CCCTCTTCACCCC CTCTTCACCCC CATCAACTTTC CATCACCCC CATCAACTTT CGGACCAG AAGGGCCAAA CCCCCCTCTTCACCC CCCCTCTTCACCCC CCTCTTTCGCC CTCTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTGGCC CTCTTTTTGGCC CTCTTTTTGGCC CTCTTTTGGCC CTCTTTTTGCC CTCTTTTGGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTGCC CTCTTTTTTGCC CTCTTTTTTGCC CTCTTTTTTTT	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC ACAGTGTTT AGTGCCCTCT GGTATTCATGC GTTGATTGC GTTGATTGC GTTGATTGC GTTGATTCA AGATCCAAGA ATTCTTCTG GCGATGACCA TTTCTAATGTT CATGATACTG CATCGAGGCT TCAATGTTT CATGATACTG CCAGGAAAAA CTCAGCACCG GCGAGAGCCT CTCACAGTCA CAGTCATGGA GTTGGCTTC CTCACAGTCA CAGTCATGGA CTTCTGGGAT CTCACAGTCA CAGTCATGGA CTTGCGGAT CTGGGAT CTGGGGTC TTCAGGACCC CACAGTCCAC CACTCTGGGAT CTGGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGTGGGTC CTGGGGTC CTGGGGTC CTGGGGTC CTGTGCTCTC	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1140 1260 1140 1560 1560 1740 1800 1980 1980 2040 2160
505560657075	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT TACGTCCGGG AGAGGGAGCA TGCTGACCACT TGCGGTGCCC ACCATGTGCA CCATCCACAT TGCGACCCG AGAGGGACCA AGGGTACCTA ATGGACAGA ATGGACAGA ATGGACGGA ATGGACGGA ATGCAGTGA ATTGCAGTGA ATTGCAGTGA ATTGCAGTGA TTGCAGTGC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTCAGAC TATCTGCAGAC TATCTCAGAC TATCT	TCAAGCAGAG AGCCAGCGGG CGCTTGCCC CACTGCCAG CACTGCCAG CACTGCCAG CACTGCCAG CACCAGCAG CTCAGAGGC TATCGGCCAG GCAATTCC CTATGGTCTG AAAGCTCTGC CTATTTTTT ATCAGGCACA ACGTCTGTC TGATGAAGGT CAAACACTTC TGATGAGGT TCCATCATCT TAAAGGTGGGT TCAATCATCT TCAATCATCT TGATGAGGT CCATTAGAG CACTTGGTC TCCATCAGT TCAATCAGT CAAACACTTC TGATGAGGT CAATCTGAGC CATTGATGAG CATCTGAGAG CATCTTGAGC CATTGAGAG CATCTTGAGC CATTGAGAG TTCCTTGAGAG TTCCTTGAGAG CATCATTGAG CATCTTGAGAG CATCATTGAGC CTTGTTTGAG CAGGGACCTC CTGGTGGAGA CTCACTTCCAC CAGGGACCTC CTGGCGGAG CTCCCTCCCCC CTGCCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCC CCTGCCCCCCCC	21 CCCAGGGGG GCTGAGGGGG GCTGAGGGGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCAGCTG ACTCTGACTT CCTGAGTTGC GCAAGACAC ACCATCATTT AAGTACATTG TGACATTC CAAGTACTTG ACTACTTC CAAGTACTTG CTGCACCTTG CAAGACGTGG GAAGAAATTT ATACAGGCA ACGGATTATA TCCTCTGTG AGGACTTG AGGACTTC ATTGCCAGTA TCCTGCGCCC CAAGACGAGC TCCATCCATC CAGGACCATC CTGCCCGTC CTCCATCCATC CGGACCGTC CTCCATCCATC CGGACCCTC CTCCATCCATC CGGACCCTC CTCCATCCATC CTCGCCCCTC CTCCATCCATC CTCGCCCCTC CTCCATCCATC CTCCATCCATC CTCCATCCA	TGCTATCGGA GCCAGGGTCT AGCTCGCGC GAGGCATGGCA GCTTCCCTGG AACCCTGGAA TGCTACCACA TCATTAAAGA GAGGAGAGCT TGTATGGAG GGGTTGGTAA TGAACAAGAC TGATCACACACACACACACACACACACACACACACACACA	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCCAT CTCTTCTGGC CCACGACGAG GCATGCTGGG GGATTATT TGACACTAT TGACACTAT TGATGCAGG GCCAGAAG TGGTTCGAC TGGATTATT TATATCATGA TGGATTCGAT TGACACTAT CGATGGATTCGAT TGAACTTCGAGT TGAACTTCGAGT TGAACTTCGA TGGATTCGAT TGAACTTCGAGT TGAACTTCGAGT TGAACTTCGA TGGATTCAC CAAAGTCCCC CATCAAGTTT GGGACAGCAG AAGGGAGGG AAGGGAGGG TCGCTTTGGGC CTTTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTGGCC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGCC CTGTCTTTGCC CTGTCTTTGGCC CTGTCTTTGGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTGCC CTGTCTTTCTC CTCTTTCTCT CTCTTTCTCT CTCTTTTTCT CTCTTTCTCT CTCTTTCTCT CTCTTCT	CGAGGGCAAG TTCCCAGACT CAGCGACCA TCAAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC ACAGTTGTTT AGTGCCTCT GGTATTCAGC CTTCAGGCATGGCTTG GTTCATGTGA AGATCCAAGA ATCCATGTTT CATGAGGCC TTCAAGTCA TTCTAACGTC TTCAACGTC TTCAACGTC TCACAGTC TCACAGTC CTCACAGTC CTCACAGTC TTCACAGTC TTCTCTGTGGGT TTCATGTGGGT TTCATGTGGGT TTTTTATGACCAC ACAGTCCATG CACTGCTTCT TATGACCAC TTCTCTGTGAGG CTCTCTGTCA TTCACAGAGG TTCTCTCTTCT TTCTCTCTTCT TCTCTTGTGAGG TCTCTCTGTCA TTCACAGAGG	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1260 1260 1320 1440 1560 1680 1740 1860 1980 2040 2160 2220
505560657075	1 GAGCTAGCGC CGGCGCGGG AGCTACCACT ACGTCCGGG AGACGGAGCA TGCTGACCACT CTGGATCCCACT TGCGAACCACT TGCGAACCACT TGCGAACCACACT TGCGAACCACACACACACACACACACACACACACACACAC	TCAAGCAGA AGCCAGGGG CGCTTGCCC CGCTGCGCT CACTGCCAGG CACTGCCAGGCT CACTGCCAGG CACTGCCAG CTACAGAGGA CTCAGAGGGA CTCAGAGGGA CTCAGAGGA CTCAGAGGA CTCAGAGGA ACGTCTGCT AAAGCTCTCC CTATTTTT ATCAGGCACA ACGTCTGGTC TGATGAGGT TCAACACTTC TCAATCATCT TCAATCATCT TAAAGGTGGG CAATCTGATC TCAATCATCT TCAATCAGG CACTTGATC CACTGCTGCAGA CATCTGGGGAG CATCTTGATC CCCCCCCCCC	21 CCCAGGGGG GCTGAGGGGG GCTGAGGGGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCCCGGG ACGCAGCTG ACTCTGACTT CCTGAGTTGC GCAAGACAC GCAAGCAC GCAAGCATG ACCATCATTT AAGTACATTG CAGTATTGAAATC CTGCACCTTG TCAGTAGTAGA AAATTGTCA ACGACTTGTG AGACCTTGG AGACCATCA ATTGCCAGTA TTCCTCTGTG AGCACCATC ATTGCCAGTA TCCTCTGGGGGGAG ATTGCAGTGG GGAAAATCT CAGGACTTGC CAGGACCATC ATTGCCAGT ATTGCCAGT TCCGCCCC GGAATAGACG CTGGCCGGTGG TCCATCCATC AAGGACGTTGG AGGACGAACC TCCGACCCGTTG CCCAAGCCCCT CCCAAGCCCCC TCCGACCCCT CCCAAGCCCCCT CCCAAGCCCCCT CCCAAGCCCCCT CCCAAGCCCCCCCCCC	TGCTATCGGA GCCAGGGTCT AGCTCGCGGC AGCTCGCGGC AGCTCGCGGC AGCTCCCTGG AACCCTGGAA TGCTGCTCAC TCATTAAAGA GAGGAGAGCT TGTATGAAG GGGTTGGTAA TGAACAAGAC CTGACAGGAGCAC ACGACACAGGT ACCAGGTGCC TGATTACAT ACACATATGA AGCATACTTG GGAACCCTCTG CTACAATGGA AGTCGACCGGT TGAACTTGCA CTGACCTGG CTGACCAGGT TGGAGCACA TGGAGCACA TGGAGCACA TGGAGCACA TTGGAGCACA TTGGAGCACA TTGACTATACT CCAACCAGGT TGAACTTGGA TTGACTTG TGAGCTATAC TTGAGCGACAA TTGGAGCACAA TTGGAGCACAA TTGGAGCACAA TTGACCAGCT TGAACTTCTC TGGAGCACAA TTGGAGCACAA TTGGAGCACAA TTGGAGCACAA TTGTAGACGA TTGAACTTCTC TGGGCTATAAA CTTTTTGACCA ACAGCAAGACT ACAGCAAGACT ACAGCAAGACT ACAGCAAGACT ACAGCAAGACT	CAGAGCCTGG GAACCCAGAT GCCTGGCGT ACTGTCTCGG GGACTTCCTC GGCCACATCC CCCTGGCAT CCCTTGCTCTCGC CCACGACGAG GCATTCTGGC GGCTATACA AGGAGGCGCT CCTTCACCCA TGGATTATT TGACACTAT CGATGATATT TGACACTAT GGATTATT GGGATTATT GTGGTTCGAG GGCTAGAGA GGATAATT GTGGTTCGAT GAAGCTCAC CTACACCGG GAGGCCCAAA GGATAATT CATGACCAG GAGTAATT CATGACCAG GAGGCCCAAA GGATAATT CATGACCAG GAGGCCCAAA GGATAATGT CATGACCAG CAACAGTT GGGACAGCAG AAGGGGAGGT TCGCTGCTC CTCTTTTGGGC CTCTTTTTGGGC CTGTCTTTGGG CAATGCTTC CAATGACCTG CTGCAAGAT CCATCAACTTT CCGCTGCTC CTCTTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGC CTACAAGTTT CAATGCTACCC CTCAACAGC CTGCAAGAT CAATGCTTGCAC CTCATCAACGC CTGTCTTTGGGC CTGTCTTTGGGC CTGTCTTTGGC CTACAAGTTT CAATGCTTGCAACAT CAATGCTTGCC CTACAAGTTT CAATGCTTGCC CTACAAGTTT CAATGCTTGCC CTACAAGTTT CAATGCTTGCC CTACAAGTTT CAATGCTTGCC CAATGCAAGTTC CAATGCTTGCC CAATGCAAGTT CAATGCTTGCC CAATGCAAGTT CAATGCTTGCC CAATGCTTGCC CAATGCAAGTT CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCAAGTT CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCTTGCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTTCCC CAATGCTACCC CAATGCTTCCC CAATGCTCCC CAATGCTTCCC CAATGCTCCC CAATGCTTCCC CAATCCAATC	CGAGGGCAAG TTCCCAGACT CAGCGACCA CTACAGGCCA ACAGTGGCTG GACCAAGACC ACAGTGGCTG GACCAAGACC ACAGTGTTT AGTGCCCTCT GGTATTCATGC GTTGATTGC GTTGATTGC GTTGATTGC GTTGATTCA AGATCCAAGA ATTCTTCTG GCGATGACCA TTTCTAATGTT CATGATACTG CATCGAGGCT TCAATGTTT CATGATACTG CCAGGAAAAA CTCAGCACCG GCGAGAGCCT CTCACAGTCA CAGTCATGGA GTTGGCTTC CTCACAGTCA CAGTCATGGA CTTCTGGGAT CTCACAGTCA CAGTCATGGA CTTGCGGAT CTGGGAT CTGGGGTC TTCAGGACCC CACAGTCCAC CACTCTGGGAT CTGGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGTGGGTC CTGGGAT CTGGTGGGTC CTGGGGTC CTGGGGTC CTGGGGTC CTGTGCTCTC	120 180 240 300 360 420 480 540 660 720 840 900 900 1020 1140 1260 1320 1440 1500 1560 1620 1620 1620 1620 1800 1900 1900 1900 1900 1900 1900 190

	GTTATTCAGA	GCACATTCCA	CTGGGAAAAT	TCTATAACAA	CCGAGCACAT	TCCAACTACC	2460
	GGGCTGGCAT	GATCATAGAC	AACGGAGTCA	AAACCACCGA	GGCCTCTGCC	AAGGACAAGC	2520
					CCAGGACGCC		2580
5	AGCCCCGGGA	GCCGGCCATC	ATCAGACACT	ACAGCTGCCG	CAAGAACCAG GTTTGCTGAC	AACCACGGGG	2640 2700
5	GCCTGACCCT	GGCCAGTGGT	GGAACCTTCC	CGTATGACGA	CGGCTCCAAG		2760
						GACAATAGGA	2820
	TCTGGGGCCC	TGGCGGCTTG	GACCATAGCG	GAAGGACCCT	CCCTATAGGC	CAGAATTTTC	2880
10	CAATTAGAGG	AATTCAGTTA	TATGATGGCC	CCATCAACAT	CCAAAACTGC	ACTTTCCGAA	2940
10	AGTTTGTGGC	CCTGGAGGGC	CGGCACACCA	GCGCCCTGGC	CTTCCGCCTG	AATAATGCCT	3000
					TGAGGACGTT GCTGGACATG		3060 3120
					GTACCCTGGC		3180
	CGAAGAATGA	CAACTGGCTG	GTCCGGCACC	CAGACTGCAT	CAATGTTCCC	GACTGGAGAG	3240
15	GGGCCATTTG	CAGTGGGTGC	TATGCACAGA	TGTACATTCA	AGCCTACAAG	ACCAGTAACC	3300
	TGCGAATGAA	GATCATCAAG	AATGACTTCC	CCAGCCACCC	TCTTTACCTG	GAGGGGGCGC	3360
					CACCCTGCAG		3420
	CCATCCACTG	GGACCAGACG	GCCCCCGCCG	AACTCGCCAT	CTGGCTCATC	AACTTCAACA	3480 3540
20	AGGGCGACTG	CANTOCCOTO	CTCAACCAAA	CCTCCAAGAC	CACCACATTC GGGCGTCTTC	GTGAGGACCT	3600
20					CCACTACTAC		3660
					GAGAGAGAAG		3720
	GCTCCATGAA	AGGCTGTGAG	AGGATAAAGA	TTAAAGCTCT	GATTCCAAAG	AACGCAGGCG	3780
0.5	TCAGTGACTG	CACAGCCACA	GCTTACCCCA	AGTTCACCGA	GAGGGCTGTC	GTAGACGTGC	3840
25					GGACCATTTC		3900
					CGACTTCGCT	ATTGACGGGA	3960 4020
	ACCAACGCCG	COTCOTOACC	CACACGAGG	TOUGGATOCA	CATTCTGCAA	GGCATACCAT	4080
	GGCAGCTTTT	CAACTATGTG	GCGACCATCC	CTGACAATTC	CATAGTGCTT	ATGGCATCAA	
30	AGGGAAGATA	CGTCTCCAGA	GGCCCATGGA	CCAGAGTGCT	GGAAAAGCTT	GGGGCAGACA	4200
	GGGGTCTCAA	GTTGAAAGAG	CAAATGGCAT	TCGTTGGCTT	CAAAGGCAGC	TTCCGGCCCA	4260
	TCTGGGTGAC	ACTGGACACT	GAGGATCACA	AAGCCAAAAT	CTTCCAAGTT	GTGCCCATCC	4320
	CTGTGGTGAA	GAAGAAGAAG	TTGTGAGGAC	AGCTGCCGCC	CGGTGCCACC	TCGTGGTAGA	4380
35	CTATGACGGT	GACTCTTGGC	AGCAGACCAG	TGGGGGATGG	CTGGGTCCCC CCAAGGGAAG	CAGCCCCTGC	4440 4500
55	ACCORGING	TGCCACCTGC	CCCTACTCAA	GTGTCTACCT	GGAGCCCCTG	GGGCGGTGCT	4560
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75		107 Protei					
, 5	1	cession #: /	NP_002731.1 21	31	41	51	
	1		1		 	EDNESS PART	
0.6						FDNEQLFTMK EDKSIYRRGA	60 120
80	RRWRKLYCAN	GHTFQAKRFN	RRAHCAICTD	RIWGLGRQGY	KCINCKTTAH	KKCHKLVTIE	180
						Resgkasssl Qtekhvfeqa	240 300
	SNHPFLVGLH	SCFQTESRLF	FVIEYVNGGD	LMFHMQRQRK	LPEEHARFYS	AEISLALNYL	360
85						IAPEILRGED RIPRSLSVKA	420 480
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			QTGFADIQGH IVRKIDQSEF			KPNISGEFGL	540
5	Nucleic Aci	108 DNA sec d Accession lence: 127	#: NM_0003	349.1			
	1	11	21	31	41	51	
	GGGACTCAGA	GGCGAAGCTT	GAGGGGCTCA	GGAAGGACGA	AGAACCACCC	TTGAGAGAAG	60
10	AGGCAGCAGC	AGCGGCGGCA	GCAGCAGCGG	CAGCGACCCC	ACCACTGCCA	CATTTGCCAG	120
			ATTCAAGCTG ACAGGCTGTG				180 240
			TAGCACGTGG				300
1.5	CTCGGTTCTC	GGCTGGAAGA	GACTCTCTAC	AGTGACCAGG	AGCTGGCCTA	TCTCCAGCAG	360
15			GGCCTTGGGC GGACAAAGTG				420 480
			GGTGGACCAG				540
	GAGCGCATGG	AAGCAATGGG	GGAGTGGAAC	CCCAATGTCA	AGGAGATCAA	GGTCCTGCAG	600
20			CATTACTCAC				660 720
20			CTTCGGGAAC				780
			GGTGCTTCAC				840
			CGACCTCAAG GGATTTTGCC				900 960
25			TTGAAGACCA				1020
			GAGAATCCCT				1080
			GGGGTTCGTG AAACAGGGAT				1140 1200
20	CACTGATTAG	CTATGACATG	AGGGTTCAGG	CCCCTAAAAT	AATTGTAAAA	CTTTTTTTCT	1260
30			AAAACCATCT TGAGAAGTCT				1320
			CAGAATCTCA				1380 1440
	GGCCGCTGCA	CAGCAACACC	ACAGAACAAG	CAGCACCCCA	CAGTGGGTGC	CTTCCAGAAA	1500
35			TGGAAAAAGA AGAATAAAGA			GTTTCCCTAT	1560
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		109 Protein					
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			KGLRQQAVMA EAMQKALGIL				60 120
			MEAMGEWNPN				180
15	PRDFVSVRCA	KRRGSTCVLA	GMDTDFGNMP	EQKGVIRAEH	GPTCMVLHPL		240
45	WLLSIDLKGW	LPKSIINQVL	SQTQVDFANH	LRKRLESHPA	SEARC		
	Seq ID NO:	110 DNA sec	quence				
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	1	1	1	1	1	1	
			GCCGGGTGAG CCTGCTGTTG				60 120
			AGAGTTCGGA				180
55			TAGCTGTTGT				240
			TCTATAATGT CTTGTGAAAA				300 360
	GGCAGAAGAC	AAATGGTGTC	CACAAAATAC	ACAGTACTGT	TTGACAGTTC	ATCACTTCAC	420
60			CCATCACCAA GAGATTCTGA				480 540
00			TACCCACCAA				600
			GCAGTGCCCC				660
						CAGCCTCTAA CTTGCACTTG	720 780
65	GTGAAGAGTG	CACATTGGAC	CTCAAGGCGA	AAGCCAGTGG	TTTGCTTGGA	TAAAATGTTC	840
						ATGGTCTGAC	900 960
						GGATCCTGGC TTGACTGCCT	
70	CAGAGGCTGC	CAGGTCAAAC	CCTCTTGTTT	ATGTGATTAG	CTCAGAGCAT	CTCTATGAAA	1080
70						CAATGAGAAA CAAATTATGG	
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						LDPTPFPNSF SRSECHFVGC	60 120
80	HHSRDSEHTE					LPVLAWVFVL	180
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	Leccorded a	CCCCAGGCGG	erecerrees	NO COTTOCCO	GGGAGGGGG	TGAGGGGGGG	60
		GTGGGCGCGG					120
5		GCTTTTAAAG					180
		GGCAACCCTC					240
		GTGCAAACCT					300
		GTGGTGCTTA CAGCATGCTG					360 420
10		AGAAAGCTGG					480
		TACACCATTT					540
		CTGCAATCGA					600
		TCATCACTTC					660
15		TGAATGTCAT					720
13		TTGCTGTGAA					780 840
		GCTTGCCTGG					900
		ACCAGCCTCT					960
20		ATCTTGCACT					1020
20		GATAAAATGT					1080
		AGATGGTCTG GAGGATCCTG					1140
		CCTTGACTGC					1200 1260
		ATCTCTATGA					1320
25		GTCAATGAGA					1380
	GAAATCTATT	TGCAAATTAT	GGGGGGAAAT	AAAGCTTTTA	AATTATAAA		
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20	1	11	21	31	41	51 I	
	MDVADYSECK	PFHCSREEPD	NHILLLKVWC	LLRRLTRYKS	SDRPAHKVSM	LLLCHALAIA	60
		WAFAKNINFY					120
25		FTSHGRSTSI					180
35	TNHTNAVFAV	MHAQRTSGSS	APTLYLPVLA	WVFVLPLL			
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40		uence: 402-1					
40	1	1 1	21	31	41	51	
	ACTTCCTGAG	CCGGGCTGGC	TCCCTCCCAA	CAGGCTCCTT	GCCGCCTCCC	CAGCGCTGGC	60
		CTGCCGCCCG					120
		GCCGGGCCCG					180
45		CGCGCCCCAG					240
		ACGCCGGCCC					300
		AGGCTCGGTG					360
		CTGGACTAGG TTTCACTGTT					420 480
50		GGACCGCCCA					540
		TGTCCAGATC					600
		TGTGAGGCCT					660
		AAACGCAGGG					720
55		TACACAGTAC					780
55		CAAAAAGTGT TGAACATACG					840 900
		CAATCACACT					960
		CCCCACACTC					1020
		CCATTCCTAG					1080
60		TGAACTTTGG					1140
		CGAAAGCCAG					1200
		GGAATTTGGC					1260
		ACGTTTGGGC GCTGAAAGGA					1320 1380
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76	MLLITLSANL	FTVPERSLTT	TFSFSRYKSS	DRPAHKVSML	LLCHALAIAV	VQIVIFSESW	60
75		VRPPLDPTPF					120
		KKCASRSECH		EHTECRSCCE	GMICNVELPT	NHTNAVFAVM	180
	ARRESESA	PTLYLPVLAW	ALAPL				
00	Seq ID NO:	116 DNA sec	quence				
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•	1	11	21	31	41	51 1	
	ATGGTATGGC	AGCAAGATTA	TGGAACCAGG	AGAGAGCACC	ATGGCTGCCG	TCTGGAATTC	60
85		CTGCAGGGTG					120
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	TCATCTGCTG	AGAGAGGTGA	GGAAGCTGCA	GAAGAAGACT	TTGAAACTAG	CAGAGGTGGG	180
		TGAAGGAAAG					240
		AAGAAGCTGC					300
_		GCATTGTACA					360
5	CAGAAGAGAT	ATTTTCAGCT	GAATATTGGA	AATGTAAAAT	GCCACACGTT	GGATGAGATG	420
	ATTATCCGAG	CTCAGACTTG	GGAAATAGTC	ATGCTTCTGG	ACCAAGTGCC	AGGTCCTGGC	480
		AGGTAGATGG					540
							600
		CCACTGATGT					
10		TTCGGACCGC					660
10	ATGGCTACAC	CATTTCCAAA	TAGCTTCAAG	TGCTTTACTT	GTGAAAACGC	AGGGGATAAT	720
	TATAACTGCA	ATCGATGGGC	AGAAGACAAA	TGGTGTCCAC	AAAATACACA	GTACTGTTTG	780
		ACTTCACCAG					840
		GTCATTTTGT					900
	AGGTCTTGCT	GTGAAGGAAT	GATCTGCAAT	GTAGAATTAC	CCACCAATCA	CACTAATGCA	960
15	CTCTTTCCCG	TAATGCACGC	TCAGAGAACA	TCTGGCAGCA	GTGCCCCCAC	ACTCTACCTA	1020
		CCTGGGTCTT					
							1080
	CAGAGACCAG	CCTCTAAAGC	ACAAGCCAAA	AACTGTGTGA	ACGGTGAACT	TTGGAGTGAA	1140
	GATCAATCTT	GCACTTGGTG	AAGAGTGCAC	ATTGGACCTC	AAGGCGAAAG	CCAGTGGTTT	1200
	CCTTCCATAA	AATGTTCCCG	CATGAGGCCA	CAGGACTGAG	GATGGGAATT	TGGCAGGGCC	1260
20							
20		GTCTGACTTC					1320
		TCCTGGCAAC					1380
	GACCTCCTTG	ACTGCCTCAG	AGGCTGCCAG	GTCAAACCCT	CTTGTTTATG	TGATTAGCTC	1440
		TATGAAATCT					1500
		TGAGAAAGGC					1560
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23	CTATTTGCAA	ATTATGGGGG	GAAATAAAGC	TTTTAAATTA	TACAATGTAA	A	
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	MVWOODYGTR	REHHGCRLEF	CRVSAGCPCL	SPLTSLVIVS	SSAERGEEAA	EEDFETSRGG	60
		HNIKVQGEAG					120
		NVKCHTLDEM					180
	KHKPTDVKYK	ETEPVCLFTI	DIRVRTAQHT	RIKQKVSITS	MATPFPNSFK	CFTCENAGDN	240
35	YNCNRWAEDK	WCPQNTQYCL	TVHHFTSHGR	STSITKKCAS	RSECHFVGCH	HSRDSEHTEC	300
		VELPTNHTNA					
	ROCCEGNICA	AND INITIAL	***********	00001111111			
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		118 DNA sec					
	Nucleic Ac	id Accession	1 #: XM_038	559.6			
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	 AGTAGGGAGG	 TGGGCAGGAG	 CCAGTGATGA	 CGGAATGGCA	 ATCACATTTG	ACCTCTGATC	60
	 AGTAGGGAGG	 TGGGCAGGAG	 CCAGTGATGA	 CGGAATGGCA	 ATCACATTTG	ACCTCTGATC	60 120
45	AGTAGGGAGG TGTTTATTTC	TGGGCAGGAG CTCCTCCTTG	CCAGTGATGA ACGTCTCCAT	 CGGAATGGCA ATAAATGTTA	ATCACATTTG CACGGGCATC	ACCTCTGATC CCCACACTCG	120
45	AGTAGGGAGG TGTTTATTTC GATACGCACC	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG	CGGAATGGCA ATAAATGTTA TAACCGTGTC	ATCACATTTG CACGGGCATC ATTTGCTTGC	ACCTCTGATC CCCACACTCG AACACTGGCA	120 180
45	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC	120 180 240
45	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC	120 180
45	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT	120 180 240
	AGTAGGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC	120 180 240 300 360
	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC	TGGGCAGGAG CTCCTCGTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CGAGTCTCCG CCTCGGGCAC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG	120 180 240 300 360 420
45 50	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG	CGGAATGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG	ATCACATTTG CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG	120 180 240 300 360 420 480
	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT	TGGGCAGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG ACTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGAGCTTCCC	CGGAATGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGG CGAGTCTCCG CCTCGGGCA GTCCACACGG TCGTGGCCGA	ATCACATTTG CACGGCATT CACGGCATGC CCGGGTCTGGG CCTGGGGAG CCGCGAGAGG TGCCCCAGGT CCAGGGGCTA CGGAACAATG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTGCTGCAG CGACCCTTGG AAGGATTGCA	120 180 240 300 360 420 480 540
	AGTAGGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGAGACCCG TGTACCGGAG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCGG CCTCGGGCAC GTCCACAGG TCGTGGCCGA AAGGAGGATC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCCGGAGAGG TGCCCCAGGT CCAGGGGCT CCAGGGACATC AAAAGAGGTG	ACCTCTGATC CCCACACTCG AACACTGGCA ACGCTTAGT GCCGGTCTCC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT	120 180 240 300 360 420 480
	AGTAGGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGAGACCCG TGTACCGGAG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCGG CCTCGGGCAC GTCCACAGG TCGTGGCCGA AAGGAGGATC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCCGGGAGGG TGCCCCAGGT CCAGGGGCT CCAGGGGACATC AAAAGAGGTG	ACCTCTGATC CCCACACTCG AACACTGGCA ACGCTTAGT GCCGGTCTCC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT	120 180 240 300 360 420 480 540
50	AGTAGGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA	TGGGCAGGAG CTCCTCCTTG CACCAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCCTCAGCT CTCCGCAGAG AGACCTAATA	CCAGTGATGA CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGCAGACCCG CGCAGCTTCCC CTGTACCGGAG GTCACACCAG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACGGGCAC GTCCACACGG TCCTGGCCGA AAGGAGGATC CTACCATTTT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGAGG CCCCCAGGT CCACGGCTA CGGAACAATG AAAAGAGGTG AAAGGGAAAAA	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA AGGATTGCA CTGGGACTT CCAGACCCCA	120 180 240 300 360 420 480 540 600
50	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCCCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT	CCAGTGATGA ACGTCTCCAT GATTCGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCGC CGAGCTTCCC TGTACCGGAG GTCACACAG GTGTTCACGG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGGGG	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTCGGGGAG CCCCCAGGT CCACGGGCTA CCGAACAATG AAAAGAGTA AAAGGAAAA AACGGAAGA AACGGAGGAAGAGAGAGA	ACCTCTGATC CCCACACTCG AACACTGGCA AGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG	120 180 240 300 360 420 480 540 600 660 720
	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCCG GTCTTCCTGC AATCCAGCCC CCGGAACCGC GGATCTGCCCT GTAACGCATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CCCGCTAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT	CCAGTGATGA ACGTCTCCACA GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG TGTACCGGAG GTCACACAC GTGTACACACGG CATATCAAGC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGC CCTCGGGCAC GTCCACAGG TCGTGCCGAACGG TCGTGCCGAACGG AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCGAGAGG TGCCCCAGGT CCAGGGGCTA AAAAGAGATG AAAAGAAAAA GACGGTGGAG CCTGTCATTG	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGC GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCTGGCT	120 180 240 300 360 420 480 540 660 720 780
50	AGTAGGGAGG TGTTTATTTC GATACGCACC CCTCTGCCCT GAATCTTCGG AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT GCACTATGCA	CCAGTGATGA CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCGG CGCAGACCGG CGAGACCGG CGAGACCAGG GTCACCACGG GTCACACCAG GTCACACCAG GTCACACCAG GTGTACAGGG GTGTACAGGC GTGGAATTAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACCACCGG TCCACACCG TCCACACGG TCCACACGG TCCACACGG TCACACTTT ATCATATGCT CTCTTCACAATTT ATCATATGCT TTCAAAGGATT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCCGGGAGG TGCCCCAGGT CCAGGGCT CAGGGGAACAATG AAAAGAGGTG AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATTT	ACCTCTGATC CCCACACTCG AACACTGGCA ACGCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG ATGGGACTTCC AGGGACTCC AGGGCTCTCCAG CCAGCCCCCA AGGGCCCCA TGGTCCTCAG CACCCTGGCT CCAGGAGTAG	120 180 240 300 360 420 480 540 660 720 780 840
50	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTAGAGTTT ATAATAAAAT	I TEGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAGC CCCCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCGCACTGTTT GCACTGTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCCCG CGAGCTCCC TGTACCGGAG GTCACACCAG GTCTTCACGGAG GTCTTCACGG CATATCAAGC GTGGAATTAT CAGCCAAACC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCCACACGG TCCTCGGCAC CTACCACATTT ATCATATGCT CTCTTCAGAA TTGAAGGATT TCAACATGGA	ATCACATTTG CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCCAGGT CCAGGGCTA CCGAACAATG AAAAGAGAAA AACGGAAAA AACGGTGGAG CCTGTCATTG TAGAATGTAT TAGAATGTAT	ACCTCTGATC CCCACACTCG AACACTGCA ACCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGC AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGCACCCCA CGGTCTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG CGCTTGCTG	120 180 240 300 360 420 480 540 660 720 780
50	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTAGAGTTT ATAATAAAAT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCTGCT TTTCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGCCCG CGAGCTCCC TGTACCGGAG GTCACACCAG GTCTTCACGGAG GTCTTCACGG CATATCAAGC GTGGAATTAT CAGCCAAACC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCCACACGG TCCTCGGCAC CTACCACATTT ATCATATGCT CTCTTCAGAA TTGAAGGATT TCAACATGGA	ATCACATTTG CACGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCCAGGT CCAGGGCTA CCGAACAATG AAAAGAGAAA AACGGAAAA AACGGTGGAG CCTGTCATTG TAGAATGTAT TAGAATGTAT	ACCTCTGATC CCCACACTCG AACACTGCA ACCTGGCTCC CAGCCTTAGT GCCGGTCTGC CGACCCTTGC AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAGCACCCCA CGGTCTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCTG CGCTTGCTG	120 180 240 300 360 420 480 540 660 720 780 840
50 55	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GGATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA ATTTTGGAACT GGAGAAACCT GGAGAAACCT TCGCAGTT TCTGCCGGTA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG TGTACCGGAG GTCACACCAG GTGTACAGGG GTGTTCACGG CATATCAGG GTGGAATTAT CAGCCAAACC TTTGACAAAC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGG CCTCCGGGCAC GTCCACACGG TCGTGGCGAA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAAACATGGA AAGACTCTT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCAGGGC TGCCCCAGGT CGGAACAATG AAAAGAGTT AAAAGAGTT AAAGGAAAAA CACGGTGGAG CCTGTCATTG GAAGGCATT TAGAATGTAT AGAGTGTATT	ACCTCTGATC CCCACACTCG AACACTGGCA CGTGGCTCCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG ATGGGGACTT CCAGACCCCA GTGGGGACTT CCAGACCCCCA CACCCTGGCT CGAGGAGTAG CGCTCTGCT CAACAGCTTG	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55	AGTAGGGAGG TGTTTATTTC GATAGGCACC CCTCTGCCT GAATCTTCGG AATCCAGCCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGAGAGA TGATGCAATC GCCACGTGTA GCTCTGCAGC CCGCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGAGAAACCT GCACTGTTT TCTGCCGGTA TCAGAGTGTTT TCTGCCGGTA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGACACCAC GTCACACAC GTCTTCACCGGAG GTCTTCACGG GTGTTCACGG CATATCAAGC CTGGAATTAT CAGCCAAAAC CTTTGACAAAG GTCCCATATT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACACGG TCCACACGG TCCACACGG TCACACGG TCACAATGT ATCATATGCT CTATTCAGAA TTGAAGGATT TCAACATGGA AAGGAGCTCTT CAACATCGC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG CCCCGAGAGG TGCCCCAGGT CAAGGGGCTA AAAGAGAATG AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT TAGTCTGTAT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCA TGGTCCTCA CGCTCTGCTC CGAGGAGTAG CGCTCTGCTG CAACACCTTG ATTCGTCCTA	120 180 240 300 420 480 540 600 720 780 840 900 1020
50	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA	I TEGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGAGAG TGATGCAGC CCCCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATCA TCAAGAATGG AACTGATT TCTGCCGGTA TCAAGAATGG AACTGAGCCT ATCAAGAATGG AACTGAGCCT ATCAAGAATGG AACTGAGCCT ATCAAGAATGG AACTGAGCCT ATCAAGAATGG AACTGAGCCT AACTGAGCCT AACTGAGCCT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CGCAGACCGC CGAGCCCG CGAGCTCCC TGTACCGGAG GTCACACAG GTCATCACGG GTATTCAAGG CATATTCAAGC CTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACC TTTGACAAACT TTCTCTTGGAG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGGG CGAGTCTCCG CTCCGGGCAC CTCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTGAAGGATT TCAACATGGA AAGAGCTCTT CACATCTGC TAACATCTGC TCAAGAAGCC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTCGGGGAG CCCCAGGT CCAGGGCTA CCGAACAATG AAAAGAGGTA AAAGGAAAA AACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTATT TAGATCTGTAT TAGCTATAT TAGATCTGTAT	ACCTCTGATC CCCACACTCG AACACTGGCA ACGCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA TGGTCCTCAG CACCCTGGCT CAGACCCCA TGGTCCTCAG CACCCTGGCT CAGAGAGTAG CACCTGGCT CAACAGCTTG CAACAGCTTG CATCGTCCTA CTGCTCCTTAG CTGCTCTTTT	120 180 240 300 420 480 540 600 720 780 840 900 1020 1080
50 55	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCACGCCC CGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT TATAATAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG TACTCTTGAG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGAG AGACCTAATA TTTTGGAACT GGAGAAACCT GGAGAAACCT TCGCCGGTA TCAAGAATGG ACTAGTTT TCTGCCGGTA CAAGAATGG AACTGAGCCT ACCAGTGGGA	CCAGTGATGA CCAGTGATGA CCACTCACAT CATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGTACCACAC GTGTACAGAG GTCTCACGGGG CATATCAAGC GTGGAATTAT TCCCCATATTTT CCTCTGGGG CCTTATTTTT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCACACGG TCCTACAGGA AAGGAGGATC CTACCATTIT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAACATGGA AAGAGCTCTT CAACATCTGC CTAGAGAGCC CAAGTAGAA	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGTCTGGG CCTGGGGGAG CCCCAGGGT CCAGGGGTA CAGAACAATG AAAAGAGAAA AGACGAAAA GACGGTGCATTG GAAGGCATTT AGAATGTAT AGAGTGTATT TAGTCTGTAT TACCAAAGC CTTTAATCCA	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC AAGGATTGCA GTGGGGACTT CCAGACCCTA GGTGCTCAG CACCTGGCT CAACAGCTCA CACCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTCT GTGCTCCTTTG GTGTCCCTGTT GTGTCCTCTTT	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140
50 55	AGTAGGGAGG TGTTTATTC GATAGGCC CCTCTGCCT GAATCTCGG AATCCAGCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TAATCAGGTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGAGAGA TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATTA TCTAGCAGTGT TCTACCGGTA TCAGACTGTTT TCTGCCGGTA TCAGAATGG AACTGAGC CAACTGATG CAACTGATG CAACTGATG CAACTGATG CAACTGATG CAACTGATGCA AACTGAGGCA CAAGTATGTA	CCAGTGATGA ACGTCTCCACAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG GTCACACCAG GTCTCACCACAG GTCTTCACGG GTGTTCACGG CATATCAAGC GTGGAATTAT CCAGCCAAACC GTCCCATATT TCTCTTGGAG CCTTATTTTT AGAGCCTGGA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGC CCTCGGGCAC GTCCACAGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTATCAGAA TTGAAGGATT CAACATCGC TCAACATGGA AAGGAGTCTTC CAACATCTGC CAACATCTC CAACATCTGC CAACATCTGC AAGATCTGC CAAGTGGAAC AAGGTGGAAC	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCGAGAGG TGCCCCAGGT CCAGGGGCTA AAAGGAAAAA AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGAGTT TAGAATGTAT TAGTCTGTAT TAGTCTGTAT TAGCCAAAGCC CTTTAATCC TGGGGACTGC	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG ATGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CGAGGAGTAG CGCTCTGCT CAACAGCTTC ATTCGTCCTA ATTCGTCCTTA TGGTCCTCTA TGGTCCTCTA ATGATCCTGT	120 180 240 360 420 480 540 660 720 780 960 1020 1020 1140 1200
50 55	AGTAGGAGG GATCTTCGC GATACTCGC GATCTCGG GTCTTCCTG AATCAGGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCTTGAG GGGCCAATC GGGAATTACGG	I TEGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAGC CCCCCAGAGA AGACCTAATA TTTTGGAACT TCGCAGAACTATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA CCCAGTGGGC CAAGAATAGACCT CCCAGTGGGA CAAGTATGTA CCAAGAATGA TCAAGAATGA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGTACCACAG GTCACCAG GTCACCAG GTCACCAG GTCACCAG GTCACCAG GTCACACCAG GTGATTAT CAGCCAAACC TTTGACAAAC CTTTGACAAAC CTTTGACAAAC TTTGACAAAC CTTTGACAAAC TTTGACAAAC CTTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAT TCTCTTGGAG CCTTATTTT ACTAGTGA TTTGCCCAAAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACCACGG TCCACACGG TCCACACGG TCACACGG TCACACTTT ATCATATGCT TCACATTT ATCATATGCT TCAACATGGAA AAGAGCTCTT CAACATCGC TCAAGAAGCCC CAAGTGGAAC AAGGTGGAAC AGGTGGAAC GTGAACAGT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG TGCCCCAGGT CCAGGGGCTA AAAAGAGTGAAAA GACGGTGAAG GCTGTCATG GAAGGCATTT TAGAATGAT TAGAATGAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGCATGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGAGGCATTC	ACCTCTGATC CCCACACTCG AACACTGGCA ACCTGGCTCC CAGCCTTAGT GCCGGTCTGCTGCAG CGACCCTTGC AAGGATTGCA AGGATCCCA TGGTCCTCAG CACCTCGGCT CCAGACCCCA TGGTCCTCAG CACCTTGGTC CAACAGCTTG CAACAGCTTG CAACAGCTTG AAGATGGCAGA TGTCCCTGT AAGATGGCAGGAGTAG TGTCACTGTCTAAGATGGCAGGAGTAG	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140
50 55 60	AGTAGGAGG GATCTTCGC GATACTCGC GATCTCGG GTCTTCCTG AATCAGGCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCTTGAG GGGCCAATC GGGAATTACGG	I TEGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAGC CCCCCAGAGA AGACCTAATA TTTTGGAACT TCGCAGAACTATGCA TCAAGAATGCA TCAAGAATGCA TCAAGAATGCA CCCAGTGGGC CAAGAATAGACCT CCCAGTGGGA CAAGTATGTA CCAAGAATGA TCAAGAATGA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGTACCACAG GTCACCAG GTCACCAG GTCACCAG GTCACCAG GTCACCAG GTCACACCAG GTGATTAT CAGCCAAACC TTTGACAAAC CTTTGACAAAC CTTTGACAAAC TTTGACAAAC CTTTGACAAAC TTTGACAAAC CTTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTTGACAAAT TCTCTTGGAG CCTTATTTT ACTAGTGA TTTGCCCAAAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACCACGG TCCACACGG TCCACACGG TCACACGG TCACACTTT ATCATATGCT TCACATTT ATCATATGCT TCAACATGGAA AAGAGCTCTT CAACATCGC TCAAGAAGCCC CAAGTGGAAC AAGGTGGAAC AGGTGGAAC GTGAACAGT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGAG TGCCCCAGGT CCAGGGGCTA AAAAGAGTGAAAA GACGGTGAAG GCTGTCATG GAAGGCATTT TAGAATGAT TAGAATGAT TAGATGTAT TACCAAAGCC CTTTAATCCA TGGGGCATGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGGGGCTGC TGAGGCATTC	ACCTCTGATC CCCACACTCG AACACTGGCA ACCTGGCTCC CAGCCTTAGT GCCGGTCTGCTGCAG CGACCCTTGC AAGGATTGCA AGGATCCCA TGGTCCTCAG CACCTCGGCT CCAGACCCCA TGGTCCTCAG CACCTTGGTC CAACAGCTTG CAACAGCTTG CAACAGCTTG AAGATGGCAGA TGTCCCTGT AAGATGGCAGGAGTAG TGTCACTGTCTAAGATGGCAGGAGTAG	120 180 240 360 420 480 540 660 720 780 960 1020 1020 1140 1200
50 55 60	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCACGCCC CCGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAT TGAGGGCAAC TGAAATTGGA CATCATCTTGAG GGGCCAATCC GGAATTACCG TCCTTGGGCT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGCT CTCCGCAGACA AGACCTAATA ATTTTGGAACT GGAGAAACCT TCTACGCTT TCTGCCGGTA TCAAGAATGG AACTGAGCT CCCAGTGGGA ACTATGCAA ACTCATCTT CTATGGAGAGA CTCATCTTT CTTATGGAGAGA	CCAGTGATGA CCAGTGATGA ACGTCTCCACT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGATTCCC TGTACCGGAG GTCTTCACAGCAG GTCTTCACAGC CATATCAAGC TTTGACAAACC TTTGACAAACG TTTGACAAACG TTTGACAAACG TTTGACAAACG TTTGACAAACG TTTGACATATT TCTCTTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCAAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACTCCG CTCACACG TCCACACG TCACACGG TACCACTTC ATCACATTTT ATCATATGCT CTCTCAGAA TTGAAGGAT TCAACAGGAT AAGAGCTCTT CAACATCTGC CAAGTAGGA AAGGGGAAC AAGGTGGAAC AAGGTGGAAC AAGGTGGAAC TCACTGAAGT TCACTGAAGT	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGTCTGGG CCTGGGGGAG CCCCAGGT CCAGGGGCTA CAGACAATG AAAAGAACAATG AAAAGAACAATG GAAGGATATTAGAATGTATAGAATGTATTAGAATGTATTAGAATGTATTAGAATGTATTAGAATGTATTAGAATGTATTAGAATGTATAATCCAAAGGC CCTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCCA CGCTGGCTCCC CTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCCA TGGTCCTCAG CACCTGGCT CAACAGCTCCA CGCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTTA GTGTCCCTGT AAGATGGAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TATTCATCTTTT	120 180 240 300 360 420 540 600 720 780 960 1020 1140 1200 1320
50 55	AGTAGGAGG TGTTATTTC GATAGGACC CCTCTGCCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGGACCGC GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGACAAC TGAAATTGGA CATTCATTGG TACTCTGAG GGGCCAATCC GGAATTACGG TCTTGTGGCT TTTACTGGAT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA ATTTGGAACT GCACTATATCA TCACACTGTT TCTGCCGGTA TCAAGAATGC AACTGAGCT CCCAGTGGGA CAAGTATGTA TCAAGAATGTA TCAAGAATGTA TCAAGAATGTA CTCATCTCTT CTTATGGAGA AAATGAAGAA	CCAGTGATGA CCAGTGATGA CCACCAT CATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGCAGACCCG GTCACACCAG GTCACACCAG GTGTACAGG CATATCAAGC CTTGACAAAG GTCCCAAAC GTCCCAAAC CTTTGACAAAG GTCCCATATT TCTCTTGGAC CCTTATTTT AGAGCCTGA TTTGCCCAAT TTTGCCCAAT TTTGCCCAAAG GAGAAGAAAG GGAGAAGAAAA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGC CCTCGGGCAC GTCCACAGG TCGTACGG TCGTACGG AAGGAGGATC CTACCATTTT ATCATATGCT CTACAGGAGT TCAACAGGAT TCAACATCTC CAACTCTC CAAGTAGGAC AAGGACCTCTT CAACATCTGC TCAAGAAGCACTT CAAGAAGCACTT CAAGAGCACTT AGGAGCACT AAGGAGCACT AAGTGGAAC AAGGTGGAAC AAGTGGAAC AAGTGGAAC AACTGAAGT AACTGAAAGT AACTGCAAACT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCGAGAGG TGCCCCAGGT CCAGGGGCTA AAAGAGATG AAAAGAGTG AAAGAGAAATG GAAAGTTAT TAGAATGTAT TAGATGTAT TAGATAGA	ACCTCTGATC CCCACACTCG AACACTGGCA GGTGGCTCC CAGCCTTAGCT GCCGGTCTGC CTTGCTGCAG CGACCCTTGGC ATGGGGACTT CCAGACCCCA GTGGGGACTT CCAGACCCCCA CACCCTGGCT CGAGGAGTAG CGCCTCTGCT CAACAGCTTC ATTCGTCCTA ATTCGTCCTTA AGATGGAG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG AATCTTTTTC GATGGCATCA	120 180 240 300 480 540 600 720 780 900 960 1020 1140 1200 1200 1320
50 55 60	AGTAGGGAGG TGTTTATTTC GATAGGCACC CCTCTGCCT GAATCTTCGG AATCTAGCC CCGGGACCGC GATCTGCCCT GTAACGGATG TTAAGGCATA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC CTGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACCG TCCTGTGGCT TTTACTGGAT TTTTCCAGGT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGAGAGA TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GGACTATTGCAGCT TCAGCTGTT TCTGCCGGTA TCAACTGTTT TCTAGCAGTGT CCAGTGGTA CAACTGATGCA ACTGAGCT CCCAGTGGGA ACTGAGCT CCCAGTGGGA ACTGAGCT CCCAGTGGGA ACTGAGCT CTCATCTCTT CTATGGAGAG AAATGAAGAGA AAATGAAGAGA AAATGAAGAGA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTCAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG GTACACCAGG GTCTTCCC TATACCAGGA GTGTACACAG GTGTACACAG GTGTACACAG GTGTACACAG GTGTACACAG GTGTACACAG GTGTACACAG GTGTACACAG GTTCCCTATATT TCTCTTGGAG CCTTATTTT AGAGCCTGAA TTTGCCCAAT GACCATCAGA CGGAAAGAG GGAAAGAG GGAAAGAG CGGTGCATTC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACACGG TCCACACGG TCCACACGG TCACACATTT ATCATATGCT TCAACATGGA AAGGAGTTC TAACATGGA AAGGAGCTCT CAACATCGC TCAAGAAGCC TCAACGGAAC GTGAAGCACT TCAACATGGA AAGGAGCTGAAC GTGAACACT TCAACTGGAAC GTGAACACT TCAACTGAAGT TCAACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCGACCTGGC	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGCATC ATTTGCTTGC CGGGTCTGGG CCCCCAGGT CCCCCAGGT CCAGGGGCTA CGGAACAATG AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATTT TAGAATGTAT TAGATGTAT TAGCCAAAGCC CTTTAATCCA TGGGGACTGC AGATAATGGG GGGAACTATG TCCCACTA ACATCAGTGG	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CTTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCA TGGTCCTCA CACCTGGCT CAACAGCTTG ATTCGTCTTA CTGCTCTTTG GTGTCCCTA CTGCTCTTTTG GTGTCCCTGT AAGATGGGAG TGTCAGCAG AATCTTTTTC GATGCACTC GATGGCATCA GGTGAATTTA	120 180 240 300 360 480 540 660 720 780 900 900 91080 1140 1260 1320 1380
50 55 60	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT AGAAATTGGA CATCATTGG TACATTGGA CATCATTGG TACATTGGA CATCATTGG TACATTGGA CATTCATGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCCTTGGGCT TTTACTGGGT TTCTCCAGG AGGTGTCAGA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATC CTCCGCAGAG AGACCTAATGA TTTTGGAACT GCACATATCA TCCACAGTTT TCTGCCGGTA TCAAGAATGG ACTAATGA CCCACTGTTT TCTGCCGGTA CCCAGTGGGA ACTGATGTT TCTGCCGGTA CCCAGTGGGA CAAGTATGTA CTCAACTGTTT CTATGGAGAG AAATGAAAGAT AGTGACAAG	CCAGTGATGA CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG GTCACACAG GTCACACAG GTCACACAG GTCACACAG GTGAATTCAGC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GGAGAAGAG GGAGAAGAG GGAGAAGAG CGGTGCATTC ACCATGGAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCGTGGCCGA AAGGAGGATC CTACCATTT ATCATATGCT CTCTTCAGAA TTGAAGGATT CAACATCTT CAACATCTT CAACATCTGC CAAGTGGAAC AAGGTGGAAC AAGGTGGAAC AGGTGGAAC TCACTGAAGT TCACTGAAGT AACTGGCAAC TCACTGCAAGT AACTGGCAAC TCACTGAAGT AACTGGCAAC TGGACCTGGC AACTGGCAAC TGGACCTGGC	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATGGGGGAG CCCCAGGGT CCACGGGCTA CCAGGGGCTA CAGAACAATG AAAAGAACAA AAAAGAACAA CACTGCACTATT TAGAATGTAT TAGAATGTAT TACCAAAGC CTTTAATCCA TAGAGGACTAC TAGAACTAT TACCAAAGC CTTTAATCCA TAGAGGACTAC TAGAACTAT TACCATATGCA CAGATAATGGG GGGAACTAT TCCTCCACTA ACATCAGTGG AGCCCTGGAG AGCCCTGGAG	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGACTTC CAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCTTG CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGCAG AATCTTTTC GATGCCAG AATCTTTTC GATGCAGTA GGTGAATTTA GGGAACAGAG	120 180 240 300 480 540 600 720 780 960 1080 1140 1260 1320 1380 1500
50 55 60	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT AGAAATTGGA CATCATTGG TACATTGGA CATCATTGG TACATTGGA CATCATTGG TACATTGGA CATTCATGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCCTTGGGCT TTTACTGGGT TTCTCCAGG AGGTGTCAGA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATC CTCCGCAGAG AGACCTAATGA TTTTGGAACT GCACATATCA TCCACAGTTT TCTGCCGGTA TCAAGAATGG ACTAATGA CCCACTGTTT TCTGCCGGTA CCCAGTGGGA ACTGATGTT TCTGCCGGTA CCCAGTGGGA CAAGTATGTA CTCAACTGTTT CTATGGAGAG AAATGAAAGAT AGTGACAAG	CCAGTGATGA CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG GTCACACAG GTCACACAG GTCACACAG GTCACACAG GTGAATTCAGC TTTGACAAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GGAGAAGAG GGAGAAGAG GGAGAAGAG CGGTGCATTC ACCATGGAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCACACGG TCACACGG TCACACGG TCACACGG TCACACGG TCACACTTT ATCATATGCT CTACACATTT CAACATCTGC CAACTGGAAC AAGGAGACCCT CAAGTGGAAC AAGGTGGAAC AGGTGGAAC TCACTGAAGT TCACTGAAGT AACTGGCAAC TCACTGAAGT AACTGGCAAC TGGACCTGGC ACTGACAAC	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATTTGCTTGC CAGGGTCTGGG CCCCAGGGT CCACGGGGCTA CCACGGGCTA AAAAGAGAAAA AAAAGAAAAA CACTAAATT AGAGTGTATT TAGAATGTAT TACCAAAGC CTTTAATCCA TAGCGGACTGC CTTTAATCCA TAGCGGACTGC CAGTAATGGG GGGAACTATT TCCTCCACTA ACATCAGTGGA AGCCCTGGAG AGCCCTGGAG AGCCCTGGAG AGCCCTGGAG	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGACTTC CAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCTTG CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGCAG AATCTTTTC GATGCCAG AATCTTTTC GATGCAGTA GGTGAATTTA GGGAACAGAG	120 180 240 300 480 540 600 720 780 960 1080 1140 1260 1320 1380 1500
50 55 60	AGTAGGAGG TGTTTATTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC CGTACGGATC GTAACGGATG TTAAGGCTAA ATAATCTGGT ACTACAGCTTT ATAATAAAAT TGAAGAATTGGA CATTCATTGG TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTTACTGGAT TCTCTCAGG ACGTTTCATCGAT TCTTCCAGG ACGTGTCAGA TGAGAGAGAGAT TGAGAGAGAGAT TGAGAGAGAG	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGCT CTCCGCAGAG AGACCTAATA ATTTTGGAACT GCACTATTC GCACTGTTT TCTGCCGGTA TCAAGAATGC AACTATGAA CTCAAGATGCT CTCATGTGT CTCATGGGA CAAGTATTT CTCATGCAGC CAAGTATTA CTCATCTCTT CTATGGAAA AGTAATGAA AGTAACAAGA AATGAAGAT AGTGACAAGG GAGATACCTC GTTTGGCTCT GTTTGGCTCT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG TGTACCGGAG GTCTACACAG GTCTACACAG GTCTACAGAG CATATCAAG GTCCCATATT TCTCTTGGAG TTTGACAAAG GTCTTTGCCAGT TTTGCCAGT TTTGCCCAAT TTTTCCCAGT TTTGCCCAAT CAGCATACT AGAGCCTGGA TTTTGCCCAAT CACCATACT AGAGCATAGA GGGAGAAGAAG CGGTGCATTCAGA GGAGAAGAAG CGGTGCATTC ACCATGGAT GACCATCAGA GGAGAAGAAG CGGTGCATTC ACCATGGATG GGTACAGCCT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCG CCAGGGGGGG CCTCGGGCAC GTCCACACGG TCGTGGCGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTTCAGAA TTGAAGGATT TCAACATCTT CAACATCTT CAACATCTT CAACATCTGC TCAAGAGC TCAAGAAGC TCAAGAAGC TCAAGAAGC AAGGTGGAAC AGGTGGAAC AGGTGGAAC AGGTGGAAC AGTGGAAC AGTGGCAAC GGACTTGACA CTGGCAAC CGGCTTGACAC CGTGTTGTTTG	ATCACATTTG CAGGGCATC ATTTGCTTGC CAGGGCATC CAGGGCATC CAGGGGAGG TGCCCCAGGG TGCCCCAGGGT CAAAAGAGGT AAAAGAGTG AAAAGAGTT AAAAGAGTT TAGAATGTAT TAGAATGTAT TACCAAAGC CTTTAATCCA TGGGGACTGC AGATAATGGG AGATAATGGG TCCTCCACTA ACATCAGTGG AGCCCTGGAG AGCCCTGGAG CCCAGTTCT	ACCTCTGATC CCCACACTCG AACACTGGCA CGCTGGCTCC CAGCCTTAGC GCCGGTCTGC CTTGCTGCAG CGACCCTTGG ATGGGGACTT CCAGACCCCA GTGGGGACTT CCAGACCCCA CACCCTGGCT CAACAGCTCAG CACCTTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCACCAG TGTCACCAG GTGAATTTT GATGGCATC GATGGATCA GGGAACAGAG GGAACAGAG GGAACAGAG GGAACAGAG GGAACAGAG GATATACTGT	120 180 240 300 420 600 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560
50 55 60 65	AGTAGGAGG TGTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GATCCCC GAATCCCGG AATCCAGCC CCGGGACCGC GTAACGGATG TTAAGGCTA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATACAAT TGAGGCAAC TGAAATTGGA TGAAATTGGA TACTCTTGGA TACTCTTGGG TCCTTGTGGCT TTTTACTGGAT TTTTCCAGG AGGTTCAGA TGAGAGAGAT ACAAGGCGA	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATTA TCTGCAGTA TCAGCAGT TCAGCTGTT TCTGCCGGTA TCAAGAATGC AACTGAGCT CCCAGTGGTA CCAGTGGTA CTCATCTTT CTATCGAGAG AAATGAAGAT AGTGACAAGG GAGATACCTC GTTTGGCTCT GACAATACAC	CCAGTGATGA ACGTCTCCACA GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG CGCAGACCCG GTCACACACG GTCTACACAG GTCTACACAG GTGTACAGG CATATCAAGC GTGGAATTAT TCTCTTGGAG GCCTAATT TCTCTTGGAG TTTGCCCAAT TTTGCCCAAT TCTCCACT AGAGCATCACA GGGGAAAGAGAG GGGTGCATTC ACCATGAGC GGGTACAGCT ATTCCAACTA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGC CCTCGGGCAC GTCCACAGG TCGACACGG TCACAGT ATACATTTT ATCATATGCT CTACATTTT CTACATTTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTT CAACATCTT CAACATCTGC TCAAGAAGCTCTT CAACATCTGC TCAAGAAGCAC TCAAGAAGCAC TCAAGAAGCAC TCACTGAAGT TCACAAC TCGACAATGG TCTGACGAATGG	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGGAG CCCCGAGGGG TGCCCCAGGT CCAGGGGCTA AAAGAGGTG AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATT TAGAATGTAT TAGTCTGTAT TCCTCACTA ACATCAGTG ACCCTTGAGA CCCCAGTTTCT TCCTAAGCTG	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGC CGCGGTCTGC CTTGCTGCAG CGACCCTTAGC ATGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTCA ATTCGTCCTAT ATTCGTCCTA ATTCGTCCTTT ATTCGTCCTTTT ATTCGTCCTTTTC AGAGAGGAG TGTCAGCAGG TGTCAGCAGG TGTCACCAGCTC AAGATGGAAC TGTCAGCAGG TGTCAGCAGC TGTCAGCAGC TGTCAGCAGC TGTCAGCAGC TGTCAGCAGC TGCAACACT TGCAAGCCGCA	120 180 240 360 480 540 660 720 780 900 900 1020 11200 1260 1320 1440 1500 1620
50 55 60	AGTAGGAGG TGTTTATTTC GATACGCAC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TTCTTCCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTAAGGAT ACAAAGGCGA TCTTAAGGAT ACAAAGGCGA TCTTAAGGAT ACAAAGGCGA TCTTAAGGAT ACAAAGGCGA TCTTAAGGAT ACAAAGGCGA TCTTTAAGGAT ACAAAGGCGA TCTTTAAGCAA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGCTCTGCAGC CTCCGCAGAT ATTTTGGAACT GCACTATGCA TCTACGCAGT TCTACGCAGA AGACTATGTA TCTACGGGTA TCAAGAATGA TCAAGATGTT TCTGCCGGTA CACAGTGTT TCTGCCGGTA AATTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACAAG GAGATACCTC GTTTGGCTCT GACAATACCA ATTAACTGAT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGGCGG CGAGACCCG CGAGACCCG CGTACCAGG GTCACACAG GTCTTCACCAG GTCATCAGGAG GTCATCAGG GTCATCAGG GTCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTCCCATATT GACCATAGA GGGGAGAGAGAG GGGGAGAGAGAG GGGGATC ACCATGGAT GTCCAATT ACCATGGAT CACCTAGAT GACCATCAGA CCGTGCATC ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACTA ATCCAACTA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCGGCAA AGGAGGATC CTACCATTT ATCATATGCT CTATTCAGAA ATGAGAGTTT CAACATCTT CAACATCTT CAACATCTT CAACATCTT CAACATCTT CAACATCTGAGAA AGGGGGAAC AGGTGGAAC AGGTGGAAC AGGTGGAAC TCACTGAGGT AACTGGCAAC TCGACTGGCAAC TGGACTGGCAAC TGGACTGGCAAC GTGTTGTTTG TGAGAATGG GAAGAAGAA	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGAGG CCTGGGGGAG CCCCAGGTT CCAGGGGCTA CCAGACAATG AAAAGAAAA AAAGAAAAA AAAGGAAAA AGAGGTGAAT TAGAATGTAT TAGAATGTAT TAGAATGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC GGGAACTATG TCCTCCACTA ACATCAGTGGA ACCTGCACTAC CCCAGTTTTT TCCCACTA CCCAGTTTCT CCAGACTGGAG CCCAGTTTCT CCAGACTGGAG CCCAGTTTCT CCAGACTGGAG CCCAGTTGCT CAGCGACTGGAG CACGGACTGGAG CACGGACTGGAG CCCAGTTCG	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGACCTTGC ATGCTCCCA CACCCTGGCT CAGACCCCA CGCTCTGCT CAACAGCTC CAACAGCTTG ATTCGTCCTA CTGCTCTTTC GTGTCCTCTT GTGTCCTTTT GTGTCCTTT GTGTCCTTTT GTGTCCTTT CAACAGCTTG AAGATGGCAG AATCTTTTC GATTGCAGG AATCTTTTC GATGGCAGG AATCTTTTC GATAGCAGG AATCTTTTC GGGAACAGAG GATATATCTGT CCAAGCCCCA ACAATTGTGC AACACTCGCA AACACTTGT CCAAGCCCGCA ACAATTGTGC	120 180 240 300 360 420 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1680
50 55 60 65	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCCG GATCTTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGT AGTTTGGAT TGAAGTTTAAAAAT TGAGGGCAAC TGAAATTGGA TGAAATTGGA TCTTTCTCAGG AGGTCTAACTTTTCTCTCAGG AGGTGTCAGAT TTTTCTTCCAGG TCTTTGACTTTTTTCTTCAGG TCTTTTACTGGAT TTTTTCTCAGG TGAAATGGAA TGAAAGGGAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TTTCATGAAT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCCGCAGTT TCTGCCGGTA TCAAGAATGG AACTGATC TCCAGTGTT TCTGCCGGTA TCAAGAATGG AACTGAGCCT CTCATGGGA CAAGTATGTA CTCATCTT CTTATGGAGAG AAATAAGAA AGTGACAAGA GGAGAATACCTC GTTTGGCTCT GACAATACACA GGAAAATAGA	CCAGTGATGA CCAGTGATGA CCACTCACAT CATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG GTGTACAGAG GTCTCACGAG CATATCAAGC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTCCCATATTTT AGAGCCTGGA TTTGCCAAT TTTCCCAAT GACCATCAGA CGGTGCATCT ACTCCAGTAGC ACCATCAGA CGGTACATCT ACCACTAGA CGGTACATCT ACCACTAGA CGGTACATCT ACCACTACC ATTCCAACTA ATCCAGTATG GGATACAATG GGATACAATG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCCACACGG TCCTCACACGG TCCTCACACGG TCACACTTT ATCATATGCT CTACCATTTT TCAACATCTT CAACATCTGC TCAAGAGGATCTCCT CAACATCTGC CTAGAGAGCTCTT CAACATCTGC TCAAGAGCC TCAAGAGCACT TCACTGAAGAC GTGAAGCAGT ACTGGCAAC GTGAACAGT ACTGGACATGG ACTTGACAAC GTGTTGTTTG TGGAGAATGG GGAGAAGAG GAAAATAGAG GAAAATAGAG	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATGGGGGAG CCCCAGGAGG CCCCAGGGGT CCAGGGGCT CAAAAGAGGAAAA AAAAGAGAAAA AAAGGAAAAT AAAAGAGAAAA ACAGTGAGG CCTGTCATTG GAAGGCATTT TAGTATGTAT TACCAAAGC CCTTTAATCCA TAGCGGACTGC AGATAATGGG AGATAATGGG AGCTATATG TCCTCCACTA ACATCAGTGGA CCCAGTTTCT TCCTCAACTA CCTCTAAGCTG CCCAGTTTCT TCCTAAGCTG CCCAGTTTCT TCCTAAGCTG GAGCACTGG GAGACTAGC	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCCA ACCTTAGT GCCGGTCTCC CTGCTGCAG CGACCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCTCA CACCTCGCT CAACAGCTCCA CACCTGGCT CAACAGCTTC CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAG AATCTTTTC GATGGCATCA GGTAATTTA GGGAACAGAG GATATACTGT GCAACCGCCA CACAGCCCCC CAACAGCCCCC CAACAGCCCCC CAACAGCCCCC CAACAGCCCCC CAACAGCCCCC CAACAGCCCCC CAACAGCCCCC CCTATGCTACTC	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1260 1380 1440 1560 1560 1680 1740
50 55 60 65	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCCG GATCTTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGT AGTTTGGAT TGAAGTTTAAAAAT TGAGGGCAAC TGAAATTGGA TGAAATTGGA TCTTTCTCAGG AGGTCTAACTTTTCTCTCAGG AGGTGTCAGAT TTTTCTTCCAGG TCTTTGACTTTTTTCTTCAGG TCTTTTACTGGAT TTTTTCTCAGG TGAAATGGAA TGAAAGGGAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TCTTGAGCAA TTTCATGAAT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGAG AGACCTAATA TTTTGGAACT GGAGAAACCT TCCGCAGTT TCTGCCGGTA TCAAGAATGG AACTGATC TCCAGTGTT TCTGCCGGTA TCAAGAATGG AACTGAGCCT CTCATGGGA CAAGTATGTA CTCATCTT CTTATGGAGAG AAATAAGAA AGTGACAAGA GGAGAATACCTC GTTTGGCTCT GACAATACACA GGAAAATAGA	CCAGTGATGA CCAGTGATGA CCACTCACAT CATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG GTGTACAGAG GTCTCACGAG CATATCAAGC TTTGACAAAC TTTGACAAAC TTTGACAAAC TTCCCATATTTT AGAGCCTGGA TTTGCCAAT TTTCCCAAT GACCATCAGA CGGTGCATCT ACTCCAGTAGC ACCATCAGA CGGTACATCT ACCACTAGA CGGTACATCT ACCACTAGA CGGTACATCT ACCACTACC ATTCCAACTA ATCCAGTATG GGATACAATG GGATACAATG	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCCACACGG TCCTCACACGG TCCTCACACGG TCACACTTT ATCATATGCT CTACCATTTT TCAACATCTT CAACATCTGC TCAAGAGGATCTCCT CAACATCTGC CTAGAGAGCTCTT CAACATCTGC TCAAGAGCC TCAAGAGCACT TCACTGAAGAC GTGAAGCAGT ACTGGCAAC GTGAACAGT ACTGGACATGG ACTTGACAAC GTGTTGTTTG TGGAGAATGG GGAGAAGAG GAAAATAGAG GAAAATAGAG	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATGGGGGAG CCCCAGGAGG CCCCAGGGGT CCAGGGGCT CAAAAGAGGAAAA AAAAGAGAAAA AAAGGAAAAT AAAAGAGAAAA ACAGTGAGG CCTGTCATTG GAAGGCATTT TAGTATGTAT TACCAAAGC CCTTTAATCCA TAGCGGACTGC AGATAATGGG AGATAATGGG AGCTATATG TCCTCCACTA ACATCAGTGGA CCCAGTTTCT TCCTCAACTA CCTCTAAGCTG CCCAGTTTCT TCCTAAGCTG CCCAGTTTCT TCCTAAGCTG GAGCACTGG GAGACTAGC	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCCA CGCTGGCTCCC CTGCTGCAGCCCTTGG AAGGATTGCA GTGGGGACTT CCAGACCCTGG GTGGTCTCCAG CACCTTGGT CACCTGGCT CAACAGCTCAG CACCTTGGT ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG GATATATT GGGAACAGAG GATATACTGT GCAACCGCA GATATACTGT GCAACCGCA ACCATGTGC CAACCGCA CACTTTTC CATGGCACT CATGGCACT CATGGCACT CATGGCACT CATGGCACT CATGGCACT CATGGCACC CATGGCT CATGGCACC CTATGCTACT	120 180 240 300 360 420 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1680
50 55 60 65	AGTAGGAGG TGTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG AATCTCGG AATCCAGCC CCGGGACCGC CGGGACCGC GTAACGGATG TTAAGGCTA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATACAAT TGAGGACAAC TGAAATTGGA GGGCCAATCC GGAATTACGG TCTTGTGGT TTTACTGGAT TTTACTGGAT TCTTCCAGG AGGTTCAGA TGAGAGAGAT ACAAGGCGA TCTTGAGCAA TACCTGAGCT TCTTCAGCAA TACCTGAGAT CCTGAGAT CCTTGAGCAA TACCTGAAT CGGACAGACT	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATTA TCTGCAGTGT TCTGCCGGTA TCAGCATGTT TCTGCCGGTA TCAAGAATGG AACTGAGCT CCCAGTGGGA CAAGTATGTA CTCATCTCTT CTATCGAGG AAATGAAGAT AGTGACAGG GAGATACCTC GACAATACCA ATTAACTGAT GTTTAACTGAT GTTTAACTGAT GGAAAATACAC ATTAACTGAT GGAAAAATAGA GTTCCATTTTG	CCAGTGATGA CCAGTGATGA ACGTCTCCACTA GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGCAGACCCG GTGACACCAG GTCTACACCAG GTGTACAGCG GTGTACAGG CATATCAAGC GTGGAATTAT CAGCCAAACG GTCCCATATT TCTTTGACAAAG GTCCATATT AGAGCCTGA TTTGCCCAAT TCTCCTAGGA GGGACAGAGA GGGTACAGCA GGGGACAGAGA GGGGACAGCAT ACCATCAGA ACGATCAGCT ATTCCACTTATC ATTCTGATTA ATTCTGATATC ATTCTGATA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGC CCTCGGGCAC GTCCACAGG TCGTCACAGG TCGTCACAGG TCACAGTA AAGAGGATT ATCATATGCT CTATCAGAA TTCAAGAGT TCAACATGT CAACATCTGC TCAAGAGCTCTT CAACATCTGC TCAAGAGCACTT TCAACATGCA AAGGGCACT TCAAGAACACAC GTGAAGCACA TCGCAACTGGCA CTGAACAGCACA TCGACACTGC TCAAGAACACACA CGTGTTGTTTG TGAGAATGG GAAGAGAAGA	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCTGGGGGAG CCCCAGGGT CCAGGGCTA AAAAGAGTG AAAAGAATG AAAAGAATA GACGGTGGAG CCTGTCATTG GAAGGCATT TAGATGTAT TAGTCTGTAT CCTTTAATCCA TGGGGACTTGC GGGACTTGG GGGACTTGG GAGCCACTGG GATACCAACT GGTACCTGTG	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGC CGCGGTCTGC CTTGCTGCAG CGACCCTTAGC ATGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTCA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTTA ATTCGTCCTTT AGATGGAGG TGTCAGCAGG TGTCAGCAGG TGTCAGCAGG ACATTTTTC CATGGCATCA AGATGGAAC AGATTTTTC CATGGCATCA ATTCTTTTTC CATGGCATCA CATGATCTTTTC CATGACTCTA CGGAACTAGA CGTAATTTTC CAAAGCTCC CATATGTGC CTATGCTACT CATAATGTAC	120 180 240 300 360 480 540 660 720 780 900 900 1020 1260 1260 1260 1380 1440 1500 1620 1680 1740
50 55 60 65	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCCTGTGGCT TTTCTCAGG AGGTGTCAGA TGAGAGAGAT ACAAAGGCGA TCTTCAGCAA TATCCTGAAT GGGACAGACT TTTCTGAGCAA TATCCTGAAT TCCTGAGCAA TTTCTTGAGCAA TTTCTTGAGCAA TTTCTTGAGCAA TTTCTTGAGCAA TTTCTTGAGTAT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGCTCTGCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCCACAGTTT TCTGCCGGTA TCAAGAATGA TCAAGAATGA TCAAGAATGA CTCATCTCTT CTATGGAGAG AAATGAAGAT AGTGACAAG GAGATACTC GTTTGGCTCT GACAATACCC GTTTAGCTGT GACAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT GGAAAATACAC ATTAACTGAT CAATGTGTTT CAATGTGTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG CGAGACCAG GTCTTCACCAG GTCTTCACCAG GTCATCACACAG GTCTTCACAG GTCATCAGAC TTGACAAAC TTTGACAAAC TTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTCCCAAT GACCATCAGA GGGAGAAGAG GGGGATCCAG CGGTGCATC ACCATGGAT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT AATTCTAGAT CAACAGTGAT CAACAGTGAT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCCGGCAC CTCACACGG TCCTCGGCAC CTACCACTTT ATCATATGCT CTCTCAGAA ATGAGAGTTT TCAACATTT ATCATATGCT CTCTCAGAA ATGAGAGTCTCT CAACATCTT CAACATCTT CAACATCTGC CAAGTGGAAC AGGTGGAAC AGGTGGAAC TCACTGAGT TCACTGAAGT TGACAAC GTGTTGTTTG TGAGAATGG GAAATAGAG GATTTCTTCT TGTTTCTCA	ATCACATTTG CACGGCATC ATTTGCTTGC CAGGGCATC ATTTGCTTGC CAGGGGAGG CCCCAGGGG CCCCAGGGG CCAGGGGCTA CAGACAATG AAAAGAGGTAA AAAGGAAAA AAAGGAAAA AAAGGAATT TAGATCTGTAT TAGATCTGTAT TACCAAAGCC CTTTAATCCA TGCGGACTGC AGGCACTGC AGCCCTGAGG CCCAGTTTCT TCCTCACTG AGCCCTGAG CCCAGTTTCT TCCTAAGCT GAGCGACTGC GAGCGACTGG GAGCACTGG GCACAGGAA	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGACCCTAG CACCCTGGCT CAGCCCCA CGCCTCGCT CAACACCCCA CCCTTGCTTG CACCCTGCT CAACAGCTTG ATTCGTCCTA CTGCTCTTTTC GTGTCCTTTTC GTGTCCTTTTC GATTGCAGA AATCTTTTC GATTGCAGA AATCTTTTC GATAGCAGC AATCTTTTC GATAGCAGC CGCAACACCCC CATAGCCCC CATAGCCCCC CATAGCCCCC CATAGCCCCC CATAGCCCCC CATAATTGTC CTATATTGTAC AATGAATTGA AATGAATTGA	120 180 240 300 360 420 660 720 780 960 1080 1140 1260 1320 1340 1560 1680 1740 1860
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCACGCCC CCGGACCGC GATCTTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTTGGATG AGTTTGGATG CATCAGCTTT ATAATAAAT TGAGGGCAACC GGAATTACGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTCTTGAGT TTTTCTCCAGG AGGTGTTCAGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TTTTTACTGAAT GGGACAGACT TTTGAGAAT TGGACAA TTTTGAGAAT TGGACAA TTTTGAGAT TTTTTACTAAA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGT CTCCGCAGAG AGACCTAATC GGAGAAACCT TCTTGCAGC TCTCGCAGT TCTGCAGC TCAGCT TCTGCAGC CACATATGCA TCAAGAATGG AACTGATC TCTATGGAAT CTCATCTT CTTATGGAGC CAAGTATGTA CTCATCTT CTTATGGAGAG AAATAATGTA AGTGACAAGG GAGAATACCTC GTTTGGCTCT GACAATACAC GCAAATACAC CATTACTGTTT TGGTGTTTCA	CCAGTGATGA CCAGTGATGA CCAGTGATGA CCAGTGAGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG CGTACCAGAG GTCTTCACAGA CGTATCAAGC CTTGACAGAAC TTTGACAACA TTTGACAAACA TTTGACAAACA GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCCAAT CAGCCAAGAC GGAGAAGAAG CGGTGCATTC ACCATCAGA CGGTGCATTC ACCATCAGA CGGTACATCAAC GGTACAGC ACCATCAGA CGGTACATCAGA ACCAGTATG AATTCCAACT GGATACAGT AATTCAACT AATTCAACT AATTGATAA CAAGAGTGAT TAACTTGGTA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACTCTCGGCAC GTCCACACG TCCTCGGGACAC GTCTACATTT ATCATATGCT CTACATTTT TCAACATTGT CAACATCTGC TCAAGAGATCTCTC CAACATCTGC CTAGAGAGCTCTT CAACATCTGC TCAAGAGCACTCTCAAGAGCACTGGAAC AGGGTGGAAC AGGGTGGAAC GTGAACAGTGGAAC GTGACATGGC ACTTGACAAC GTGTTGTTTG TGGACAATGG GAATTGTTTC TGGAGAATGG GAATTCTTCACAAC GTGTTGTTTTG TGGAGAATGG GAATTCTTTCACAAC GTGTTTCTTTACAAC GTGTTTCTTTCACAAC GTAGTTACTTTCACAC GTAGTTACTTCACAC GTAGTTACTTCACAC GTAGTTACTTCACAC GTAGTTACTTCACAC GTAGTTACTTCACAC GTAGTTACTTCACAC GTAGTTACTTCAC GTAGTTACTTCAC GTAGTAACTT	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATGGGGGAG CCCCCAGGAG CCCCCAGGT CCAGGGGCTA CCAGGGGCTA AAAAGAGGAAAA GACGGTGGAG CCTGTCATTG GAAGGCATTT TAGTATGTAT TAGTCTGTAT TACCAAAGC CCTTTAATCCA TAGCGGACTGC AGATAATGGG AGCACTAGG AGCACTAGG AGCACTAGG AGCACTAGG CCCAGGAG CCCAGTTCT TCCTAAGCTG GAGCACTGG GAGCACTGG GATACCAAGC GCTACCTGTACCTG TGCCAGAGA ACCTTTACCTT	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GCAGCCCTTAG ATGGGGACTT CCAGACCCTA GTGGGGACTT CCAGACCCTGC CACCTGGCT CAACAGCTTC CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AGATCCCTGT AGATCGCAG ATTCTTTC GTGTCCTGT GATGGCAGC AACACTTTTC GATGGCACC GATGATTTT GGGAACAGAG GATATACTGT GCAACCGCG GTATGTATTA GCGAACAGC GTATGCTACT CATAATTGTAC AATGAATTGCA AACCATTAGAAAAA	120 180 240 300 360 420 540 660 720 780 960 1020 1140 1200 1380 1440 1560 1560 1680 1740 1800 1800 1920
50 55 60 65	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC CGTACGGATCG GTACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAACC TGAAATTGGA GGGCAATCC GGAATTACGG TTCTTCAGG AGGTGTCAGA TCTCTCAGG AGGTGTCAGA TCTCTCAGG AGGTGTCAGA TCTCTCAGAT TCTCTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT ACAAAGGCGA TCTTGAGAT ACAAAGGCGA TTTTGTAGAT AATCATCAAA ACATTAATGT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATTA TCAGCAGTTTT TCTGCCGGTA TCAGAGATGTTT TCTGCCGGTA CCAGTGTGTA TCAAGAATGG AAATGAGCAT CTCATCTCTT TCTATCGAGAG AAATGAAGAT AGTGACAAGG GAGAATACTC GTTTGGCTCT GACAATACAC ATTAACTGAT CTATAACTGAT GTTGCTCTT GACAATACAC ATTAACTGAT CGAAAATAGA GTTGCATTTT CAATGTTTTA TGGAAATAGA TGGATATTTA TGGTTTTCA AAGCCATATA	CCAGTGATGA ACGTCTCCAC GATTCGGGGG AGTGAGCAG ACTCACCAT ACTCCACCAT CGCTAGGTCG CCGCGCGC CGCAGACCCG GTGACCAGA GTCACACAG GTCACACAG GTGATCACGG GTGATCACGG GTGATCACGG GTGATCACG GTGCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGGA CCTTATTTTT AGAGCCTGGA TTTGCCCAAT ATTCCACTAGA GGGACACC ATTCCACTAGA GGGACACC ATTCCACTAGA ACCATGATA ACCATGGAT AATTCCAGTAT AATTCTATTA AATTCTGATA AATTGTGATA AATTGTGATA AACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCG CCAGGGGGGG CCAGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTACATCTT TCAACATCTC CAACTGGAACACTCT CAACATCTTC CAACTGGAACACTCT CAACATCTTC CAACTGGAACACT TGGACACGGACACACACACACACACACACACACACTCTCT TCACAATTGCAACT TGAACATCTTC TCAAGAATACACACACACACACACACACACACACACACAC	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCAGGGG TGCCCCAGGT TCCCCAGGGCT AAAAGAGGTG AAAAGAGGTG AAAAGAGTG AAAAGAATG AAAGAGATT TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TACAAAGC CTITAATCCA TGGGGACTGC AGATAATGGG AGCCACGAG ACCCTGGAG ACCCTGGAG ACCCTGCAACT TCCTAAGCTG GATACCAACT GCTACCATT TCCTAAGCTG GATACCAACT GCTACCTTA TCCTTACTTT TCCTAAGCTG GATACCAACT GCTACCTTT TCCTTACTTT TCCTAAGCTG TGCCAGAGAA ACCTTTACTTT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGTGGCTCC CAGCCTTAGC GCGGTCTGC CTTGCTGCAG CGACCCTTGGC ATGGGGACTT CCAGACCCCAG CTGCTCAG CGCCTCAGC CACCTGGCT CAAGACTCCA CACCTGGCT CAAGACTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG GTGTCACCTGT CAACAGCTTG CTAGCAGG GTGAATTTT GGAACAGGA GATATACTGT GCAAGCGCA ACAATTGTG CTATATGTACC CATAATGTAG AATGAATTG AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATACTC CATAATGTAG AATGAATACTC CATAATGAAAA ACTCCTTTTTGT	120 180 240 300 420 420 660 720 780 900 900 1020 1140 1260 1380 1440 1500 1620 1680 1740 1860 1980
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC CGTACGGATCG GTACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAACC TGAAATTGGA GGGCAATCC GGAATTACGG TTCTTCAGG AGGTGTCAGA TCTCTCAGG AGGTGTCAGA TCTCTCAGG AGGTGTCAGA TCTCTCAGAT TCTCTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT TCTTCAGAT ACAAAGGCGA TCTTGAGAT ACAAAGGCGA TTTTGTAGAT AATCATCAAA ACATTAATGT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATTA TCAGCAGTTTT TCTGCCGGTA TCAGAGATGTTT TCTGCCGGTA CCAGTGTGTA TCAAGAATGG AAATGAGCAT CTCATCTCTT TCTATCGAGAG AAATGAAGAT AGTGACAAGG GAGAATACTC GTTTGGCTCT GACAATACAC ATTAACTGAT CTATAACTGAT GTTGCTCTT GACAATACAC ATTAACTGAT CGAAAATAGA GTTGCATTTT CAATGTTTTA TGGAAATAGA TGGATATTTA TGGTTTTCA AAGCCATATA	CCAGTGATGA ACGTCTCCAC GATTCGGGGG AGTGAGCAG ACTCACCAT ACTCCACCAT CGCTAGGTCG CCGCGCGC CGCAGACCCG GTGACCAGA GTCACACAG GTCACACAG GTGATCACGG GTGATCACGG GTGATCACGG GTGATCACG GTGCAAACC TTTGACAAAG GTCCCATATT TCTCTTGGGA CCTTATTTTT AGAGCCTGGA TTTGCCCAAT ATTCCACTAGA GGGACACC ATTCCACTAGA GGGACACC ATTCCACTAGA ACCATGATA ACCATGGAT AATTCCAGTAT AATTCTATTA AATTCTGATA AATTGTGATA AATTGTGATA AACTTGGTA ACATGGGATT TAACTTGGTA ACATGGGATT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCG CCAGGGGGGG CCAGGGCGC CCTCGGGCAC GTCCACACGG TCGTGGCGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTACATCTT TCAACATCTC CAACTGGAACACTCT CAACATCTTC CAACTGGAACACTCT CAACATCTTC CAACTGGAACACT TGGACACGGACACACACACACACACACACACACACTCTCT TCACAATTGCAACT TGAACATCTTC TCAAGAATACACACACACACACACACACACACACACACAC	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCAGGGG TGCCCCAGGT TCCCCAGGGCT AAAAGAGGTG AAAAGAGGTG AAAAGAGTG AAAAGAATG AAAGAGATT TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TACAAAGC CTITAATCCA TGGGGACTGC AGATAATGGG AGCCACGAG ACCCTGGAG ACCCTGGAG ACCCTGCAACT TCCTAAGCTG GATACCAACT GCTACCATT TCCTAAGCTG GATACCAACT GCTACCTTA TCCTTACTTT TCCTAAGCTG GATACCAACT GCTACCTTT TCCTTACTTT TCCTAAGCTG TGCCAGAGAA ACCTTTACTTT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGTGGCTCC CAGCCTTAGC GCGGTCTGC CTTGCTGCAG CGACCCTTGGC ATGGGGACTT CCAGACCCCAG CTGCTCAG CGCCTCAGC CACCTGGCT CAAGACTCCA CACCTGGCT CAAGACTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG GTGTCACCTGT CAACAGCTTG CTAGCAGG GTGAATTTT GGAACAGGA GATATACTGT GCAAGCGCA ACAATTGTG CTATATGTACC CATAATGTAG AATGAATTG AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATTGA AATGAATACTC CATAATGTAG AATGAATACTC CATAATGAAAA ACTCCTTTTTGT	120 180 240 300 420 420 660 720 780 900 900 1020 1140 1260 1380 1440 1500 1620 1680 1740 1860 1980
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCAC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGACAC TGAAATTGG TACTCATTGG TACTCTTGAG GGGCCAATC GGAATTACGGT TTTTACTGGAT TCTTCAGG AGGTGTCAGA TGTTGAGAGAGAT TTTCTTGAG AGGTGTCAGA TCTTGAGCAA TCTTGAGTAAATGTAAAAAAAAAA	I TEGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTCGGAGAG TGATGCAATC GCCACGTGTA AGCCTCAGCT CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTATGCA TCCACAGTGTT TCTGCCGGTA TCAAGAATGA AACTATGCA TCAAGAATGG CACAGTGGAA AATGAAGATGGA CAATATCATCTT CTATGGAGAG GAGATACTCTT CTATGGAGAG GAGATACTCTT GCACATACCC GTTTGGCTCT GACAATACAC ATTAACTGAT GGAAAATAGA GTTGCATTT CGATTTTCCATTGCATTT TGCATTTT TGGTGTTTTC AAGCCATATA AGCCATATA	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CGCAGACCGC CGAGACCGG CGAGACCGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTATTCAAGG GTCACACAG GTCACACAG GTCATATT TCTCTTGGAG GTCACACAGA GTACACAGA GAGAAGAGAG GAGAGAGAGA GAGAGAGAGA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACAGGG CCACACGG TCCACAGG TCCACAGG TCACAGTA AAGGAGGATC CTACCATTT ATCATATGCT CTACATATGCT CAACATCTGC TCAACAGGAGACA AAGGAGGATC TCAACATCTGC TCAACATCTGC TCAACATCTGC TCAACATCTGC TCAACATCTGC TCAACATCTGC TCAACATCTGC TCAACATCTGC ACTTGACAAC AGGTGGAAC AGGTGGAAC TGGACCTGGC ACTTGACAAC TGGACATGGC GTGTTGTTTG TGGAGAATAGAG GAAATAAGAG GAAATAGAG GATTTCTTCA TGTTTCTTCA TTCCTCAATG TCTTTAATAT	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGCATC ATTTGCTTGC CGGGTCTGGGGAG CCCCGAGAGG TGCCCCAGGT CCAGGGGCT AAAGAGACAATG AAAGGAAAAA GACGGTGGAG CCTGTCATTG GAAGGCATT TAGATGTAT TAGTCTGTAT TACCAAAGCC CTTTAATCCA TGGGGACTGC AGATCATG GGGACTATG TCCTCCACTA ACATCAGTG TCCTCACTA ACATCAGTG GGGAACTATG TCCTCACTA ACATCAGTG GGGACTTGC GGGCCCTGGAG GCCCTGGAG GACCATCG GAGCCACTG GAGCCACTG GAGCCACTG GAGCCACTG GAGCCACTG GAGCCACTG GAGCCACTG TCCTACCTT TCCTAAGCTG TCCTACCTT TCCTAACCT TCCTACCTT TCCTACCTT TCCTACCTT TTCTTAGTGC AAGTTACATT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGC CGCGGTCTGC CTTGCTGCAG CGACCCTTAGC GAGCCCTAGC TGGTCCTCAG CACCCTGGCT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CAACAGCTTG ATTCGTCCTTA ATTCGTCCTTTTC ATTCGTCCTTTTC CATGCAGCAGG TGTCAGCAGG CATATCTTTTT CATGACTCTA CGTGAACTTA GGTGAACTTA CGTGAACTTA CGTAATCTTTC CTATATGTAC AATTGACT AATGAATTGC ACCTTAGTAG AATGAATTGC CTCTTTTTTC CTGCCTCTCA	120 180 240 360 420 660 720 780 900 900 1080 1120 1260 1380 1500 1560 1580 1620 1680 1740 1860 1920 1920
50 55 60 65 70	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTTGGATG AGTTTGGATG AGTTTGGATG CATCAGCTTT ATAATAAAAT TGAGGGCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TTCTCCAGG AGGTGTCAGA TGAGAGAGAT TCTCTCAGGAA TCTTCAGCAA TCTTTGAGCAA TCTTTGAGCAA TCTTTGAGCAA TCTTCAGCAA TCTTTGAGCAA TCTTTGAGCAA TCTTCAGCAA TCTTTGAGCAA TATCCTGAAT AGGACAGACT TTTGTTAGTAT AATCATCAAA ACATTAATGT ACTTCACTCA AACAAATGCA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATA TTTTGGAACT GGAGAAAACCT GGAGAAAACCT TCCACAGTGTT TCTGCCGGTA TCAAGAATGA TCAAGAATGA TCAAGAATGA TCAAGAATGCT CTATGGAGA AAATGAAGA AAATGAAGA GAGAATACCT GACAATAACT GAAAAATGA GGAAAATACT GGAAAATAGA GGTACATTC TCATGGAGAG AAATGAAGA CAATAACT GAAAATACTAAT TCAACTGTT TCATGAGAGA CAATAACT GAAAATAAT TCAATTGAAAT TCAATTGAATAAT TCAATTGAATAAT TCAATTGAATAAT TCAATTGAATAAT TCAATTGAATAAT TCAATTGATAAT TGGTGTTTCA AAGCCATATAA AATTTTTTTGTG	CCAGTGATGA ACCTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG CGAGACCAG GTCTTCACCAG GTCACACAG GTCACACAG GTCACACAG GTGAATTAT CAGCCAAACC TTTGACAAAG GTCCCATATTT AGAGCCTGGA TTTCCCACT AGCCATCAGA GGGAATAC ACCATCAGA GGGAATAC ATTCCACT ATTCACT ACATGGATT TAACTTGGTA ACATGGATT TAACTTGGTA ACATGGATTAT TGTGTTTTGAA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCACACGG TCTCACACGG TCTCACACGG TCTCACACGG TCTCACACTTT ATCATATGCT CTATCAGAA ATGAAGGATTC CAACTTTCACAATTT CAACATCTGC CAAGTGGAAC AGGTGGAAC AGGTGGAAC TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAAC GTGTTGTTTG TGAGAATGG GAAATAGAG GAAATAGAG GATTTCTTTTTTCTCAATG TTCTCAATG TCTTTAACAT TTCCTCAATG TCTTTAATAT AGCTAATTTG	ATCACATTTG CACGGGCATC ATTTGCTTGC CACGGGCATC ATTTGCTTGC CACGGGCAGAGG CCCCCAGGT CCACGGGGCTA CCACGGGCTA AAAAGAGAAA AAAAGAAAAA ACACTAAATT AGAGTGTATT TAGAATGTAT TACCAAAGC CTTTAATCCA TACCACAAA ACATCACTAC TCCCCAGTT TCCTCACTA ACATCAGTGG AGCCCTGGAG CCCAGTTTCT TCCTAAGCC TCCTAAGCC GCTACCTGG GATACCACT GCTACCTT ATTTTAGTGC AAGTTACCTT ATTTTAGTGC AAGTTACCTT ATTTTAGTGC AAGTTACATT ATTTTAGTGC AAGTTACATT ATTTTAGTGC AAGTTACATT AAAAAATTTC	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGGATTGCA GTGGGGACTT CCAGACCCCA TGGTCCTCAG CACCCTGGCT CACCCTGGT CACCCTGGT CACCCTGGT CACCCTGGT CACCCTGGT AAGACTTG ATTCGTCCTA ATTCGTCCTT GTGTCCTGT CAACAGCTTG AAGATGGAAT TGTCAGCAGG AATCTTTTC GATGCATCA GGTAATTTA GCAAGCCGC ACAATTGTGC GTATGTACT CATAATGTAC CTCTTAGTATTTGC CATAATGTAC CTCTTTTGT CATAATTTAC CTCTTTTGT CACCCTCAAAAAA CTCCTTTTTTC ATTAGCAAAA	120 180 240 300 360 420 660 720 780 960 1080 1140 1260 1320 1380 1560 1560 1740 1860 1920 1980 2010
50 55 60 65 70	AGTAGGAGG TGTTTATTC GATAGGACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGACCGC CGGACCGC GATCTGCCT GTAACGCATC GTAACGCATC GTAACGGATG AGTTTGGATG AGTTTGGATG AGTTTGGATG CATCAGCTTT ATAATAAAT TGAGGGCAACC GGAATTCGG TCCTTGAGG ACGTGTCAGA TCTTCACGGA TCTTCACGGA TCTTCACGAT TTTTCTCAGG ACGTGTCAGA TCTTCAGCAT TTTTGTGAGT TTTTTGAGAT TCTTCAGGA TCTTGAGCAA TCAAAAGGCAA CCAAAATGAA ACATTAATGT ACTTCACAA ACAAATGCA ATTCCTCAGA	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTGTTT TCTGCCGGTA TCAAGAATGG AACTGATGCA CTCATGCTG CTCAGCTCTCTCTCTTCTTCTATGCAGAT GAATATGAA AATGAAGAT GGTGATAACTAA ATTAACTGAT GGAAAATAGA GTTGCATTT CAATGATTTT GGAAAATAGA GTTGCATTTT AAGATATTTT AATGATTTT AAGCCATATA AAGCCATATA AAGCCATATA ATTTTTTTTTGTG CCTATCTTTTA ACTCTTTTA AAGCCATATA ATTTTTTTTTGTG CCTATCTTTTA	CCAGTGATGA ACCTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG GTGTACCAGAC GTCACACAG GTCTACACAG GTCTACAGAC CATATCAAGC GTGAAACC TTTGACAAAC GTCCCATATT TCTCTTGGAG CCTTATTTT AGACCTGAA TTTGCCCAAT TTTGCCCAAT ATTCCACAGA GGAGAACAC ACTTCAACAG GGAGACAGC ATTCCAACT ATTCCAGTAG GGATACAGT ACCAGTAGA ACCAGTAGT ATTCCAGTAT ACAGTAGT AATTCTGATA AATCAGTAT AATTGTGATA AATTGTGATA AATTGTGATA AATTGTATA AATTGTATA ACATGGGATT TAACTTGTAT ACATGGGAT TTGTTTTGAA TCCACAGAAA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CCTCGGGCAC GTCCACACGG TCGTGGCGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTGAAGGATTCTC CAACATCTT CAACATCTGC TCAGAGAGCC TCAAGAAGC TCAAGAGCACT TCAAGAAGCACTT TCAATGAGA AGGAGCAGAA AGGACAGAAG AGTTGTTTGTTG TGAGAATAGGA GTAGAATAGGA GTAGTTTTTTG TGAGAATAGAG GAAATAGAG GATTTCTTTC TGTTTCTTCA	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC CATGGGGGAG CCTCGAGGGGCAG CCCCAGGGGT AAAAGAGGTA AAAAGAGTG AAAAGAGTAT AAAAGAGTAT TAGATGTAT TAGATGTAT TACCAAAGC CTTTAATCCA TGGGGACTAC TGCGGACTACT TCCACTA ACATCAGTG AGCCCTGGAG CCCTGCATT TCCACTA ACATCAGTG TCCTCACTA ACATCAGTG AGCCCTGGAG CCCAGGAC CCCAGTTCT TCTTAATCCA ACATCAGTG AGCCCTGGAG CCCAGGAA ACCTTACCTT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGTGGCTCC CAGCCTTAGC GCGGTCTGC CTTGCTGCAG GCGGTCTGC GTGGGGACTT CCAGACCCTCAG CACCCTGGCT CAGACCCTCAG CACCCTGGCT CAACAGCTCAG CACCTTGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAGG GTTCAGCAGG GATATACTGT GCAACAGCTG GCAACAGCGCA ACAATTGTG GCAACAGCGCA ACAATTGTG CTATGGTCACT CATAATGTAC AATGAATTGC AATGAATTGC CATAGAAAA CTCCTTTTGT CTTTTGTCTCTCAAAAAA CTCCTTTTGT CATAGGTAAAA CTCCTTTTGT CAAGGCTCAC ACAAGACTTTT	120 180 240 300 420 600 720 780 960 1080 1140 1200 1380 1440 1560 1560 1680 1740 1800 1980 2040 2160
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC TGAAATTGGA TGCTTTACTGGAT GGGACAATC TGAAATTGGA TCCTGTGGCT TTTACTGGAT TTTCTTCAGG AGGTGTCAGA TCTTGAGAGAGAT TTTCTTCAGG AGGTGTCAGA TCTTGAGTAAATCTGAAT AATACAAAAAAAAAA	I TIGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCACGCGGG TGATGCAATC GCCACGTGTA AGCCTCAGCT CTCCGCAGAG AGACCTAATA TITTGGAACT GCACATATA TCAGCATGTTT TCTGCCGGTA TCAAGAATGA AACTATGTA CTCATCTTT CTATGAGAGA AAATGAAGAT ATTTTGGACT GACAATACTCTT CTATGAGAGA GAGATACTCT GTATGAGCT GCATATCACT GACAATACAC ATTAACTGAT CGATATACAC ATTAACTGAT TGGTGTTTC CAATGTTT TGGTGTTTT CAATGTTT TGGTGTTTTA AGCCATATA AGCCATATA AGTACTAAAT ATTTTTTTTTG CCTTTTTTTTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CGCAGACCGC CGAGACCGG CGAGACCGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTATTCAAGG GTCACACAG GTCACACAG GTCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GAGAAGAGAG GAGAGAGAGAG CATTCAACT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCAGTATG CATGGATT CAGGGGTT AACTTGGAT ACAGGGGTT AACTTGGAT ACAGGGGTT AACTTGGAT ACAGGGGTT TAGTTTTTAT AGTAGTTTTAT TGTGTTTTAT TGTGTTTTAT TCACAGAAA CACTGGTTTT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACAGGGCAC GTCCACAGG TCGACGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTACTCAGAA TTGAAGGATT CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTGC TCAAGAAGCTCTT CAACATCTGC TCAAGAAGCACTT TCACTGAAGT AACTGGCAAC GGGAGCAGA AGGAGAGAAGA GAAATAGAG GAAATAGAG GAAATAGAG GAATTCTTTG TGTTTTCTTCA TTCCTCAATG TTCCTCAATG TCTTTAATAT AGCTAATTTG TCTTTTAATAT AGCTAATTTG TTTTTTTTTT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGGAG CCCCGAGGGG TGCCCCAGGT CCAGGGGCTA AAAAGAGTG AAAAGAGTG AAAAGAATG AAAGAGTTAT TAGATGTAT TAGATGTAT TAGTCTGATT TCCTAAGCCG GGGAACTATG TCCTCCACTA ACATCAGTGG GGTACCAGTG TCCTAAGCT GAGCGACTGG GATACCAGT TCCTTAGCTG TGCCAGAGAA ACCTTACCTT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGC CGCAGCCTTAGC CGAGCCTTAGC CGAGCCTTAGC CGAGCCTTAGC CGAGCCCTAG CGCCCTGGCT CGAGGACTTC CAGGACCCCA CGCCTCGCC CAGGACTTG ATTCGTCCTA ATTCGTCCTTTC CAGAGCGCA AGATTGTC CGTGAACTTTTC CGTGAACTTTTC CGTGAACTTTTC CGTGAACTTTTTC CATGCCTCTTTTC CATGCCTCTA AGATGGCAC CATTCTTTTC CATGCACTC ATTCTTTTC CATGCACTC CATAGCATCA CATGCTCTC ATTAGCTACT ATTAGGTTAC ATTGGCTCCTC ATTAGGTTAC ATTGGCTCCTC ATTAGGTTACA CACAGCTTTT CTTCTCTCCTC ATTAGGTTACA CAAGACTTTT CTTTAGGTTAA	120 180 240 360 420 660 720 780 900 900 1080 11200 1260 1380 1500 1560 1680 1740 1620 1680 1740 1860 1920 2040 2040 2020 2020
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCCC CCGGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGCAAC TGAAATTGGA TGCTTTACTGGAT GGGACAATC TGAAATTGGA TCCTGTGGCT TTTACTGGAT TTTCTTCAGG AGGTGTCAGA TCTTGAGAGAGAT TTTCTTCAGG AGGTGTCAGA TCTTGAGTAAATCTGAAT AATACAAAAAAAAAA	I TIGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCACGCGGG TGATGCAATC GCCACGTGTA AGCCTCAGCT CTCCGCAGAG AGACCTAATA TITTGGAACT GCACATATA TCAGCATGTTT TCTGCCGGTA TCAAGAATGA AACTATGTA CTCATCTTT CTATGAGAGA AAATGAAGAT ATTTTGGACT GACAATACTCTT CTATGAGAGA GAGATACTCT GTATGAGCT GCATATCACT GACAATACAC ATTAACTGAT CGATATACAC ATTAACTGAT TGGTGTTTC CAATGTTT TGGTGTTTT CAATGTTT TGGTGTTTTA AGCCATATA AGCCATATA AGTACTAAAT ATTTTTTTTTG CCTTTTTTTTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT CGCTAGGTCG CGCAGACCGC CGAGACCGG CGAGACCGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTACACAGG GTATTCAAGG GTCACACAG GTCACACAG GTCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GAGAAGAGAG GAGAGAGAGAG CATTCAACT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCACTATT ATCCAGTATG CATGGATT CAGGGGTT AACTTGGAT ACAGGGGTT AACTTGGAT ACAGGGGTT AACTTGGAT ACAGGGGTT TAGTTTTTAT AGTAGTTTTAT TGTGTTTTAT TGTGTTTTAT TCACAGAAA CACTGGTTTT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGCGG CCACAGGG CCTCACAGG TCGACGG TCGACGG TCGACGG AAGGAGGATC TCACATTT ATCATATGCT CTACATTTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTC CAACATCTGC TCAAGAAGCTCTT CAACATCTGC TCAAGAAGCACTT TCACATCTGC TCAAGAAGCAGACA AGGTGGAAC AGGTGGAAC TGGACTGGC ACTTGACAAC TGGACATGG GAAGAGAAGA	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGGGGAG CCCCGAGGGG TGCCCCAGGT CCAGGGGCTA AAAAGAGTG AAAAGAGTG AAAAGAATG AAAGAGTTAT TAGATGTAT TAGATGTAT TAGTCTGATT TCCTAAGCTG GGGAACTATG TCCTCCACTA ACATCAGTGG GGTACCAGTG TCCTAAGCTG GATACCAGT TCCTAAGCTG TCCTAAGCTG GATACCAGT TTTTTAGTGC AAGTTACAT ACATTACAT ACTTACCTT TTTTTAGTGC AAGTTACAT CCAAGTCCGT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGTGGCTCC CAGCCTTAGC GCGGTCTGC CTTGCTGCAG GCGGTCTGC GTGGGGACTT CCAGACCCTCAG CACCCTGGCT CAGACCCTCAG CACCCTGGCT CAACAGCTCAG CACCTTGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AAGATGGAG TGTCAGCAGG GTTCAGCAGG GATATACTGT GCAACAGCTG GCAACAGCGCA ACAATTGTG GCAACAGCGCA ACAATTGTG CTATGGTCACT CATAATGTAC AATGAATTGC AATGAATTGC CATAGAAAA CTCCTTTTGT CTTTTGTCTCTCAAAAAA CTCCTTTTGT CATAGGTAAAA CTCCTTTTGT CAAGGCTCAC ACAAGACTTTT	120 180 240 300 420 600 720 780 960 1080 1140 1200 1380 1440 1560 1560 1680 1740 1800 1980 2040 2160
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATACGCAC CCTCTGCCT GAATCTTCGG GTCTTCCTGC AATCACGCCC CCGGACCGC GATCTTGCCT GTAACGGATG TTAACGCTAA ATAATCTGGT AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAAC TGAAATTGGA CATCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTTTCCTGAG AGGTGTCAGA TTTCTTCAGG AGGTGTCAGA TTTCTTCAGG AGGACAGACT TTTGTTAGTAT AATCATCAAA ACATTAATGT ACTTCAGCAA TATCCTGCAG AAACACGGA AACACAGCG TTTCCTCAGA AACACAGCA TTTCCTGCAG AACACAGCA TTTCCTGCAG AACACAGCA TTTCCTCCAGA AACACAGCA TTTCCTCCAGA AACACAGCA TTTCCTCCAGA AACACAGCA TTTCCTCCAGA AACACACGGA AACACAGGA AACACAGGA AACACAGGA AACACAGGA AATTCCTGTTT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGCTCAGCT CTCCGCAGAG AGACCTAATA ATTTTGGAACT GCACTATTT TCTGCCGGTA TCTAGAGATGC CTCAGCT CCCAGTGTA AATGAAGCT CCAGTGTT TCTGCCGGTA TCTAGAGATGC CCAGTGGGA AATTATGTA CTCATCTCTT CTATGGAGAG AAATGAAGA AATGAAAGA CTCATCTCTT GACAATACCC GTTTGGCTCT GACAATACCT ATTAACTGAT GGAAATACT CATTAACTGAT TGGTGTTTC AAGCCATATA AGTGCTAAAT ATTTTTTGTG CCTATCTTTA ATTTTTTTGTG CCTATCTTTA ATTTTTTTTGTG CCTATCTTAA TTCCTCCCAT TCTTCCTGAT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGAGACCCG CGAGACCCG CGAGACCAG GTCTTCACCAG GTCTTCACCAG GTCTTCACAG GTCATCAGC CATATTCAGC CTTGACAAAA GTCCCATATT TCTCTTGGAG CCGTACTTTT AGAGCCTGGA TTTCCAATAT GACCATAGA GGAGAAGAG GGAGAAGAG CGGTGCATTC ACTCAGAT ATTCCAATAT ATTCCAATAT AATCCAGTATG AATTGTGAT ACATGGGAT TAACTTGGTA ACATGGATT TAGTAGTTTTGA ACTTGGTA ACATGGATT TAGTAGTTTTTGAA CCACAGAAA CACTGTTTTT GTCACAGCCCT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCGGCAC CTCACACGG TCTCACACGG TCTCACACGG TCTCACACGG TCTTCAGAA ATGAGAGTTT CAACATTTT CAACATCTT CAACATCTT CAACATCTGC CAAGTGGAAC AGGTGGAAC AGGTGGAAC TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAGT TCACTGAAC GTGTTGTTTG TGAGAATGG GAAATAGAG GATTTCTTCA GTAGTTCTTCAATG TTCTCAATG TCTTCAATG TCTTCATTCAATG TCTTTACTAATT TCCTCAATG TCTTTTCTCAATG TCTTTTACATT TCCTCAATG TCTTTTACTATTT TCACTGATTTCTTCAATG TCTTTTAATAT AGCTAATTTG GTGTTTTCTT TGAAGGTCCT GAGCATACTC GAGCATACTC GAGCATACTC	ATCACATTTG CACGGGCATC ATTTGCTTGC CACGGGCATC ATTTGCTTGC CACGGGGAG CCCCCAGGT CCACGGGGCT CCACGGGGCT CCACGGGGCT AAAGACAATG AAAAGAAAA ACACGAAATT TAGAATGTAT TACCAAAGCC CTTTAATCCA TACCACAAAGC CCAGTTTC TCCCACTA ACATCACTGG ACCCTGGAG CCCAGTTTCT TCCTAAGCC TCCCAGTTTC TCCTAAGCC TCCCAGTTTCT TCCTAAGCC TCCCAGTTTCT TCCTAAGCT ACACTGGAACCTGC ACCCTGGAGAACCTGC AACTTACCTT ATTTTTAATCC TTTTTTTTAATT CCAAGTCCGT TCCACTAAGTCCT TCTTAACCTT TTTTTTTTAATT TCTTTTTTTAATTCC TCCAGTCGT TCCAGTCCTT TCCAGTCCTT TCCAGTCCTT TCCTAAGTCCTT TCTTTTTTTTAATTC TCCAAGTCCTT TCCAAGTCCCTT TCCAGTCCTT TCCAAGTCCCTT TCTGCCATTAG	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGACTCCA GTGGGACCCTAG GTGGGACCTCAG CACCCTGGCT CAGACCCCA CGCTCTGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA ATTCGTCCTA CTGCTCTTTC GTGTCCCTGT CAACAGCTTG CAACAGCTTG CATTCGTCCTA CTGCTCTTTTC GTGTCCCTGT CATAGCAGC CATATGTGC CATATGTGC CTATGCTACT CATAATGTGC CTATGCTACT CATAATGTAC CCCTTTTGC CATAATGTCC CATAATGTCC CATAATGTCC CATAATGTCC CATAATGTCC CATAATGTCC CATAATGTCC CATAGCTTCT CTGCTCCTCC ATAGGTTAC CAAGACTTTT CTGCTCCTCC CAAGACTTGT CTGCTCCTCC CAAGACCTGA GAAGACCTTG	120 180 240 360 420 660 720 780 960 1080 1140 1260 1320 1500 1560 1560 1740 1890 1920 1920 2160 2280
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATACGCACC CCTCTGCCT GAATCTTCGG GTCTTCCTGC ATCCAGCCC CCGGACCCG GATCTTGCCT GTAACGGATC GTAACGGATC TTAAGGCTAA ATAATTGGT AGTTTGGAT TGAGGGCAAC TGAAATTGGA CATTCATTGG TACTCTTGAG GGGCCAATCC GGAATTACGG TCTCTTGAGA ACGAATACGG TTTTACTGGAT TTTACTGGAT TTTTCTCCAGG AGGTGTCAGA TGAGAGAGAT TTTTGTAGTA ACAAAGGCGA TCTTGAGCA TTTTGTAGTA ACAAATGCA ACAAAATGCA ACTTCATCAA ACAAATGCA ACTTCATCAA ACAAATGCA ATTTCTTCAGAG ACTTCATCAA ACAAATGCA ATTTCTTCAGAG AACAATGCA ATTTCTTCAGAG AACAATGCA ATTTCCTGCAG AAAACTGCAT TTTCTTCAGAG AAAACTGCAT TTTCTTCAGAT ATTCTTCTTCTGTGTT TTTCTTGCAG AACAATGCA ATTCTCTTCAGGAAACTGCAT TTTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTCTAGAT TTTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCTTCTAGTT TTCCTTCCTGCAG AAAACTGCATTCCT TTTCCTTCTTCTTCTT TGTCCATTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGA AGACCTAATA TTTTGGAACT GGAGAAACCT TCGCCGGTA TCAAGAATGA ACACTATTA TCTGCCGGTA CCAGTGTAT TCTGCCGGTA TCAAGAATGG AACTGAGCCT CCCAGTGGGA CAAGTATGTA CTCATCTCT TTATGGAGAG AAATGAAGAT GGAGAATACTC GTTTGGCTCT GACAATACAC GTTTGGCTCT GACAATACAC GTTTGGCTCT AAGAATTGA GATAACTTGA TTTAACTGAT TTTAACTGAT TTCTCTCATTA TTCTTCCTCAT TCCTCCATT TCCTCCATT TCTCCCGTAT CCACATTCCTCT TCTCCTGAT CCACATTCTCT TCCTCCATT TCTCCCCAT TCTCCTGAT CCACATTCTC	CCAGTGATGA ACCTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGACCCG GTGTACCAGAG GTCTCACCAG GTGTACAGAG GTCTCACGAACC TTTGACAAAC TTTGACAAAC GTCCCATATTTT AGAGCCTAATTTT AGAGCCTGGA TTTGCCAAT GACCATCAGA GGAGAAGAG GGTACATCTGGAG GGAGAAGAG GGAGAAGAGAGAGAGAGAGAGAGA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CGAGTCTCCG CTCCGGGCAC GTCCACACGG TCGTGGCGGA AAGGAGGATC CTACCATTTT ATCATATGCT CTCTTCAGAA TTGAAGGATTTCAACATCTGC CAACTGGACACGG TCAGAGAGC TCAGAGAGC TCAGAGAGC TCAGAGAGC GTGAAGCAGT TCACTGAGA AGGTGGAAC GTGACTGGC ACTTGACAAC GTGTTGTTTG TGGAGAATGG GAATTGGT TCATTGATTTC TTGAGATTTCTTC TGGAGAATGG GAATTTCTTCA GTGTTTCTTCA GTGTTTCTTCA GTGTTTTCTT TGAAGGTCCT TGGAGATTGG GTGTTTCTTT TGAAGGTCCT TGGAGATTGG TCTTTTAATAT TCCTCAATG TCTTTTAATAT TGGAGATTTCT TGAAGGTCCT TGGAGCATCT TGGAGCATCT TTGAAGGTCCT TGGAGCATCT TGGAGCATCT TGGAGCATCT TGGAGCATCT TGGAGGTCCT TTATTATTAT TGGAGGTCCT TTGGAGGTCCT TTATTATTAT	ATCACATTTG CACGGGCATC ATTTGCTTGC CGGGTCTGGG CCTGGGGGGAG CCCCCAGGGT CCACGGGGTA AAAAGAGTG AAAAGAGAAAA GACGGTACTGAG CCTGTCATTG GAAGCATTT TAGATGTAT TACCAAGCC CTTTAATCCA AGATAATGGA GGGAACTATG GGAACTATG TCCTCACTA ACATCAGTGG CCCTGTACTTG TCCTCACTA ACATCAGTGG CCCAGTTCT TCCTAAGCTG GAGCACTGC GAGACTACT TCCTCACTA ACATCAGTGG AGCCTGGAG CCCAGTTTCT TCCTAACTG TCCTCACTA ACATCAGTGG AGCCTTGCACTA TTTTTAGTGC AAGTTACTT ATTTTAGTGC AAGTTACTT TTTTTTAAAT CCAAGTCCGT TGCAAGTACT TTTTTTAAAT CCAAGTCCGT TTTTTTAAAT CCAAGTCCGT TTTTTTAAAT CCAAGTCCGT TTTTTTAAAT CCAAGTCCGT TTTTTTAAAT CCAAGTCCGT TTTTTTAAAT CCAAGTCCGT TTTTTTAATT CCAGCTGCT TCTTGCATTAG CTGCCTGCT TCTGCATTAG CTGCCTGCCT TCTGCATTAG CCTGCCTGCT TCTGCTTACTT TTTTTTAAAT CCAAGTCCGT TCTGCCTTGCT TCTGCCTTGCT TTTTTTAATT CCAGCTGCCT	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCCA ACACTGGCTCC CAGCCTTAGT GCCGGTCTCC CTGCTGCAG ATGGGGACTT CCAGACCCTGG GTGGGGACTT CCAGACCCCAG CCCTGGCT CAACAGCTCAG CACCTGGCT CAACAGCTTG ATTCGTCCTT AGAGAGGTTG ATTCGTCCTT AGAGAGGAGA CTGTCAGCAG GATATACTGT GCGAACAGAG GATATACTGT CATAATGTAG AATGATTGC CATAATGTAG AATGATTTG CATGATTTGCTCTT CATAATGTAG AATGATTGCACTCT CATAATGTAG AATGATTTGC CATGATTTGCTCCTCA AATGATTGC CCTCTTTGT CTTTTGTCTCTCTC CATAATGTAG AATGATTTGC CATGATATACTGC CATGATTTTC CATAATGTAG AATGATTTGC CACTGGAAAA CTCCTTTTGT CTGTCCCTCA CAAGACCTTT GTTAAGGTAA GAGACCTGA GTCAGGCAGA GTCAGGCAGA	120 180 240 360 420 540 660 720 780 960 1080 1140 1200 1380 1440 1560 1740 1680 1740 1980 2010 2010 2010 2010 2010 2010 2010 20
50 55 60 65 70	AGTAGGAGG TGTTTATTTC GATAGGACC CCTCTGGCCT GAATCTTCGG GTCTTCCTGC AATCCAGCCC CCGGAACCGC CGGAACCGC GATCTGCCT GTAACGGATG TTAAGGCTAA ATAATCTGGT AGTTTGGATG CATCAGCATT ATAATAAAAT TGAGGGCAACCC GGAATTCGGG GGGCCAATCC GGAATTACGG TTCTTCTGAG AGGTGTCAGA TCTCTGAGT TCTTCAGGA TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGGAT TCTTCAGAT ACAAAGACAGAT ACATTAATGT ACTTCATTAG ACAAAATGCA ACAATTAATGT ACTTCACTGAAT ACTTCACTGAAT ACTTCACTGAAT ACTTCACTGA ACAAATGCA ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCCTGCAG AAAACTGGAT ATTCTTCTCGCAG AAAACTGGAT ATTCTGTATTC CTGCATTCC TTCACACACACTC TTCACACACACTC TTCACACACA	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGAG AGACCTAATA TTTTGGAACT GCACTGTT TCTGCCGGTA TCAGAGTGTT TCTGCCGGTA TCAAGAATGG AAATGAGCT CTCATCTCTT TCTATCCAGCT CTCATCTCTT GACAATACA AAATGAGAT AGTGACAGG GAGATACTC GACAATACAC ATTAACTGAT TCATCCTCT GACAATATGA AGTGACATG CCATTTTC CAATGTTT CAATGATTT CAATGATTT CAATGATTT CAATGATTT CAATGATTT CAATGATTT CAATGATTT CAATGATT TCTTCCCAT TCTTCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCTTCCCCAT TCCTCCCAT AGGGTCTTGT	CCAGTGATGA ACCTCTCCAT GATTCGGGGG AGTGAGCAG ACTGCACCAT CGCTAGGTCG CCGCAGACCCG CGCAGACCCG CGCAGACCCG GTGACCAGAC GTGACACAG GTCTACAGAG GTCTACAGAG GTCTACAGAG GTCCCATATT TCTCTTGGAC GCCTATATTT AGAGCCTGA CCTTATTTT AGAGCAGAA CCGTGCATAC ATTCCACTAG GGTACATAGA GGTACATCAGA GGATACAGA ACCTGTTTCACAGA ATTCCAGTATT ATTCCAGTATT AGAGATGAT ATTCCAGTATT AGAGATGAT TAACTTGGTA ACATGGGATT AGTAGTTTTAACAGAAA CACTGTTTTT GTCACAGAAA CACTGTTTTT GTCACAGAAA CACTGTTTTT CTTTCCACAT ACCACAGAAA CACTGTTTTT CTTTCCACAT GCCTTATAGA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGG CCACACGG CCTCACACGG TCGTGGCGA AAGGAGGAT ATACATTTT ATCATATGCT CTACATTTT TCAACATCTT CAACATCTC CAACATCTT CAACATCTGC TCAAGAGC TCAAGAGC TCAAGAGCACT TCAAGAGCACT TCAAGAGCACT TCAAGAGCACT TCAAGAGCACT TCAAGAGCACT TCACATGCAAC AGGTGGAAC AGGTGGAAC AGTGTTTTTT TCACATGC ACTTTTTTT TCACATGC TCAAGTACAC GTGTTTTTTT TCTCAAGT TCTTTTTT TCCTCAATG TCTTTTAATAT AGCTAATTTG TGTTTTTCT TGAAGGTCCT TCAAGTACT TTTTTTTTTT	ATCACATTTG CACGGCATC ATTTGCTTGC CACGGCATC ATTTGCTTGC CGGSTCTGGG CCTGGGGGAG CCCCAGGGG TGCCCCAGGT CCAGGGCTA AAAGAGGTG AAAAGAGTG AAAGAGATG AAAGAGTT TAGAATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGATGTAT TAGTCTGATTG GAGACACTG GCGACACTG GCGACTACG GGGACTACG GCTACCACTA ACATCAGTGG AGCCACGAG AGCCACGAG TCCTACACTA CAATCAGTGG AGCCACTGAG TCCTACACTT TCCTAAGCTG GATACCAACT GCTACCTT TCTTAGTCC TTCTTTAGTCC TTTTTTTAGTC TTTTTTAGTC TTTTTTAGTC TTTTTTAGTC TTTTTTAGTC TTTTTTAGTC TTTTTTAAT CCAAGTCCGT TTTTTTAAT CCAAGTCCGT TGTGCATTAG CTGCCTGCT CCCCATGGCT CCCCATGGCT CCCCATGGCT	ACCTCTGATC CCCACACTCG AACACTGGCA ACACTGGCA CGCTGGCTCC CAGCCTTAGC GCCGGTCTGC CTTGCTGCAG CGACCCTTAGC GTGGGGACTT CCAGACCCCCA GTGGGGACTT CCAGACCCCCA CACCTGGCT CAACAGCTCC ATTCGTCCTCA ATTCGTCCTT AAGATGGAG GTGACTTT GTAAGCAGA GATATACTGT CCTAGAACCCCA ACAATTGTGC CTATGATACTAC CTCTCTTTT GCAAGCCGCA ACAATTGTGC CTATGATACTAC CTCTCTTTTT CTATATGTAC ATTGGTTAC CTCTTTTTTTTTT	120 180 240 360 480 660 720 780 900 900 1020 1260 1260 1260 1260 1560 1680 1740 1680 1740 2040 2040 2280 2340 2340
50 55 60 65 70	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCCC CGGGACCGC GATCTTGCCT GTAACGGATA TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTTGGATG AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAATCC GGAATTACGG TACTCTTGAG GGGCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TTCCTCAGG AGGTGTCAGA TGAGAGAGAT TTCTTCAGGAA TATCCTGAAT ACAAAGCCGA TTTTGTTAGTAT AATCATCAAA ACATAATGT ACTTCACTCA AACAAGTCGA TATCCTGCAG TATCCTGCAG AAACTCGGAT AATTCTGTTT GTGCATTTCC TACAAGACT TTCCTTCAGG AAACTCGGAT ATTCCTGTTT GTGCATTTCC TACAAGACT TACAGACT TACAAGACT TACAAGACT TACAAGACT TACAAGACT TACAAGACT AGGTACTCAG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATC GCCACGTGTA AGACCTAATC GCACATGTAT TCTGCAGCT GCACTATGCA TCAAGAATGC TCAAGAATGC TCAAGAATGC CCCAGTGGA AATTATGCAGC CCAGTGGA AATTATGT TCTGCCGGTA TCAAGAATGG AAATTATGTA CTCATCTCT CTATGGAGAG AAATGAAGA GATATCCT GACAATACCT GACAATACCT GACAATACT GGAAAATGAA GGTGCTACT TCATCGATT TCATCCTATCATTT TGGTGTTTC AAGCCATATA AGTTACTAAAT ATTTTTTGTG CCTATCTTTA TCTCCCCAT TTAATGGTTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG CGAGACCAG GTCTTCACCAG GTCACACAG GTCACACAG GTCATCAGGAG CTTTGACAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTCCACT ACCATCAGA GGAGAAGAG GGAGAAGAG CGGTGCATT ACTCCACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCACT TAGCTGTA CACTGGTAT TACTCACT TACTCACAC CATTGTTT TACTCACAC CACTGTTTT TGTCACACAGAA CCACTGTTTT TGTCACACACC CTTTCCACAT TCCACAGAAA CCACTGTTTTT GTCACAGCCCT CTTTCCACAT TGTCACAGCCT CTTTCCACAT TGTCACAGCCT CTTTCCACAT TGCCTTATAGAT TTTACACAT TTTACACACAT TTTACACAT TTTACACAT TTTACACAT TTTACACAT TTTACACACAT TTTACACACAC	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCGGCAC CTCACACGG TCTCACACGG TCTCACACGG TCTTCAGAA ATGAAGACTCTT CAACATTTT CAACATTGAAGACT CTACATGAA AAGAGCTCTT CAACATCTGC CAAGTGGAAC AAGGTGAAC TGGACATGGC ACTTGACAAC GTGATGTTTTTG TGAGAATGG GAAAATAGAG GATTTCTTCT TTCCTCAATG TCTTCTCAATG GTGTTTCTTCACAC GTGTTTCTTCT GTAGTAACTT TTCCTCAATG GTAGTTCTTCT TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG TCTTTTACTAC TTTCTTCATCAC GTGTTTCTTC TTCCTCAATG TCTTTTCTCA TTTCTTCATCC TATGTTTCTC TTTCTTCATCC TATGTTTCTC TTTCTTCTC TTTCTTCTC TTTCTTCTC TTTCTTC	ATCACATTTG CACGGGCATC ATTTGCTTGC CACGGGCATC ATTTGCTTGC CACGGGCATC CACGGGGAGG CCCCCAGGT CCACGGGGCT CCACGGGGCT CCACGGGGCT AAAAGAGGAA AAAGGAAAA ACACTATT TAGAATGTAT TACCAAAGC CTTTAATCCA TACCACAAA ACATCACTGG GGAACTTT TCCTCCACTA ACATCACTGG GGAACTTTC TCCTCACTA ACATCAGTGG AGCCCTGGAG CCCAGTTTCT TCCTAAGCC TTCTAACCTG TACCTGGAACTTC TCCTAAGCT CACTACTTT TCTTAACTAC CACTACTTT TCTTAACTAC AACTTCCTT ATTTTTAATGC AAGTTCCTT TTTTTTTAATT CCAAGTCCGT TCTGCCTCGT TCTGCTCCTT TCTGCTCCTT TCTGCTCCTT TCTGCTCCTT TCTGCTTCTT TTTTTTAATTC TCCACTGCT TCCCACTGCT TCCCACTGCT TCCCACTGCT TCTGCCCATTGCT TCTGCCCATGCT TCTGCCTCCT TCTCCCACTGCT TTTTCCTTCTA	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCA ACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGACTCCA GTGGGACCTTGC AGGCCTCAG CACCCTGGCT CAGACCCCA GGTCTCTCGC CACCCTGGCT CAACAGCTTC CAACAGCTTG ATTCGTCCTA ATTCGTCCTT GTGTCCCTG AAGATGGCAG AATCTTTTC GATTGCACCAC CATACTTTTC GATTGCACCCA ATACTTTTC GATTGCACCCA ATACTTTTC CATAATGTAC CATAATGTAC CACCTTAGAAAA CTCCTTTTGT CATAATGTAC CACTAGAAAA CTCCTTTTGT CTGCTCCTCA ATAGGTTAC CAGACCTGA ATAGGTTACA CAGACCTGA GTCAGCTGA CTGCTCCTCA ATAGGTTACA CAAGACTTTT GTTAAGGTTAC GAAGACTTGT GTTAAGGTTAC GACATATAGT GGAAGCCTGA GGCACATATAGTTAC GGCACC GACATATAGTTA	120 180 240 360 420 540 660 720 780 960 1080 1140 1200 1380 1440 1560 1560 1740 1860 1980 2210 2210 22340 2340
50 55 60 65 70 75	AGTAGGAGG TGTTTATTC GATACGCAC CCTCTGCCT GAATCTCGG GTCTTCCTGC AATCACGCCC CGGGACCGC GATCTTGCCT GTAACGGATA TTAAGGCTAA ATAATCTGGT AGTTTGGATG AGTTTGGATG AGTTTGGATG CATCAGCTT ATAATAAAAT TGAGGGCAATCC GGAATTACGG TACTCTTGAG GGGCAATCC GGAATTACGG TCCTGTGGCT TTTACTGGAT TTCCTCAGG AGGTGTCAGA TGAGAGAGAT TTCTTCAGGAA TATCCTGAAT ACAAAGCCGA TTTTGTTAGTAT AATCATCAAA ACATAATGT ACTTCACTCA AACAAGTCGA TATCCTGCAG TATCCTGCAG AAACTCGGAT AATTCTGTTT GTGCATTTCC TACAAGACT TTCCTTCAGG AAACTCGGAT ATTCCTGTTT GTGCATTTCC TACAAGACT TACAGACT TACAAGACT TACAAGACT TACAAGACT TACAAGACT TACAAGACT AGGTACTCAG	TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA AGACCTAATC GCCACGTGTA AGACCTAATC GCACATGTAT TCTGCAGCT GCACTATGCA TCAAGAATGC TCAAGAATGC TCAAGAATGC CCCAGTGGA AATTATGCAGC CCAGTGGA AATTATGT TCTGCCGGTA TCAAGAATGG AAATTATGTA CTCATCTCT CTATGGAGAG AAATGAAGA GATATCCT GACAATACCT GACAATACCT GACAATACT GGAAAATGAA GGTGCTACT TCATCGATT TCATCCTATCATTT TGGTGTTTC AAGCCATATA AGTTACTAAAT ATTTTTTGTG CCTATCTTTA TCTCCCCAT TTAATGGTTTT	CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CTCGCCGCCG CGAGACCCG CGAGACCCG CGAGACCAG GTCTTCACCAG GTCACACAG GTCACACAG GTCATCAGGAG CTTTGACAAG GTCCCATATT TCTCTTGGAG CCTTATTTT AGAGCCTGGA TTTCCACT ACCATCAGA GGAGAAGAG GGAGAAGAG CATCAGAT GACCATCAGA CCGTGCATT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCAACT ATTCCACACT ATTCCACACT TAACTTGGAG CACTGGTTTT CAGCTGTT TACTTGTA CCACAGAAA CCACTGGTTTT TGTCTTTGAA CCCTGTTTTT GTCACAGCCT CTTTCCACAT TCCACAGAAA CCCTGTTTTT GTCACAGCCT CTTTCCACAT TGTCACAGCCT CTTTCCACAT TGTCACAGAAT TCCACAGAAA CACTGTTTTT GTCACAGCCT CTTTCCACAT TGTCTCACAT TGTCACAGAAT TCCACAGAAT TCCACAGAAT TCCACAGAAT TCCACAGAAT TCCACAGCCT CTTTCCACAT TCCACAGAAT TCCACA	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGCGC CCTCGGGCAC CTCACACGG TCCTCGGCAC CTCACACGG TCTCACACGG TCTCACACGG TCTTCAGAA ATGAAGACTCTT CAACATTTT CAACATTGAAGACT CTACATGAA AAGAGCTCTT CAACATCTGC CAAGTGGAAC AAGGTGAAC TGGACATGGC ACTTGACAAC GTGATGTTTTTG TGAGAATGG GAAAATAGAG GATTTCTTCT TTCCTCAATG TCTTCTCAATG GTGTTTCTTCACAC GTGTTTCTTCT GTAGTAACTT TTCCTCAATG GTAGTTCTTCT TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG GTGTTTCTTC TTCCTCAATG TCTTTTACTAC TTTCTTCATCAC GTGTTTCTTC TTCCTCAATG TCTTTTCTCA TTTCTTCATCC TATGTTTCTC TTTCTTCATCC TATGTTTCTC TTTCTTCTC TTTCTTCTC TTTCTTCTC TTTCTTC	ATCACATTTG CACGGGCATC ATTTGCTTGC CACGGGCATC ATTTGCTTGC CACGGGCATC CACGGGGAGG CCCCCAGGT CCACGGGGCT CCACGGGGCT CCACGGGGCT AAAAGAGGAA AAAGGAAAA ACACTATT TAGAATGTAT TACCAAAGC CTTTAATCCA TACCACAAA ACATCACTGG GGAACTTT TCCTCCACTA ACATCACTGG GGAACTTTC TCCTCACTA ACATCAGTGG AGCCCTGGAG CCCAGTTTCT TCCTAAGCC TTCTAACCTG TACCTGGAACTTC TCCTAAGCT CACTACTTT TCTTAACTAC CACTACTTT TCTTAACTAC AACTTCCTT ATTTTTAATGC AAGTTCCTT TTTTTTTAATT CCAAGTCCGT TCTGCCTCGT TCTGCTCCTT TCTGCTCCTT TCTGCTCCTT TCTGCTCCTT TCTGCTTCTT TTTTTTAATTC TCCACTGCT TCCCACTGCT TCCCACTGCT TCCCACTGCT TCTGCCCATTGCT TCTGCCCATGCT TCTGCCTCCT TCTCCCACTGCT TTTTCCTTCTA	ACCTCTGATC CCCACACTCG AACACTGCA ACACTGCA ACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC CAGCCCTTGC AAGACTCCA GTGGGACCTTGC AGGCCTCAG CACCCTGGCT CAGACCCCA GGTCTCTCGC CACCCTGGCT CAACAGCTTC CAACAGCTTG ATTCGTCCTA ATTCGTCCTT GTGTCCCTG AAGATGGCAG AATCTTTTC GATTGCACCAC CATACTTTTC GATTGCACCCA ATACTTTTC GATTGCACCCA ATACTTTTC CATAATGTAC CATAATGTAC CACCTTAGAAAA CTCCTTTTGT CATAATGTAC CACTAGAAAA CTCCTTTTGT CTGCTCCTCA ATAGGTTAC CAGACCTGA ATAGGTTACA CAGACCTGA GTCAGCTGA CTGCTCCTCA ATAGGTTACA CAAGACTTTT GTTAAGGTTAC GAAGACTTGT GTTAAGGTTAC GACATATAGT GGAAGCCTGA GGCACATATAGTTAC GGCACC GACATATAGTTA	120 180 240 360 480 660 720 780 900 900 1080 11200 1260 1380 1500 1500 1680 1740 1860 1980 2040 2280 2240 2400
50 55 60 65 70	AGTAGGAGG TGTTTATTC GATAGGACC CCTCTGCCT GAATCTCGG GTCTTCCTGC ATCCAGCCC CCGGACCGC GATCTGCCT GTAACGGATG TTAAGGCTA ATAATCTGT AGTTTGGAT AGTTTGGAT TGAAATTGGA TGAAATTGGA TGAAATTGGA TCTTCTCAGG GGGCCAATCC GGAATTACG TTTTCTTCAGG AGGTGTCAGA TCTTCATGGAT TCTTCAGGAT TTTTTCTCAGG AGGTGTCAGA TGAAATGGA TCTTGAGAT TCTTCAGGAT TCTTCAGGAT TTTTTACTGAT TTTGTAGTAT AACAAAAGCGAA ACAAAATGCA TTTTGTAGTAT AATCACAAA ACAAATGCA TTTCTCAGAA ACAAATGCA TTTCTCAGAA ACATTAATGT ACTTCACCAA AACAAATGCA TTTCCTGCAG AAAACTGAAT ATTTCCTGTAG TACAAAAGCACT TTTCAGTAT ACATTCACTCA AACAAATGCA TTTCCTGCAG AAAACTGAAT ATTCCTGTAG TACAAAAGCACT ACACACAC TTCACTCAAC ACACACT TTCCTGCAG AAAACTGCAT TTTCCTTTCTTCTTCT TACAAGACTGA CCTTCTTTTTT	I TGGGCAGGAG CTCCTCCTTG CACAGTGGCT GCACCCGGG GCTGGGAGAG TGATGCAATC GCCACGTGTA GCTCTGCAGC CTCCGCAGGT TTTTGGAACT GGAGAAACCT GGAGAAACCT TCTGCCGGTA TCTGCAGC CCCACTGTTT TCTGCCGGTA TCAAGAATGGA ACATATGTA TCTAGCAGGA CAAGTATGTA CTCATCTTT CTATGGAGAG AAATAATGGA AAATAACTGT GGAGAATACAC GTTTGGCTCT GACAATACAC GTTTGGCTTT TGTGCTTT TGTGCTTT TGTGCTTT TCTTCTTATTTTTTTTTT	CCAGTGATGA CCAGTGATGA ACGTCTCCAT GATTCGGGGG AGTGAGCAGT ACTCCACCAT CGCTAGGTCG CGCAGACCCG CGCAGACCCG CGCAGACCCG CGTATCCACCAG GTCTTCACAGA GTCATCAGCAG CATATCAAGC TTTGACAAACA TTTGACAAACA TTTGACAAAA GTCCCATATTT AGAGCCTGGA TTTGCCCAAT TTCCTACTGGAG CGGTGCATTC ACACTGGAA CGGTGCATTC ACATGGAGA CGGTGCATTC ACATGGAGA ATTCCAACT GACATCAGA AATTCCAACT GACATTGGAA CAATGGATT TAACTTGGTA ACATGGGATT AGTAGTTTTT TGTCACAGAA CACTGTTTTT GTCACAGCT CTTTCCACT GCCTTATAGAA TCTACAGCT CTTTCCACT TTTCCACAT TTTCACACT CTTTCCACAT TTTTCACACT TTTTTCACACT TTTTTTTT	CGGAATGGCA ATAAATGTTA TAACCGTGTC GAGTGAGGCT CTGGGGGGGG CCACTCCG CTCACACG TCCTCACACG TCTCACACT ATACATTTT ATCATATGCT CTTCTCAGAA TTGAAGGATT CAACATCTT CAACATCTGC CTAGGGACAC CTAGGAGACAC AGGGGACAC AGGGGACAC AGGGGAACA AGGGTGGAAC AGGGTGGAAC AGGGTGGAAC AGGTGGAAC GTGACATGG ACTTGACAAC GTGTTGTTTG TGGAGAATGG GAATTTCTTC TGGAGAATGG GAATTCTTCT TGGAGAATGG GAATTCTTCT TTCCTCAATG TCTTTTAATAT TCCTCAATG TCTTTTAATAT AGCTAATTTG TCTTTTAATAT TCTTTAATAT TCTTTTATTCT TGAAGACAT TTATTTAGAACACT TATTTTTATAG TCTTTTTTTATAG TCTTTTTTTAG TCTTTTTTTTTT	ATCACATTTG CACGGGCATC ATTTGCTTGC CAGGGGCATC ATTTGCTTGC CAGGGGCATC CAGGGGGCATC CAGGGGGCATC CAGGGGGCATC CAGGGGGCATC CAGGGGCTACATG CAAAAGAGGAAAAA CAGGAGAATT AAAAGAGAAAA AAAGAGTGTATT TAGTATGTAT	ACCTCTGATC CCCACACTCG AACACTGCA AACACTGCA CGCTGGCTCC CAGCCTTAGT GCCGGTCTGC GCAGCCCTTAG ATGGGGACTT CCAGACCCTA GTGGGGACTT CCAGACCCTGCT CAACAGCTTG CACCTGGCT CAACAGCTTG ATTCGTCCTA ATTCGTCCTT AGATGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG TGTCAGCAG AATCTTTT GATGGCATC GAAGCCTGC GAAGCCGCA GATAATGTAG AATAATTGT CACTTTTGT CATGAATTGT CACTTTTGT CATGACTTT CATGACTTT CATGACTTT CTTTAGGAAA CTCCTTTTG TTTAAGGTAA CTCCTTTTG TTTAAGGTAA CACATTGTAC CAAGACCTGA GTCAGGCAC GACATATAGT TTTAAGGTAA CTCCTTTTGT TTTAAGGTAA CACATTGTAC CAAGACTTTT GTTAAGGTAA CAAGACCTGA GTCAGGCAC GACATATAGT TTAAGGTAA TTCTGACAGT TTAGAAGTTA TTCTGACAGT TTTAAGGTAA TTCTGACAGT TTAGACAGT TTTAGACAGT TTTAGACAGT TTTAGACAGT TTTAGACAGT TTTAGACAGT TTTTAGACAGT	120 180 240 360 480 540 660 720 780 960 1080 1140 1260 1380 1560 1560 1740 1520 1680 1740 1620 1740 1620 1740 1620 1740 1740 1740 1740 1740 1740 1740 174

	CTGAAGCATA	GTTAGTTTAG	GAAATCACTT	CATATTGATT	GTATTAGAAT	TATCTTGGAA	2640
	TTGAAGATAT	ATCCCTAGAG	CAGGGGACCC	CAACCCCCAG	GCCATGGGCC	ACACAGCAGG	2700
	AAGAGGTGAG	TGGTGGGCCA	TTGAGGAGCT	TCATCTGTAT	TTATGGCTAC	TTCCCATCAC	2760
			CACCTCTTGT				2820
5							
5			ACTCTGCATG				2880
			TGAGGTGTAA				2940
	GCAGTCTGTG	GAAAAATTGT	CTTCCACAAA	ACTGGTCCCT	GGTGCCAAAA	ATGTTGGGGA	3000
	CCACTCCTCT	AGAGAGAGGT	CATGATATCA	TACCAACCAA	ATCCAAATCA	CAAATCTTTT	3060
10 -			AAATAAATCT				3120
10.	GGCATACTCT	GATTTTTATA	CTCTGTTTTT	GCAGGTGCTC	TTTTCTTTGA	ATGGAGATTT	3180
	GATGAGCAAG	TGGTTAGGAT	GCAGGGAGAG	CTACTATGGG	TGATATTTTC	CTTGTTTAGG	3240
			TCCTTTGTGG				3300
			TCAACTCTCA				3360
1 ~			CATATTTTAT				3420
15	TTCTAAAAGT	TTGATGCATT	GGAAAAATTT	CCTTGAGGCA	TTTAGCAACA	CATAGAAAAT	3480
	GGGCTTTGAT	TCTTTTCCAA	AACTTTTAGC	CATAGGGTCT	TTTATAGACA	GGGATAGTAA	3540
			AGATGAAAAG				3600
			TGGGAGAAGC				3660
	TGTCGCCTGC	GCACTGTGTA	CCCCGAGCAA	CATTCTAAGG	GTGTGCTTTC	GCCTTGGCTA	3720
20	ΔΟΨΟΌΨΨΩΔ	CCTCATTCTT	CATATAGTAG	TCTAGGAAAA	AGTTGCAGGT	AATTTAAACT	3780
20							
			TAAATTTCTA				3840
	CCATCAACAC	ATTTTATACT	TTGCATCTCC	AAATTTATTG	TGGCGAGACT	TGTCCATTGT	3900
	GAAAGTTAGA	GAACATTATG	TTTGTATCAT	TTCTTTCATA	AAACCTCAAG	AGCATTTTTA	3960
			GTGAAAACTA				4020
25							
23			ACCATTGTCA				4080
	ACGCTTTCTT	GTTAAATAGA	TTTAACAGGA	ACATCTGCAC	ATCTTTTTTC	CTTGTGCACT	4140
	ATTTGTTTAA	TTGCAGTGGA	TTAATACAGC	AAGAGTGCCA	CATTATAACT	AGGCAATTAT	4200
			ATTGTCACAC				4260
20			CTAATCTGCT				4320
30	GATATTTGCA	TAATTGGCTG	CAATTATTTA	ATGTTTAATT	GGGTTGATCA	AATGAGATTC	4380
	AGCAATTCAC	AAGTGCATTA	ATATAAACAG	AACTGGTGGC	ACTTAAAATG	ATAATGATTA	4440
			TCCTTTCACT				4500
			CATCAGTAGA				4560
~ ~	AAAGGCAAAA	CCTGAGCAGT	TCCTAAAAAG	ATTTGCTGTT	AGAAATTTTC	TTTGTGGCAG	4620
35	TCATTTATTA	AGGATTCAAC	TCGTGATACA	CCAAAAGAAG	AGTTGACTTC	AGAGATGTGT	4680
			AATGAATAAA				4740
			AAAGGGAAAG				4800
	GAATCAGGTT	TTTTCTACCT	GGTAAACATT	CTCTATTCTT	TTCTCAAAAG	ATTGCTGTAA	4860
	GAAAAAATGT	AAGAC					
40							
-10	C TD 170	110 Deskade					
		119 Protein					
	Protein Acc	ression #:]	KP N38659.2				
	1	11	21	31	41	51	
				31 	41 	51 	
45	1	11	21	1	1	l	60
45	1 MKDCSNGCSA	11 ECTGEGGSKE	21 VVGTFKAKDL	IVTPATILKE	 KPDPNNLVFG	 TVFTDHMLTV	60
45	1 MKDCSNGCSA EWSSEFGWEK	11 ECTGEGGSKE PHIKPLQNLS	21 VVGTFKAKDL LHPGSSALHY	 IVTPATILKE AVELFEGLKA	 KPDPNNLVFG FRGVDNKIRL	 TVFTDHMLTV FQPNLNMDRM	120
45	1 MKDCSNGCSA EWSSEFGWEK	11 ECTGEGGSKE PHIKPLQNLS	21 VVGTFKAKDL	 IVTPATILKE AVELFEGLKA	 KPDPNNLVFG FRGVDNKIRL	 TVFTDHMLTV FQPNLNMDRM	
45	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE	 IVTPATILKE AVELFEGLKA WVPYSTSASL	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK	120 180
45	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN	21 VVGTFKAKDL LHPGSSALHY 1QQLVKLDQE PVSLWANPKY	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN	120 180 240
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	21 VVGTFKAKDL LHPGSSALHY 1QQLVKLDQE PVSLWANPKY MNLFLYWINE	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
45 50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GCQQVLWLYG WGEFKVSERY	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GCQQVLWLYG WGEFKVSERY	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG GCQQVLWLYG WGEFKVSERY	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEPKVSERY LASRILSKLT	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS	 IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO:	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA See	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY PVSLWANPKY EGNRVREMFG WTIVLS Quence	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA See	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300
50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005	IVTPATILKE AVELFEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT	 TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ	120 180 240 300
50	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVILSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA see id Accession uence: 121.	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGMRVREMFG WTIVLS Quence n #: NM_005 .1194	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300
50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequent	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession uence: 121. 11	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK	120 180 240 300 360
50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA see id Accession uence: 121. 11 GGTCGCGCGC	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 I TTGTGCGCGT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC	120 180 240 300 360
50 55	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGCGC GGGGAACTAG	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC	120 180 240 300 360
50	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession uence: 121. 11 GGTCGCGGG GGGGAACTAG ACTCGTACCA	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEESLATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACCGCGGGGA ACCGCGGGGA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC	120 180 240 300 360
50 55	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding sequ 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession uence: 121. 11 GGTCGCGGG GGGGAACTAG ACTCGTACCA	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEESLATPP SGTACVVCPV 377 31 ITTGTGCGCGT GTGGCAAGCT TACGACTATG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACCGCGGGGA ACCGCGGGGA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC	120 180 240 300 360
50 55	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLEVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG	11 CONTROL OF CONTRO	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE ECHRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC GGACATCTGG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG ARGAAATTCG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTTGGTGCC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG	120 180 240 300 360 60 120 180 240
50 55	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQCVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTGCACGA ACTTGGGTCC	11 CONTROL OF CONTRO	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE n. #: NM_005 .1194 21 CTCGGTGGCCG TCTGCTCCAG TCACTATITC GGGACATCTGG ACCCAGCCCT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 I TTGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT	RPDPNNLVFG RFGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGGGGGGC CTCCTGGAAC CTCCTGGAAC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GCGCCCCTGG GTGGCCGGTA	120 180 240 300 360 60 120 180 240 300
50 55	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCCACGA ATGGACCGCG CGCTCCACGA ACTTGGGTCC	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCAGCGGGA GCGACGAGCGGA GCGACGAGAC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC GGACATCTGG ACCCAGCCCT GGAATCCCAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TGTGCGAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT CAGCTATGGT GACTACTGGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCCTGAGCAA ACCGCGGGGA ACTTGGTGGAC CTCCTGGAAC CAGCTTGGGA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGFK 51 CCCTGCTGCC GCAAGCCAAC GCAGTTTCTAC GCGGCCTGG GTGGCCGGTA CGCGAACTAC	120 180 240 300 360 60 120 180 240 300 360
50 55 60	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequilated ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG CGCTCCACGA ACTTGGGTCC GGGTGCGCTG GCCTCCCCCCA	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession LECT 121. GGTCGCGCGC GGGGAACTAG ACTCGTACCA CGCCAGCGA GCAGCCGGGA GGGACGAGAC TCCGCCGTGA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCCAG TCACTATTTC GGACATCTCG ACCCAGCCT GGAATCCCAG CTGCATGGG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGAATTCTCAC GCCGCCCTGG GTGGCCGGTA CGCGACTAC GCCGCTGAG GCCGCTGAG	120 180 240 300 360 60 120 180 240 300 360 420
50 55	MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequilated ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG CGCTCCACGA ACTTGGGTCC GGGTGCGCTG GCCTCCCCCCA	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession LECT 121. GGTCGCGCGC GGGGAACTAG ACTCGTACCA CGCCAGCGA GCAGCCGGGA GGGACGAGAC TCCGCCGTGA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC GGACATCTGG ACCCAGCCCT GGAATCCCAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGAATTCTCAC GCCGCCCTGG GTGGCCGGTA CGCGACTAC GCCGCTGAG GCCGCTGAG	120 180 240 300 360 60 120 180 240 300 360
50 55 60	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQCVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTTCGACGA ACTTGGGTCC GGGTGCGCTGA AGAGCGGTGA	11 ECTGEGGSKE PHIKPLQNLS VFDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLITAL DIQYGREESD 120 DNA sec id Accession uence: 121. 11 GGTCGCGCG GGGGACTACA ACTCGTACCA GCACCGGGA GCACCAGGA CTCCCCGTGA GTGACCTGCT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE n. #: NM_005: .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATITC GGAACTCTGG ACCCAGCCCT GGAATCCCAG CTGCATGTGG TGCCATGTGG TGCCATGTGG TGCCATGTGG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGT AGCGGCTTCT GCGCCCTCGG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCCTGAGCAA ACCGCGGGGA ACTTGGTGCC CTCCTGGAAC AAGCTTGGGA CCACCAGGA GATACTCGCC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCCGTA CGCGAACTAC GCCGCTGGAG CAAGGAGTTC	120 180 240 300 360 60 120 180 240 300 360 420 480
50 55 60	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq 1 ACAGAGGGCG CCCAGGGA ATGGACCGCG CGCTCCACGA ACTGGGTCC GCCTCCCCCA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGAGCGGTGA AGACCCCCCCG	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCAGCGGGA GCACCGGGGA GCGACGGGA GCGACGGCGA ACTACACTCC	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGGTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATGTGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CCGAGCCTCGAA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGT GACTACTGGA AGCGCTTCGT GCCCCCCGG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGFK 51 CCCTGCTGCC GCAAGCCAAC GCATTTCTAC GCGGCCTGG GTGGCCGGTA GCGGAACTAC GCGGAACTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT	120 180 240 300 360 60 120 180 240 360 420 480 540
50 55 60	MEDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding sequing ACAGAGGGCG CCCACGCTGGA ATGGACCGCG CGCTCCACGA ACTTGGGTCC GGGTGCGCTG GCCTCCCTCA AGAGCGGTGA AGCAGCTCCCCCC TTGTTGGGCCG TTGTTGGGCG	11 ECTGEGGSKE PHIKPLQNLS VFDKELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession uence: 121. 11 GGTCGCGGG GGGAACTAG ACTCGTACCA CGCCAGCGA CGCAGCAGCA TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAAGAT	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCTT GGAATCCTAG CTGCATGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CTGCATTGGC CCAGCCTTGGC CCAGCCTTGGC CCAGCCTTGGC CCAGCCTGCA CCAGCCTGCA CCAGCCTGCC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAATTCG CAGCTTTGGT GACTACTGGA AGCGCCTCGG GCCCCTCGG GCCCCTCGG TCCAGGTCTG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTCGGGAA ACGTCGGGAA CCACCAGAA GATACTCGCC TAGCGCCCAT AGAGCCCAAAG	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTGAC GCGGCCTGGAC CAAGGAAGTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT CGACTCCCAG	120 180 240 300 360 60 120 180 240 300 420 480 540 600
50 55 60	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac Coding seq 1 ACAGAGGGCG CCCAGCTGGA ATGGACCGCG ACTTGGGTC GGGTGCGTCC AGAGGGGTGG GCCTCCCTCA AGAGCGGTGA ACTTGGGTC GGGTGGAGAAGAAA	11 CONTROL OF CONTRO	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE ECHRVREMFG WILVIS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATITC GGACATCTGG ACCCAGCCCT GGACATCCGG ACCCATGGC CTGCATGGC CGGCATTGGC CGACATCGGC ACGCCTGC ACGCCTGC ACGCCTGC ACGCCTGC ACGCCTGC ACTAAAGAAGAAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGT ACGACTACTGGT GACTACTGGT GACTACTGGT GACTACTGGT ACGACATCT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGGCAGTCTT AGGCAGTCTT AGGCAGTCTT AGGCAGTCTT	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA ACTTGGTGCC CTCCTGGAAC CCACCTAGGA GATACTCGCC TAGGGCCCAT TGAGTACGCC TGAGTACGCC TGAGTACGCC TGAGTACGCC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCCTGG GTGGCCGGTA CGCGACTAC GCCGCTGGAC CAAGGCAGTC CTTCCCCTGT GAAGCCAGC GAAGCCAGC	120 180 300 360 60 120 180 240 300 360 420 480 540 660
50 55 60 65	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq ACAGAGGGCG CCCAGGA ATGGACCGCG GCTCCACGA ACTGGGCCCCCCG GGTGCACTGC GCCTCCCCCC TGTTGGGCG TGTTTGGGCG GGTGAAGAAA ATCATCGCGG	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGGGG ACTGGTACCA ACTCGTACCA GCCCAGGGA GGGACGAGAC TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAGGAT TCCACGTGAC TCCACGTGA TCCACGTGA TCCACGTGAC TCCACGTGA TCCACGTGAC	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WILLOS TURNE TURNE TURNE TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATGGG CGAGCTTGGA CCAGGCCTGA CCTTCTGGAT CCTTTTGGAT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGT GCGCCCTCGG GCCGCCTCGG GCCGCAACC TCCAGGTCTT AGGACTTTC CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGFK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGGG GTGGCCGGTA CGCGAACTAC GCCGCTGGAG CCAAGGAGTTC CTTCCCCTGT CGAACTCCCAG GAAGCCAAC CCCCTGT CGACTCCCAG GAAGCCAGTC CATCTCCATC	120 180 240 300 360 120 180 240 300 360 420 600 600 720
50 55 60	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac: Coding seq ACAGAGGGCG CCCAGGA ATGGACCGCG GCTCCACGA ACTGGGCCCCCCG GGTGCACTGC GCCTCCCCCC TGTTGGGCG TGTTTGGGCG GGTGAAGAAA ATCATCGCGG	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGGGG ACTGGTACCA ACTCGTACCA GCCCAGGGA GGGACGAGAC TCCGCCGTGA GTGACCTGCT ACTACACTCC AGCCCAGGAT TCCACGTGAC TCCACGTGA TCCACGTGA TCCACGTGAC TCCACGTGA TCCACGTGAC	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WILLOS TURNE TURNE TURNE TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCAGCCT GGAATCCCAG CTGCATGGG CGAGCTTGGA CCAGGCCTGA CCTTCTGGAT CCTTTTGGAT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGT GCGCCCTCGG GCCGCCTCGG GCCGCAACC TCCAGGTCTT AGGACTTTC CCCCGCATGA	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGFK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGGG GTGGCCGGTA CGCGAACTAC GCCGCTGGAG CCAAGGAGTTC CTTCCCCTGT CGAACTCCCAG GAAGCCAAC CCCCTGT CGACTCCCAG GAAGCCAGTC CATCTCCATC	120 180 300 360 60 120 180 240 300 360 420 480 540 660
50 55 60 65	1	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LTMDDLTTAL DIQYGREESD 120 DNA seid Accession Lence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA ACTCGTACCA GCGCCAGGGA GCGACGAGAC GCGCCGGGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAC TCGACGTGAC AGCACAACTA AGCACAACTA	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGTCCAG TCACTATTTC GGACATCTGG ACCTATTGG GGAATCCCAG CCGAGCCT CGAGCTCGAA CCAGCCTT CGAGCTCGAA CCAGCCTTGGA CCAGCCTTGGA CCAGCCTTGGA CCAGCCTTGGA CCAGCCTTGGAT CCAGCCTTGGAT CCAGCCTTGGAT TGCTGCCCCT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGCTTCGG GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCAGGTCTT CCCCGATGA TTTCCTCCAG	KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGCCCTGG GTGGCCGGTA CGCGACTAC GCGCTGGAG CAAGGAGTAC CCCTGCTGCC CTTCCCCTGT CGACTCCGAG GAAGCCACT CCACCTCCATC CCACAGAAGGG	120 180 240 300 360 120 180 240 420 480 600 660 780
50 55 60 65	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GCGTCCCACA ACTTGGGTCC GGGTGCGCTGA TTGTTGGGC GCCCCCCCA AGAGCGGTGA ACTATCGCG GCTCACACA ACTATCGCG GCTCACACA ACTATCGCG GCTCACACAC GCTCACAACA ACCAGCAAC	11 CONTROL OF CONTRO	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE ECHRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTIC GGACATCAG ACCCAGCCCT GGACATCAGG CTGCATGGT CGGCTTGGC CGACGCTGG ACCAGCCTGG ACCAGCCTGG ACTAAAGAAG CCTTCTTGGAT TGCTGCCCCT AAAAGAAGCT AAAAGAGGCT AAAAGAGGCT AAAAGAGGCT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAGGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA GCCCCTCGG GCCCCTCGG GCCCCCCGCAGCA TCCAGGTCTT AGGCAGTCT AGGCAGTCT CCCGCATGA CTTAGAGAGAGAG CTAGAGAGAGAG		TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGGTA CCGCCTGG GTGGCCGGTA CCCGCTGCAG CCAGCACTAC GCCGCTGCAG CCAGCAGCTC CATCCCCAGG GAAGCCAGTC CATCTCCATC CCAAGAAGGAG GGGAAAGGAT	120 180 300 360 60 120 180 360 360 480 540 660 720 780 840
50 55 60 65	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq ACAGAGGGCG CCCAGCTGGA ATGGACCGCG GGTCCACCG ACTTCGGTCC GGGTCCCCCCG TTGTTGGGCG GCTCCCCCG TTGTTGGGCG GCTCACAGA ATCATCGCGG CACCAGCAACA GCTCCAAGAA ATCATCGCGG CACCAGCAACA GCTCCAAAGA GGTCAAGAAGA GGTCAAAGA GGTCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCAAAGAAAG	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA second accession uence: 121. 11 GGTCGCGGGG GGGGAACTAG ACTCGTACCA GCACCAGGAA GCACCAGGGA GGGACAGAC TCCGCCGTGA GTGACCTGCT ACTACACTC AGCCCAAGGA TCGGCCGAGAA TCGGCCAAGGA TCGGCGGAA GTGACCTGCT ACTACACTCC AGCAGAACTA AGGATGCCCC ATGAAGAGAT	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTC GGAATCCCAG ACCCAGCCCT GGAATCCCAG CTGCATGTGG ACCCAGCCTGGACCTGGACCTGGA CCAGGCCTGGACTCGAA CCAGGCCTGGA CCAGGCCTGGA TGCTGCTGGAT TGCTGCCCCT AAAAGAGGCT TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGGCAGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG CCACCTGTAG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RCILDLAHQ HIPTMENGPK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGGTA CGCGCCTGGA CCAGGCCAC GCAGCCAC CCAGCCTGGA CAAGACTAC CCAGCCCTGT CGACTCCCATC CCAAGAAGGG GAAGCCAGT CCAAGAAGGG GGGAAAGGAT TGCCCAGTCC TGCCCAGTC	120 180 240 300 360 120 180 240 300 360 420 540 660 720 780 840 900
50 55 60 65	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCOQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq ACAGAGGGCG CCCAGCTGGA ATGGACCGCG GGTCCACCG ACTTCGGTCC GGGTCCCCCCG TTGTTGGGCG GCTCCCCCG TTGTTGGGCG GCTCACAGA ATCATCGCGG CACCAGCAACA GCTCCAAGAA ATCATCGCGG CACCAGCAACA GCTCCAAAGA GGTCAAGAAGA GGTCAAAGA GGTCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCCAAAGA GGTCAAAGAAAG	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA second accession uence: 121. 11 GGTCGCGGGG GGGGAACTAG ACTCGTACCA GCACCAGGAA GCACCAGGGA GGGACAGAC TCCGCCGTGA GTGACCTGCT ACTACACTC AGCCCAAGGA TCGGCCGAGAA TCGGCCAAGGA TCGGCGGAA GTGACCTGCT ACTACACTCC AGCAGAACTA AGGATGCCCC ATGAAGAGAT	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE ECHRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTIC GGACATCAG ACCCAGCCCT GGACATCAGG CTGCATGGT CGGCTTGGC CGACGCTGG ACCAGCCTGG ACCAGCCTGG ACTAAAGAAG CCTTCTTGGAT TGCTGCCCCT AAAAGAAGCT AAAAGAGGCT AAAAGAGGCT AAAAGAGGCT	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GACTACTGGA AGCGGCTTCT GCGCCCTCGG GCCGCAACC TCCAGGTCTG AGGCAGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG CCACCTGTAG	KPDPNNLVFG KPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RCILDLAHQ HIPTMENGPK 51. CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGGTA CGCGCCTGGA CCAGGCCAC GCAGCCAC CCAGCCTGGA CAAGACTAC CCAGCCCTGT CGACTCCCATC CCAAGAAGGG GAAGCCAGT CCAAGAAGGG GGGAAAGGAT TGCCCAGTCC TGCCCAGTC	120 180 300 360 60 120 180 360 360 480 540 660 720 780 840
50 55 60 65 70	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCAGGA ACTGGGTCCACGA ACTGGGTCCACGA ACTGGGTCGCTG GCCTCCACGA AGAGCGGTGA ACTGGTCG GCTCACGA AGAGCGTGA CCTCCACGA AGAGCGTGA CCACCCCCG GTGAAGAA ATCATCGCG CACCACCAGC CACCAGCAAC GCTCCAAAGA GTTCAAAGAA TGATAAGGAAG TGCCAGCCCA	11 ECTGEGGSKE PHIKPLQNLS VPDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLTTAL DIQYGREESD 120 DNA secid Accession uence: 121. 11 GGTCGCGGGC GGGGAACTAG ACTCGTACCA GCCCAGGGA GCGACGGGA GCGACGGGA GCGACGGGA GCGACGGGA GCGACGGGA GCGCCAGGGA TCCGCCGGGA GTGACCTGCT ACTACACTCC AGCCCAAGAT TCGACGTGAA AGCACAACTA GGATGCCCCA ATGAAGAGAT AACCCATCCA	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTC GGAATCCCAG ACCCAGCCCT GGAATCCCAG CTGCATGTGG ACCCAGCCTGGACCTGGACCTGGA CCAGGCCTGGACTCGAA CCAGGCCTGGA CCAGGCCTGGA TGCTGCTGGAT TGCTGCCCCT AAAAGAGGCT TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC TGTGAGCCTC	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACATATG AAGAAATTCG CAGCTTTGGT GCGCCTTCGGT GCCCCTCGGT GCGCCGTCGT TCCAGGTCTT TCCCCGAGTAGT TTCCTCCAG TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTGGA GAGAATTGGA	RPDPNNLVFG FRGVDNKIRL YIRFTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACCGCGGGAA ACTTGGTGCC CTCCTGGAAC AAGCTTGGGA GATACTCGCC TAGGGCCCAT AGAGCCCAAG TGAGTACCCC AAAGCTGCTT AAGCTCCAGA AAAGCTGCTT AAGCTCCAGGA AAAGCTGCTT AAGCTCCAGGA AAAGCTGCAT CAAGAAGAAAAAACAAAAC	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCGGCCTGGA GTGGCCGGTA CGCGCTGGAG CAAGGAGTTC CTTCCCCTGT CGACTCCCAG GAAGCCAAC GAAGCCAAC GCAGGAGCAAC CTTCCCATC CCAAGAAGGA GGAAACGAT TCCCAGGCGGAACCAAC CCAAGAAGGG GGGAAACGAT TGCCCAGGTCC GTACCACACC	120 180 240 300 360 120 180 240 300 360 420 540 660 720 780 840 900
50 55 60 65 70	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GCGTCCCTCA AGAGCGGTGA ACTTGGGTCC GGGTGCAGCA GCCCCCCG GGTGAAGAAA ATCATCGCGG GCTCCAAGA ATCATCGCGG GATAAGAAG ATCATCGCGG GATAAGAAG ATCATCGCGG GATAAGAAG ATCATCGCAGCCAAC AGACCAAC ACACCAAC AGACCAAC	11 CONTROL OF CONTRO	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE ECHRVREMFG WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTG GGACATCAG ACCCAGCCCT GGAATCCCAG CTGCTTGGAT CCAGCCTGGACTCGAA CCAGCCTGC AGTAAAGAAG CCTTCTTGGAT TGCTGCCCCT TGAAGACGCT TGTGAGCCTC TTATGATACT GAATGATCAA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATGA AAGAATTCG CAGCTTTGGT GCCCCTCGG GCCCCTCGG TCCAGGTCTT ACGACTTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CCACCTGTAG GAGAATTGGA CCTTCCCGGT	RPDPNNLVFG PRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGTGGGGA AGTTGGTGCC CTCCTGGAAC CTAGCGCCCAT AGAGCCCAAG TGAGTACGCC TAGCGCCCAT AGAGCCCAAG ATACTCGCC ATCTCTTCCA AAAGCTGCTT AAGCTCCAGG AAAGTGAGGC CCAAGAAGAA CTTGGCCCT CCCAAGAAGAA TCTTGGCCCT AAGTTCGCCC CCAAGAAGAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTGAG CAAGCAAC CCTTCCCCTG CTTCCCCTGT CGACTCCCAG GAAGCAGTC CATCTCCATC CCAAGAAGGA GGGAAAGGAT TGCCAGTC CCAAGAAGGA TGCCAGTC CCAAGAAGGA TGCCAGTC GACTCCAGC GAGGACAGC GGGAAAGGAT TGCCAGTC GACTCCAGC GAGGACAGC GAGGGACAGG	120 180 300 360 360 120 180 360 480 540 660 720 780 900 900 1020
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50 55 60 65 70	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP ALLFVLLSPV GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq ACAGAGGGCG CCCAGGA ATGGACCGCG GGTCCACGA AGAGCGGTGG AGCCCCCCG TTGTTGGCCG GGTGAAGAA ATCATCGCGG CACCACGAAC GCTCCAAGA GCTCCAAGA GTAAGGAAC GTCCAAGGA TGCCAGCCC GATACTTGCCG GGTCCAAGGA CACCAGCAAC GCTCCAAGGA CACCAGCAAC GCTCCAAGGA TGCCAGCCC GATACTTAC	11	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE EGNRVREMFG WTIVLS Quence n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTC GGACATCTGG ACCCATGCGC TGCATGTGG CCGAGCCT GGAATCCCAG CCGAGCCTGC AGTAAGAAG CCTTCTGGAT TGCTGCCCCT TAAAAGAAG TGCTGCCCT TATGATACT GAATCATACT GGAATCATACT GGAATCATACT GGAATCATACT GGAATCATACT TGTGAGCCTC TTATGATACT GGAATCATACGAT CCTAGGGTT GGAAGCCGAG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEEBLATPP SGTACVVCPV 377 31 ITTGTGCGCGT TACGACTATG AAGAAATTCG CAGCTTTGGT GCGCCTTCGG GCCGCAACC TCCAGGTCTG AGGAGTTTCCTCCAG TTTCCTCCAG TTTCCTCCAG CTAGAGAAGA TTTCCTCCAG CTAGAGAAGA CCACCTGTAG GAGAATTGGA GAGAATTGGA CCACCTGTAG GAGAATTGGA GAGAATTGGA CGTTCGCGGT TCCAAAGTAA GAGAGATGGA AGCAGGATGA	RPDPNNLVFG FRGVDNKIRL YIRFTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACCGCGGGA ACTTGGTGCC CTCCTGGAAC AAGCTTGGGA GATACTGCC TAGGGCCCAT AGAGCCCAG AATCTCTCCA AAAGCTCCTG AAAGCTCCTG AAAGCTCCTG AAAGCTCCTG TGATACGC CCAAGAAGAA TCTTGGCCT TGATCCTAGT TGATCCTAGT CCAAGAAGAA TCTTGGCCT TGATCCTAGT CTACGGAGAA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGGA GTGGCCGTTAC GCCGCTGGAG CAAGGAGTTC CTTCCCCTGT CGACTCCAG GAAGCCAGC GAAGCCAGC GAAGCCAGC GAAGCCAGC GAAGCCAGC GAAGCCAGC CATCTCCATC CCAAGAAGGG GGGAAAGGAT TGCCCAGTC GTACCACAGC GAGGGACCAG AAGGCAAGCT ACACACACC AAGGCACCAC AAGGCACCC CAAGCACCC CAAGCCACCC AAGGCACCC CAAGCCACCC CAAGCCACCC CAAGCCACCC CAAGCCACCC CAAGCCACC CAAGCCACCC CAAGCCACCC CAAGCCACCC CAACCCACC CAAGCCACCC CAACCCC CAACCCACC CAACCCCC CAACCCACC CAACCCCCC	120 180 240 300 360 60 120 180 240 300 360 420 720 780 840 900 960 1020 1080 1140
50 55 60 65 70	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GCCTCCACGA ACTTGGGTCC GGGTGCACTGA ACTTGGGTCC GGGTGCACTGA ACTACTGGGG GCCTCCTCA AGAGCGGTGA ACTACTGGGG GCACCCCCG GGTGAAGAAA ATCATCGCGG GATAAGGAAG GCTCCAAGA GCTCCAAGA GATACTACG GAATACTAC GAATACTAC GAATGCCAGCA GAATACTAC	11 CONTROL OF CONTRO	21 VVGTFKAKDL LHPGSSALHY IQQLVKLDQE FVSLWANPKY MNLFLYWINE ECRIVEREM WTIVLS QUENCE n #: NM_005 .1194 21 TCGGTGGCCG TCTGCTCCAG TCACTATTTC GGACATCTAG ACCCAGCCT GGAATCCCAG CTGCTTGGA CTGCTTGGA CTGCTTGGAT CAGAGCTTGAAAGAAG CTTATGATACT GAATGATCAA CTCTAGGTT GGAACCCAG CCTTATGATACT TGCTGCACCT TGTAGATCT TGAATGATACT GAATGATCAA CTCTAGGGTT GGAAGCCGAG GCAGAAAAGA	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGCCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GCCCCTCGG GCCCCTCGG GCCCCTCGG TCCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CCACCTGTAG CGAGAGATGA CGTTCGCGGT TCCCAAGTATGAGAGAGA CGTTCGCGGT TCCCAAGTATGAGAGAGAGATGAGAGATGAGAGATGAGAAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAAGA	RPDPNNLVFG PRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTA ACCGCGGGA AGTTGGTGCC CTCCTGGAAC CAACCCAGA GATACTCGCC TAGCGCCCAT ACAGCCCAT ACAGCCCAT ACAGCTCCAG ATCTCTCCA AAAGCTGCTT AAGCTCCAGG AAAGTGAGGC CCAAGAAGAA TCTTGCCC TGATCCTAGT TGATCCTAGT TGATCCTAGT TGATCCTAGT TGATCCTAGT TGATCCTAGT TCTACGAGAA TCTTGGCCCT TGATCCTAGT TCTACGGAGAA TCACTAGCTA	TVFTDHMLTV FQPNLNMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTGAC GCAGCCAAC GAAGCCAAT CCAAGCAAGC GAAGCAAGC GAAGCCAAC GGAAAGGAC GGAAAGGAC GGAAAGGAC GAAGGCACC GAAGGCAAC CAAGGCCACC CAAGGCAACAAA	120 180 300 360 60 120 180 240 300 360 420 480 540 660 720 780 900 900 900 1080
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50 55 60 65 70 75	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GCGTCCACGA ACTTGGGTC GGGTGAGAAAA ATCATCGCGG CACCCCCG TTGTGGGC GGTCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCCAAC GGTCCAGCAAC GGTCCAGCCAAC GGATGCCAGCCA GAATACTTAC GAATGCCAGC AGGTAACTTAC AGATGCTACAC AGTAACTTGT GCAGCCCGCC GAATACTTAC AGATGGTACC AGATGCTACAC AGTACTGTACAC AGTACTAGAC CTCTTCCCC GCAGCTGACT AGATGGTATG CTCTTACATGA	11 CTGTGEGGSKE PHIKPLONLS VEDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLITAL 120 DNA seid id Accession uence: 121. 11 GGTCGCGGG GGGGAACTAG ACTCGTACCA GCACGGA GCACCAGGA GCACCAGGA GCACCAGGA TCGCTGCTACTAC TCGCTGCAGA AGCACTAG TCGACCAGGA AGCACAGAT TCGACGTGA AGCACAGTA ACCATCA TCGAAGAGACA GCAAGAGACA TCGCTGCAGA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCCACCAC TCAAGAGACA TCGACCACCC ATGAAGAGAC TGCCTGCTA ACACTTTTGG TCACAACAAT TCACTTATGG GACGGCAATT TCCACAACAAT TCACTTATGG GAGGGACCTT CACAACAGTGG ACTTTTAGG GACGGTGG ACTTTTAGG GACGGTGG ACTTTTAGG ACTTTAGG ACTTTTAGG ACTTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTTAGG ACTTTTAGG ACTTTT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE ECRIVERED TOGETGGCG TCTGCTCCAG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGACATCGG ACCCAGCCT GGACATCGG ACCCAGCCT GGACATCGG ACTCAGGT TGCTGCCCT TGATGGCT TGTGAGCT TGATGATCT TGATGATCT TGATGATCT GGAAGCCAG CCTTATGGAT TGCTGCCCT TGAAGAAGA ACCCAGCCT TGAAGCACC TGAAGCCAGC TGAAGCTCAG ACCCAGCCT TGAAGCT TGAAGCT TGAAGCT TGAAGCT TGAAGCT TGAATCT GGAAGCCAGG ATAAAGAGCT TGAAGCT TGAATCAT CTTAGGT TGAATCT TGAATCAT CTTAGGT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATGT TACAGCAGGA ATAAAGGCT TGGATGTT TGGGTGTTTT TGGGTGTTTT TGGGTGTTTT TGGGTGTTTT TGGATGTTGT TGGATGTT TGGATGT TGGATG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GGCTCCTGGG CTCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CTAGAGAGAG CCACCTGTAG GAGAATTGAGAGAGAG CCACTGTAG GAGAATGA AGAGATGA AGAGATGA AGTTCTCTCCAG CTAGAGTAGT TCCAAAGTAA GAGAGATGG ATTTCTTT CACTCTGGG TGTTTCTTT CACTCTGGG TGTTTTCTGG TGTTTTCTGG TGGTTCACTA	RPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA AGTTGGTGCC TCCTGGAAC CAGCCCATG AAGCTCGCC TAGCGCCCAT AAGCTCCTG AAAGCTGCTT AAGCTCCAGG AAAGTAGGCG TCAATGCTCT CCAAGAGAA TCTTGGCCT TGATCTTCCA TGATCTTGCC AGTAGATTGC AGTCTAGTT TCACTAGTT TCACTAGTT TCACTAGTT TCACTAGTT CACTAGTT CTACGGAGA CCATTGGC AAACTTTGAC CACTTTGGC TCTCCAAAGA AGCCTGGAGG TCTTCCAAAGA AGCCTGGAGG TGATGCAAGG TGATGCAAGG	TVFTDHMLTV FQPNLMMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51 CCCTGCTGCC GCAAGCCAAC GGATTTCTAC GCCGCCTGG GTGGCCGTGAC GCAGCCAAC GCAGCCAAC GCCCTGGAG CAAGGAGTTC CATCTCCATC CCAAGAAGGG GGAAAGGAT TGCCCAGTC GTACCACAGC GAGGCAGCAG CAAGGCAGC CAAGGCAGCT CTACCCCAGT CCAAGGCAGC CAAGGCAGCT CTACCCAGCT CTACCCAGCT CTACCCAGCT CTACCAGCT CTACCAGCT CTACCAGCT CTACCAGCT CTACCAGCT CTACCAGCT CTACCAGCT CTACCAGCT AAAGGCT AAAGGCT AAACCT AAATCTACA AAACTCACA ACAGCTGGT	120 180 240 300 360 120 180 240 300 360 420 480 540 660 720 780 900 900 900 1020 11200 1200 1200 1320 1440 1560 1560 1560 1620
50 55 60 65 70 75	1 MKDCSNGCSA EWSSEFGWEK YRSAVRATLP GCQVLWLYG WGEFKVSERY LASRILSKLT Seq ID NO: Nucleic Ac. Coding seq 1 ACAGAGGGCG CCCAGCTGGA ACTGGACCGCG GCGTCCACGA ACTTGGGTC GGGTGAGAAAA ATCATCGCGG CACCCCCG TTGTGGGC GGTCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCAAC GGTCCAGCCAAC GGTCCAGCAAC GGTCCAGCCAAC GGATGCCAGCCA GAATACTTAC GAATGCCAGC AGGTAACTTAC AGATGCTACAC AGTAACTTGT GCAGCCCGCC GAATACTTAC AGATGGTACC AGATGCTACAC AGTACTGTACAC AGTACTAGAC CTCTTCCCC GCAGCTGACT AGATGGTATG CTCTTACATGA	11 CTGTGEGGSKE PHIKPLONLS VEDKEELLEC GPYFSSGTFN EDHQITEVGT LIMDDLITAL 120 DNA seid id Accession uence: 121. 11 GGTCGCGGG GGGGAACTAG ACTCGTACCA GCACGGA GCACCAGGA GCACCAGGA GCACCAGGA TCGCTGCTACTAC TCGCTGCAGA AGCACTAG TCGACCAGGA AGCACAGAT TCGACGTGA AGCACAGTA ACCATCA TCGAAGAGACA GCAAGAGACA TCGCTGCAGA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCGACCAGCA TCCACCAC TCAAGAGACA TCGACCACCC ATGAAGAGAC TGCCTGCTA ACACTTTTGG TCACAACAAT TCACTTATGG GACGGCAATT TCCACAACAAT TCACTTATGG GAGGGACCTT CACAACAGTGG ACTTTTAGG GACGGTGG ACTTTTAGG GACGGTGG ACTTTTAGG ACTTTAGG ACTTTTAGG ACTTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTAGG ACTTTTTAGG ACTTTTAGG ACTTTT	VVGTFKAKDL LHPGSSALHY IQQLVKLDQE PVSLWANPKY MNLFLYWINE ECRIVERED TOGETGGCG TCTGCTCCAG TCTGCTCCAG TCACTATTTC GGACATCTGG ACCCAGCCT GGACATCGG ACCCAGCCT GGACATCGG ACCCAGCCT GGACATCGG ACTCAGGT TGCTGCCCT TGATGGCT TGTGAGCT TGATGATCT TGATGATCT TGATGATCT GGAAGCCAG CCTTATGGAT TGCTGCCCT TGAAGAAGA ACCCAGCCT TGAAGCACC TGAAGCCAGC TGAAGCTCAG ACCCAGCCT TGAAGCT TGAAGCT TGAAGCT TGAAGCT TGAAGCT TGAATCT GGAAGCCAGG ATAAAGAGCT TGAAGCT TGAATCAT CTTAGGT TGAATCT TGAATCAT CTTAGGT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATCT TGAATGT TACAGCAGGA ATAAAGGCT TGGATGTT TGGGTGTTTT TGGGTGTTTT TGGGTGTTTT TGGGTGTTTT TGGATGTTGT TGGATGTT TGGATGT TGGATG	IVTPATILKE AVELPEGLKA WVPYSTSASL VRAWKGGTGD DGEELATPP SGTACVVCPV 377 31 ITGTGCGCGT GTGGCAAGCT TACGACTATG AAGAAATTCG CAGCTTTGGT GGCTCCTGGG CTCCAGGTCTT CCCCGCATGA TTTCCTCCAG CTAGAGAGAG CTAGAGAGAG CCACCTGTAG GAGAATTGAGAGAGAG CCACTGTAG GAGAATGA AGAGATGA AGAGATGA AGTTCTCTCCAG CTAGAGTAGT TCCAAAGTAA GAGAGATGG ATTTCTTT CACTCTGGG TGTTTCTTT CACTCTGGG TGTTTTCTGG TGTTTTCTGG TGGTTCACTA	RPDPNNLVFG FRGVDNKIRL YIRPTFIGTE CKMGGNYGSS LDGIILPGVT SDILYKGETI 41 GTGTGGAGTG GCGTGAGCAA ACGGCGGGGA AGTTGGTGCC TCCTGGAAC CAGCCCATG AAGCTCGCC TAGCGCCCAT AAGCTCCTG AAAGCTGCTT AAGCTCCAGG AAAGTAGGCG TCAATGCTCT CCAAGAGAA TCTTGGCCT TGATCTTCCA TGATCTTGCC AGTAGATTGC AGTCTAGTT TCACTAGTT TCACTAGTT TCACTAGTT TCACTAGTT CACTAGTT CTACGGAGA CCATTGGC AAACTTTGAC CACTTTGGC TCTCCAAAGA AGCCTGGAGG TCTTCCAAAGA AGCCTGGAGG TGATGCAAGG TGATGCAAGG	TVFTDHMLTV FQPNLIMDRM PSLGVKKPTK LFAQCEAVDN RRCILDLAHQ HIPTMENGPK 51. CCCTGCTGCC GCAGGCCAGC GGATTTCTAC GCGCCCTGG GTGGCCGGTA CCGAGGACTAC GCGCCTGGAG CAAGGAGTTC CTCCCCTGT CGACTCCGAG GAAGCAACA GGAACTAC CCAGAGAGGG GGAAAGGAT TGCCCAGTC CTACCCCAGC GAGGGACGAG CAAGGCCAGC GAGGGACGAG CAAGGCCAGC GAGGGACGAG CAAGGCCACT TTCCCCTTT AGAATCGATT ACCCAGCTC TTCTCAGCAG AAAGCTACA AAATCTCACA	120 180 240 300 360 120 180 240 360 420 480 960 960 1020 1080 1140 1200 1140 1200 1320 1380 1490 1500 1500

				CATTACCTCA			1740
	CTGAGGAGTT	GGAAACCTTA	CATATATGTA	TATATATATG	TATGTATATA	TGTATATATG	1800
				TGTATATATA			1860
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,				TAAGAGAACT			1980
				GAGGGAACTT			2040
	TGTCTCATTC	TGCCTCTGTT	ATGCAATGGG	TTCTACAGCA	CCCTTTCCCG	CAGGTTAGAA	2100
	ATATTTCCCT	AAGACACAGG	GAAATGGGTC	TTAGCCTGGG	GCCTGGGGAA	AGTTCCCAAG	2160
				GTGTTTTCTG			
10							2220
10				AGGGAGAACT			2280
	CCTGCCTCTC	ATCTCAATCC	TTGACTGATG	AATTTGAAGT	TCTACTAGAA	CCATGAAAAC	2340
	TTGTTCCTTT	CGTGCATCTC	CAAGGAGCTT	GCTGGCTCTG	CAGCCACGCT	TEGGCCCTCG	2400
				ACAGAATCTG			
							2460
1 5				CAACGTGGAC			2520
15	AAGGATCCTC	CAGGAGCTCT	GCTTAGCCAA	TCATCATGAT	GGATTTTTTT	TTTTTTTTT	2580
				CTGGAGGTTA			2640
				TCTCCTGCCT			2700
				ATTTCTGTAT			2760
	CACCACATTG	GCCAGGCTGG	TCTTGACCTC	CTGACCTAGG	TGATCCACTG	CCTCCATGAT	2820
20	AGATTTTGCC	CCAGCTGGAC	TCTGCAGCTC	CACGTGGAAT	CCAGGTGCCT	GCCTCCAGTC	2880
				GTGGGTAACT			
	IGGGAMAGIC	ACCAACCCGC	AGCITGICAL	GIGGGIAACI	ICIGAACCCI	ANGCE	
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				KKFELVPPPW		-	60
	GCAGDETESQ	DYWKAWDANY	ASLIRRDCMW	SGFSTQEPLE	RAVSDLLAVG	APSGYSPKEF	120
	ATPDYTPELE	AGNLAPIFPC	LLGEPKIOAC	SRSESPSDSE	GEEIDVTVKK	ROSLSTRKPV	180
30				FPPESCFQEG			240
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				ENWTKKKYHS			300
	VPALASCSRV	SKVMILVKAT	EYLHELAEAE	ERMATEKRQL	ECQRRQLQKR	IEYLSSY	
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	CACCETTICCC	VCCCCCCCCC	CATCTCCACC	CTGGGCTGGT	dececcecce	dececceses	60
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40				GCCCGAGGCT			120
	TTGCCTTCTT	GATCTTCCGT	CCTTCTTGGA	GACGACTGGC	GAGAGGAAGA	GGGACTAGGT	180
	CCAAACGCTA	GGTGGCTGGG	TCCAGCCGGA	GACCCGCACC	AAGGAGGAGA	TCATCGAGCT	240
				CCCTGAAAAG			300
15				CACTCTGCTG			360
45				GACCAGCGAC			420
	AAGAGAGTCC	TCACCACCTC	ACTCAGTCCA	TTCTTTCAGT	GGTGACCGGG	ACTGGGACCG	480
				AGACCGCTGG			540
				TCCTGTGGTG			600
50				TTATGAGTCC			660
50	ATACCAAAAT	GTGGTGGACC	TCGCTGAGGA	CAGGAAACCT	CACAACACAA	TCCAGGACAA	720
	CATGGAAAAC	TACAGGAAGC	TGCTCTCCCT	CGGAGTGCAG	CTTGCTGAAG	ACGATGGCCA	780
				ATCCAAGAGA			840
				AAAATCAACC			900
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55	CAAATCGGGA	AGAGCAAGGG	AGTCAAGCGA	CCGGTCACAG	AGATTCCCCA	GAATGTCAGA	1020
	TGATAACTGG	AAGGACATTT	CATTGAACAA	GAGGGAGTCA	GTGATCCAGC	AGCGGGTTTA	1080
						CCAGAAAGAG	1140
				TGACACAGAT			1200
60				TGAATGTGGT			1260
60	GAGCGTGAGC	AGCCTGAGCA	GCCTCAGCTC	CCCCTCCTTT	ACCGAGTCAC	AGCCAATTGA	1320
	TTTTGGGGCA	ATGCCATATG	TATGTGATGA	GTGTGGGAGG	TCGTTCAGTG	TCATCTCAGA	1380
				AGAGAACCTC			1440
				GAAAAGTCAG			1500
C F				GAGTGCCGCC			1560
65	TCATGCTAGA	GGTTATCTTG	TGGAATGTAA	GAATCAGGAA	TGTGAGGAAG	CCTTCATGCC	1620
	TAGCCCCACC	TTTAGTGAGC	TTCAGAAAAT	ATATGGCAAA	GACAAATTCT	ACGAGTGCAG	1680
						AAATCCACTT	1740
						AGCGCGGGGA	1800
70				GTTTCAGAAA			1860
70	GTACGAATGT	AAGGTGTGTG	GGGAGACTTT	CCTTCATAGC	TCATCCCTGA	AAGAACATCA	1920
-				AAACAAGGGT			1980
						AGCTCTGTGA	
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						ATCAGAAAAT	2100
	TCATTCTCGA	AAGAACCTCT	TTGAAGGCAG	AGGGTATGAG	AAATCTGTCA	TTCATAGTGG	2160
75						GTGATGAGGA	2220
							2280
						CCTCTGTGGA	2340
						CAGAGTCTAC	2400
	CATTCAGAGC	TTCGATGCTA	TCAACCATCA	GAGAGTTCGT	GCTGGAGGGA	ACACCTCTGA	2460
80						CTCCAAGAAG	2520
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						AAGGGGGCAG	2640
	TAAGAATCGC	AACTATGAAG	ACTCTGTCAT	ACAGAGTGTA	TTCCGTGCCA	AACCTCAGAA	2700
						CTGTTCCCAG	2760
85						AGCATAGGAG	

	CAATGAGACC	TCTGTAATTC	ACTCTCTGCC	TTTTGGTGAA	CAAACATTTC	GCCCTCGAGG	2880
	GATGCTCTAT	GAATGTCAGG	AGTGTGGGGA	GTGCTTTGCT	CATAGCTCTG	ACCTCACTGA	2940
			GGGAGAAGCC				3000
5			CTGACCCTCA				3060
5			GTAAGGACTT ATGACCAAGA				3120
			CCCACAGCGA				3180 3240
			ACATGGAAGA				3300
			GCCTGGGCTT				3360
10	GAAAGTCCAC	AGCAGGAAGT	GCCTGGTTGA	CAGTCGGGAG	TACACACATT	CTGTAATTCA	3420
			ATCAGAGAGA				3480
	AAAGTGTGGG	GAATCTTTTA	TTCATAGCTC	ATTCCTTTTC	GAGCATCAGA	GAATCCATGA	3540
			TGAAGGGGTG CTGCAGAGAG				3600
15			GCTTCATTCA				3660 3720
			TGGAGCAGAG				3780
			AGAGAAGTCA				3840
			ACCCAGCAGA				3900
20			CCTCCTATAC				3960
20			AATGCAAGGA				4020
			TTCATCTGGA				4080
			AAGTTGAAGC AGGCTGCTGA				4140
			TGGAGGCTGC				4200 4260
25			TTGGAGAGGC				4320
			CAGATGGTGC				4380
			AAGAGCCAGA				4440
			GTGAAGATCA				4500
30			CCTTCACTTC				4560
30			TTGAGCCTGC				4620
			CAGGTGGTGC TCAATGACCG				4680 4740
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			CAATCCATGA				4860
35			TCTCTAAACT				4920
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40			TGACAGAACA CAGAGGTACC				5160 5220
70			ACAAATTTGA				5280
			TGAACCCTGT				5340
			GAAGCTGTAG				5400
15			CTTTAGCTTC				5460
45			AAGGCTTTAC				5520
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			TAGTGCCTAA				5760
50			GGCTAATAAC				5820
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60			RRESSPPHSV				120
			MDREDDRDSR				180
			HSHMTQGHSS				240
			SKSGRARESS RVLERKRRYH				360 360
65			DEGAMPYVCD				420
			ECKDCGETFN				480
			RVCKETFLHS				540
			MYECKVCGET				600
70						RGYEKSVIHS	660
70			DEKAFTISSN				720
			TIQSPDAINH				780
			SDLNDKRQKI SSNVREYQKA				840 900
			EHQKIHDREK				960
75			LNTNQKIYDQ				1020
	MAN			FVDLTDLTDH	QKVHSRKCLV	DSREYTHSVI	1080
	DPVIQGSDME				DODOT WOME		1140
	DPVIQGSDME HTHSISEYQR	DYTGEQLYEC	PKCGESFIHS				
	DPVIQGSDME HTHSISEYQR MKPRRNRAAE	DYTGEQLYEC RNPALAGSAI	PKCGESFIHS RCLLCGQGFI	HSSALNEHMR	LHREDDLLEQ	SQMAEEAIIP	1200
·80	DFVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS	DYTGEQLYEC RNPALAGSAI QTEERLFECA	PKCGESFIHS RCLLCGQGFI VCGESFVNPA	HSSALNEHMR ELADHVTVHK	LHREDDLLEQ NEPYEYGSSY	SQMAEEAIIP THTSFLTEPL	1200 1260
. 80	DFVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS KGAIPFYECK	DYTGEQLYEC RNPALAGSAI QTEERLFECA DCGKSFIHST	PKCGESFIHS RCLLCGQGFI VCGESFVNPA VLTKHKELHL	HSSALNEHMR ELADHVTVHK EEEEEDEAAA	LHREDDLLEQ NEPYEYGSSY AAAAAAQEVE	SQMAEEAIIP THTSFLTEPL ANVHVPQVVL	1200 1260 1320
80	DFVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS KGAIPFYECK RIQGLNVEAA	DYTGEQLYEC RNPALAGSAI QTEERLFECA DCGKSFIHST EPEVEAAEPE	PKCGESFIHS RCLLCGQGFI VCGESFVNPA	HSSALNEHMR ELADHVTVHK EEEEEDEAAA AEPNGEAEGP	LHREDDLLEQ NEPYEYGSSY AAAAAAQEVE DGEAAEPIGE	SQMAEEAIIP THTSFLTEPL ANVHVPQVVL AGQPNGEAEQ	1200 1260
.80	DPVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS KGAIPFYECK RIQGLNVEAA PNGDADEPDG DCHECTETFT	DYTGEQLYEC RNPALAGSAI QTEERLFECA DCGKSFIHST EPEVEAAEPE AGIEDPEERA SSTAFSEHLK	PKCGESFIHS RCLLCGQGFI VCGESFVNPA VLTKHKELHL VEAAEPEVEA EEPEGKAEEP THASMIIFEP	HSSALNEHMR ELADHVTVHK EEEEEDEAAA AEPNGEAEGP EGDADEPDGV	LHREDDLLEQ NEPYEYGSSY AAAAAAQEVE DGEAAEPIGE GIEDPEEGED	SQMAEEAIIP THTSFLTEPL ANVHVPQVVL AGQPNGEAEQ QEIQVEEPYY	1200 1260 1320 1380
	DPVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS KGAIPFYECK RIQGLNVEAA PNGDADEPDG DCHECTETFT	DYTGEQLYEC RNPALAGSAI QTEERLFECA DCGKSFIHST EPEVEAAEPE AGIEDPEERA	PKCGESFIHS RCLLCGQGFI VCGESFVNPA VLTKHKELHL VEAAEPEVEA EEPEGKAEEP THASMIIFEP	HSSALNEHMR ELADHVTVHK EEEEEDEAAA AEPNGEAEGP EGDADEPDGV	LHREDDLLEQ NEPYEYGSSY AAAAAAQEVE DGEAAEPIGE GIEDPEEGED	SQMAEEAIIP THTSFLTEPL ANVHVPQVVL AGQPNGEAEQ QEIQVEEPYY	1200 1260 1320 1380 1440
80	DPVIQGSDME HTHSISEYQR MKPRRNRAAE GLALTEFQRS KGAIPFYECK RIQGLNVEAA PNGDADEPDG DCHECTETFT	DYTGEQLYEC RNPALAGSAI QTEERLFECA DCGKSFIHST EPEVEAAEPE AGIEDPEERA SSTAFSEHLK	PKCGESFIHS RCLLCGQGFI VCGESFVNPA VLTKHKELHL VEAAEPEVEA EEPEGKAEEP THASMIIFEP	HSSALNEHMR ELADHVTVHK EEEEEDEAAA AEPNGEAEGP EGDADEPDGV	LHREDDLLEQ NEPYEYGSSY AAAAAAQEVE DGEAAEPIGE GIEDPEEGED	SQMAEEAIIP THTSFLTEPL ANVHVPQVVL AGQPNGEAEQ QEIQVEEPYY	1200 1260 1320 1380 1440

	·	124 DNA sec		96			
		id Accession Lence: 180		. 36			
5	1	11	21	31	41	51	
,	GTTCCCAGAA	GCTCCCCAGG	CTCTAGTGCA	GGAGGAGAAG	GAGGAGGAGC	AGGAGGTGGA	60
		TAAAAGGCTC					120
		GGTCCGAATC					180 240
10	CCTGGGCAGG	CCGACCTCGT					300
	CCCATTCGCA	GCCTTGGCAG	GCGGCCTTGT	TCCAGGGCCA	GCAACTACTC	TGTGGCGGTG	360
		TGGCAACTGG					420
		AGACCACAGC CCCACACCCC					480 540
15	TGATGCTTCT	TCAACTGCGT	GACCAGGCAT	CCCTGGGGTC	CAAAGTGAAG	CCCATCAGCC	600
		TTGCACCCAG					660
		AGAGAATTTT TGAGGATGCT					720 780
00	GCAGCAAAGG	GGCTGACACG	TGCCAGGGCG	ATTCTGGAGG	CCCCTGGTG	TGTGATGGTG	840
20		CATCACATCC					900
		CATCTGCCGC TAAGCACTAG				AGCAAGGGCT	960
25		125 Protei: cession #: 1		-			
	1	11	21	31	41	51	
	1	1		<u> </u>	1		
		TWMFLLLLGG AAHCKKPKYT					60 120
30		SLGSKVKPIS					180
		QITDGMVCAG	SSKGADTCQG	DSGGPLVCDG	ALQGITSWGS	DPCGRSDKPG	240
	VITNICRILD	WIKKIIGSKG					
35		126 DNA sec					
33		id Accession uence: 171.		791.1			
	1	11	21	31	41	51	
]					60
40		GAAGCGGCCA TCAGGACAGC					60 120
	TCCGCCCCTC	AGGTTCTTTT	TCTAATTCCA	AATAAACTTG	CAAGAGGACT	ATGAAAGATT	180
		TCTCAAATAT					240 300
		AGGGAGTGAT					360
45		GCATATATGT					420
		GTACTGCCCT GGAGACCCGG					480 540
		CTATGCTCAC					600
50		GCTGATTGAC					660
50		ATGCTGTGGG ATCAGAGGCA					720 780
	GTGGATTTCT	ACCATTTGAT	GATGATAATG	TAATGGCTTT	ATACAAGAAG	ATTATGAGAG	840
		TGTTCCCAAG					900
55		CCCAAAGAAA CAACTATCCT					960 1020
	ATGATTGCGT	AACAGAACTT	TCTGTACATC	ACAGAAACAA	CAGGCAAACA	ATGGAGGATT	1080
		GTGGCAGTAT AAAACCAGTT					1140 1200
		CACAGACATC					1260
60	ATAAAAATTA	TGTGGCGGGA	TTAATAGACT	ATGATTGGTG	TGAAGATGAT	TTATCAACAG	1320
						AATGGGGTGG AAGAACAAAG	1380 1440
	AAAATGTATA	TACTCCTAAG	TCTGCTGTAA	AGAATGAAGA	GTACTTTATG	TTTCCTGAGC	1500
65						CCAAATCGTT	1560
05						AAAATACCAG AGGCGGTGCC	1620 1680
	GCTCAGTGGA	ATTGGATCTC	AACCAAGCAC	ATATGGAGGA	GACTCCAAAA	AGAAAGGGAG	1740
						CTCACCAGGA TATAATGTGA	1800 1860
70						ATTCTTCCAA	1920
	AGAAGCATGT	TGACTTTGTA	CAAAAGGGTT	ATACACTGAA	GTGTCAAACA	CAGTCAGATT	1980
						CCCGATGTGG	2040 2100
						GATGAGTGTG	2160
75	GGTGTGATAC	AGCCTACATA	AAGACTGTTA	TGATCGCTTT	GATTTTAAAG	TTCATTGGAA	2220
						TTAAACAAAA CTGTCTTTTT	2280 2340
						TCCATATGTG	2400
80			TCTCTTTGTA	ATGTGTAATT	TCTTTCTGAA	ATAAAACCAT	2460
OU	TTGTGAATAT	-					
	Seq ID NO:	127 Protei	n sequence				
	Protein Ac	cession #:	NP_055606.1 21	31	41	51	
85	ī	<u>†</u>	1 .	1	ī	j.	
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					T1.00.000		
	WKDADEPTKA	YELHETIGTG	GFAKVKLACH	ILTGEMVAIK	IMDKNTLGSD	LPRIKTEIEA	60
	LKNLRHQHIC	QLYHVLETAN	KIFMVLEYCP	GGELFDYIIS	QDRLSEETR	VVFRQIVSAV	120
	ayvhsqgyah	RDLKPENLLF	DEAHKTKTID	FGLCAKPKGN	KDYHLQTCCG	SLAYAAPELI	180
_	QGKSYLGSEA	DVWSMGILLY	VLMCGFLPFD	DDNVMALYKK	IMRGKYDVPK	WLSPSSILLL	240
5	QQMLQVDPKK	RISMKNLLNH	PWIMQDYNYP	VEWQSKNPFI	HLDDDCVTEL	SVHHRNNRQT	300
	MEDLISLWQY	DHLTATYLLL	LAKKARGKPV	RLRLSSFSCG	QASATPFTDI	KSNNWSLEDV	360
		LIDYDWCEDD					420
		SAVKNEEYFM					480
	KIDOMETETO	KLMTGVISPE	PRCPQVELDI.	NOAHMEETEK	RKGAKVEGSI.	ERGLDKVITV	540
10		RDGPRRLKLH					600
10		FELEVOQLQK					000
	QSDFGKVIMQ	PELEVOQUQK	PDAAGTKKŐK	DEGUMATER	PAPPITIZZCY	•	
		128 DNA sec					
15		id Accession		luence			
15	Coding sequ	lence: 169-1	.323				
	1	11	21	31	41	51	
			1	1	1	1	
	GGGATCCTTT	CTGGAATGGA	GGTCTTATGA	GCTGCTATTG	AACACGGCAG	AGCCTGTTGG	60
	TGACCTGCAC	ACAGGAGCCC	TCCAGTCAGT	ACTGATTGAA	TTACTCAAGG	CTGCCTCTCT	120
20	GCAAAGTTGA	GCACTACAGG	ACGTCGGGAC	TGGGCATTTC	CTTCCAACAT	GGCCGCCACT	180
		AGCCACTCGC					240
		TGGATGAAGT					300
		TCCTCCCAGT					360
	GGCAAAGTCT	TCCTCCCAGT	CITCIAIAGC	CIGATITITO	CCCCC BCCC	MCACAGGAAC	420
25	CTCCTTCTTC	TCATGGTCTT	GCTCCGTTAC	GIGCUICGCA	GGCGGATGGT	TUAGATCIAI	
25	CTGCTGAATC	TGGCCATCTC	CAACCITCIG	TTTCTGGTGA	CACTGCCCTT	CIGGGGCATC	480
		GGCATTGGGT					540
		TTTACAGTGG					600
	GAGATCGTTC	ATGCTCAGCC	CTACCACAGG	CTGAGGACCC	GGGCCAAGAG	CCTGCTCCTT	660
	GCTACCATAG	TATGGGCTGT	GTCCCTGGCC	GTCTCCATCC	CTGATATGGT	CTTTGTACAG	720
30	ACACATGAAA	ATCCCAAGGG	TGTGTGGAAC.	TGCCACGCAG	ATTTCGGCGG	GCATGGGACC	780
	ATTTGGAAGC	TCTTCCTCCG	CTTCCAGCAG	AACCTCCTAG	GGTTTCTCCT	TCCACTCCTT	840
	GCCATGATCT	TCTTCTACTC	CCGTATTGGT	TGTGTCTTGG	TGAGGCTGAG	GCCCGCAGGC	900
	Cycccccccc	CTTTAAAAAT	AGCTGCAGCC	TTGGTGGTGG	CCTTCTTCGT	GCTATGGTTC	960
	CCATACAATC	TCACCTTGTT	TCTCCATACC	CTGTTGGACC	TCCAACTATT	CGGGAACTGT	1020
35	CCATACAATC	AGCATCTAGA	CTGCATACG	CIGITOGACC	ACACCAMOCC	COCCURCIO	1080
33							1140
-		CCCCCATCCT					
		CTGCCGTGCT					1200
		CTGAGAGCAG					1260
40		GGCAGTCTGA					1320
40		AATTTTGGTC					1380
	TCAAAGTGCT	CTCTCCAGGG	GCCTCAGTGA	CTGTGTTGCT	AAACCCAGTG	GTCAGTTCTC	1440
	AGTTCTCAGC	CATCAGCAGC	ATTTGCTCGC	CCCGCCTTCT	TCCTCCACTT	TCTTCACTTG	1500
	CTTCCAGGAT	ACCACGCTTT	CTTTTCTGAA	TTGCTACAAT	CTTTCTTCCT	TCCTTCCTTG	1560
	CTTCCTTCCT	TCCTTCCTTC	CCTCTCTCCC	TCCCTCCCTC	CCTCGCTTCT	TCCCTTCCTC	1620
45	CTTTCCTCCC	TTCCTACTTT	CCTTCCTTCC	TTCTGACAGG	GTCTTGCTCT	ATTGCTCTGT	1680
		GGAATGCAGT					1740
		TCATGCCTCA					1800
		TTTTGTATTT					1860
		TCACTCTTGT					1920
50		CTCCCGGATT					1980
50		TGCCACCACG					2040
		CAGGATGATC					2100
	AAAGTGCTGG	GATTACAGGT	GTGAGCCACC	ATGCCTGGCC	CTAATTTTTG	TGTTTTTATT	2160
<i>C C</i>	AGAAACAGAG	TTTCACCATG	TTGGCCAGGC	TGGAGAATTG	CTGTAATAGT	TTTCCAACTG	2220
55	GCCCCTGTCC	TTCCTCTCTC	TTGCTCTCCT	CCCATCTCAT	CTGCACCTAG	CAGCCAGAGT	2280
	GATCCTGATA	CTCTCGGCCT	TTACTTCCGC	CTCCCTCAGA	GCAGCAGCCT	GTCAAAACAC	2340
	CAGATTACAA	CAAATTTAGT	TTAAAGGTCT	CAATTAGCGT	TATTGGCAAT	TCTAGAATCA	2400
	GGCAACAGAC	TCATTGAATC	AGGAACAGAT	TCACTCCATA	AAATACAGAG	AGTGCTGCAA	2460
	TGAGCTGGGT	AGAAGAGGTT	AGTTTTATAG	ACAGGAAGGG	GCTGTCAAAG	GCAGAAAGAA	2520
60	ATGAAGAACA	AAAAAAAAGA	TTGATTTTTT	TTTTTTTGAG	ACAGGATCTC	ACTCTGTCAT	2580
	CCAGGCTGAA	GTCCAATCCC	ACAATCATGG	CTCACTGCAG	CCACCACCTC	CTGAGCTCAA	2640
	GTGATCCTC	CATCTAAGCC	CCCAAGTAGC	TAGGACTACA	GGAGCACACC	ACCACACCTG	2700
	CCTAAmmen	GTATTTTTT	TGGAGACAGG	GTCTCAGTAT	GTTACCCAGG	TTGGACTGGA	2760
	AACCOMMOGC	TCAAGCAATT	TOCAGACAGO	ACCUTCCCAA	ACTCCTCCCA	TTACAGGCGT	2820
65		ACAGGGCCAG					2880
05							2940
		ACATCAGTTT					
	TCATTATCAT	GAGCATGGTT	ACTGTCTGCA	TTATTACGCC	AACTGAAACT	GTCATGTTTG	3000
	GGAATTTGGC	TGTTAACTCT	GTCTCCAGGA	GTCTCAAAGG	TCAGATAACA	ACTTAGTTTT	3060
70		CATGGAACTT					3120
70		CAGGAGGTTA					3180
	CCAACTCCTT	ACGGTAATCC	TTTAAGGCCT	ATGTGATCTG	CCCTCACCCT	GGCTACACTC	3240
	TTTGCCCTTA	TGTCCACCAG	CCTCCAGTGC	TCCAGACACA	ACTGATCTCA	AATACTCCTG	3300
	ACACATCCCC	CTGGGGATTC	CTCTTCCTGG	ATTGCTCTCC	TCTCAGCTGT	CTGCTTGGCT	3360
	CACTCTCTCA	CCTTCTGAGG	TCTTAGCTCA	GATACCACCT	TTCACTCACC	TGTCCAACCT	3420
75						TATTTTTAAA	3480
. –						TTGTGATGTT	3540
	CAGTGGGTAG	TGTCCCTACC	CACATTGTCC	CAGGTGAATT	CCACAAGGTA	GGGATCTTGG	3600
	TTAGGGGGAG	***********	NACCOCCUES S	CACACIGICO	CCTCTCTACC	TTTTCAGAAA	3660
							3720
80	GTATCTGTAA	MATGCATGGG	TOP CONCINCION	MCCVCXCX	TICIGGCACI	GCTGGGGAAA	
OU	AAGAACCTAA	GGCCCTCCAC	CACCAGGGT	I CLACATICI	CIGIAGICCA	GCTGGGAAAT	3780
	GCTATTAAAA	GGACCATTCT	CGTAGCCTTG	ATGGTGGACC	CAGCATCTGG	CAATCAGGAG	3840
	GGCCTTGAAG	TACTCTGCCT	AGGGAATGTC	CCAGGACCAT	ATACAGTCTG	CAGAAGGAGG	3900
						TGGGACCTGC	3960
0.5	ACAATCAAGT	CCAAAATCTT	TGTCTGATGT	CAAGGCTAGG	GCTTTTGCAA	ATAGGATCCC	4020
85	ATACATCTTC	CAGCCCTCAT	ACTCCTCCAC	TCCCTTTTCA	TTTCCTGAAC	ATTCCAACTT	4080
			-				

5	CTATGCCTTT CCTCACCCTT TGCCCTGTGC ACATTTCCCT GAAGTGCAAT TGAGATCTGG GTGAGTGAGC AGTCCCAATC	GTTTTACAAC TTTGAGAGGA GGTCACGGTG ATCACTAGAA AGCTACTCCT AGATCCCGAG	TGAATCCCAC GGTTGGGTGG ATTTTTTTAG CATGTGAGAA TCCTCCACCC GGCACTGTTT	TTTCTCTGGG AGCATGGGAC GGGTGGGCAC GAGAGGCATG AAACTTCAGA GAGCCTCAGA	ACTCCACTGC ATGGGCCATT ATGACCTAGG AAACCGAAGC AGGTGAAGGA ATCAAAGCAC	TTGGTCACTC TACTGCCTTC TAGAGCCAAT TGAGAGGGTT GATAGTGCAT TTCTGAAGCT	4140 4200 4260 4320 4380 4440 4500
10	Seq ID NO: Protein Acc			31	41	51	
15	LSGNLLLLMV STLYTINFYS VFVQTHENPK RPAGQGRALK	LLRYVPRRRM GIFPISCMSL GVWNCHADFG IAAALVVAFF	VEIYLLNLAI DKYLEIVHAQ GHGTIWKLPL VLWFPYNLTL	SNLLFLVTLP PYHRLRTRAK RFQQNLLGFL FLHTLLDLQV	VVSFGKVFLP FWGISVAWHW SLLLATIVWA LPLLAMIFFY FGNCEVSQHL	VFGSFLCKMV VSLAVSIPDM SRIGCVLVRL DYALQVTESI	60 120 180 240 300
20	GMNDLGERQS Seq ID NO:	ENYPNKEDVG	NKSA	LGWHLAPGTA	QASLSSCSES	SILTAGEEMI	360
:		d Accession	1 #: NM_0027	774			
25	1	11	21	31	41	51	
	AGCCCGGGGC	AGGGGCGGG	GCCAGTGTGG	TGACACACGC	CGCGCCTGGG TGTAGCTGTC AGCACACAGA	TCCCCGGCTG	60 120 180
30	CGGCCATGAA AGAATAAGTT TCTACACCTC	GAAGCTGATG GGTGCATGGC GGGCCACTTG	GTGGTGCTGA GGACCCTGCG CTCTGTGGTG	GTCTGATTGC ACAAGACATC GGGTCCTTAT	CCGGAGGCCT TGCAGCCTGG TCACCCCTAC CCATCCACTG	GCAGAGGAGC CAAGCTGCCC TGGGTCCTCA	240 300 360 420
35	AAAGGGAGAG ATGCCGCCAG CTGAACTCAT ACATCCTGGG	TTCCCAGGAG CCATGACCAG CCAGCCCCTT CTGGGGCAAG	CAGAGTTCTG GACATCATGC CCCCTGGAGA ACAGCAGATG	TTGTCCGGGC TGTTGCGCCT GGGACTGCTC GTGATTTCCC	GGGGAAGCAT TGTGATCCAC GGCACGCCCA AGCCAACACC TGACACCATC	CCTGACTATG GCCAAACTCT ACCAGCTGCC CAGTGTGCAT	480 540 600 660 720
40					CCCTGGCCAG		780
40					CTGCCAGGGT ATGGGGTAAC		840 900
					ATACACGAAC		960
					CTCCCGACCT		1020
45					CCTCCTCTCC		1080 1140
73					AGGACTTGGG		1200
	TACCCCCACC	ACTAAGAGAA	TACAGGAAAA	TCCCTTCTAG	GCATCTCCTC	TCCCCAACCC	1260
					TGTCTGGAAT ACTGCAGATT		1320 1380
50					GCTGTTGGAA		1440
	TTTCACACCT TATTTT	ATGACATACA	TGGGATAGCA	CCTGGGCCGC	CATGCACTCA	ATAAAGAATG	1500
	rp wo.	131 Buch-4					
55		131 Protei: 2ession #: 1					
	1	ļ1	21	31	41	51	
	MKKI-MVVI.SI.	I TAAAWAEEON	 KLVHGGPCDK	TSHPYOAALY	TSGHLLCGGV	LIHPLWVLTA	60
CO	AHCKKPNLQV	FLGKHNLRQR	ESSQEQSSVV	RAVIHPDYDA	ASHDQDIMLL	RLARPAKLSE	120
60					HLVSREECEH KEKPGVYTNV		180 240
	IQAK	DacQGDaGGF	DACGDUREGR	VSWGMIFCGS	REREGULIAV	CKIIKWIQKI	230
	Sea ID NO:	132 DNA sec	nuence				
65	Nucleic Ac	id Accession	n #: AY0380	71.1			
	Coding sequ	uence: 110	585 21	31	41	51	
	Ī	1		1	1	1	
70					CCGAGTGCAA	CCCGTGCAAA	60 120
70						CGCCGACCCG	180
	GAAAAGGCCG	TGCAAGGCTC	CCCTAAGAGC	AGCAGCGCCC	CGTTCGAGGC	CGAGCTGCAC	240
					GCCGCCTCCT	TCAGGGTGCG	300 360
75					GGCCCGGGGA		420
	GGCGCAGGGG	CCGCCGCGGC	AGCCGCGGCC	GCGGCCGCCG	CGGCCTGGGA	CACGCTCAAG	480
						GAACGGGGCG	540 600
						CGTCACGCAC GGGTGGTGGC	660
80	ACCGGCACCG	AGGACGACGA	GGAGGAGCTG	CTGGAGGACG	AAGAAGATGA	GGACGAGGAA	720
					ACGACGCCCG	CGCGCTGCTC AGCTGCCGCT	780 840
						GCACCCGGAA	900
05	GACGCTGAGG	GCAAGGACGG	CGAGGACAGC	GTGTGCCTCT	CTGCGGGCAG	CGACTCGGAG	960
85	GAGGGGCTGC	TGAAACGCAA	ACAGAGGCGC	TACCGCACCA	CGTTCACCAG	CTACCAGCTG	1020

5	CTGGCCATGA GCCAAGTGGC CCGGGGCCACCACC TTCCCGAGCC GGCCTGAGCA TTCGGCAGGC CTGAGACAGC CTGAGACAGC	AGCGGGCCTT GGCTGGACTT GCAAGCGGA TCTCCGCCAC TACCTCCGC CTTTCCTCGC TCTTTCCTCGC CCACACCCGC CCGCAGACAG CGCAGCTCAC	GACCGAGGCC GAAGGCAGGC CCACCGCTC CTCCGCTTGG TCCGGGCTCG AGCGGCAGTG AATGGCCCCC CGTGGAGGGC ACGCGCCTCT	CGAGTCCAGG GCGCAGACCC AGCCCCTACC ACTGCCGCTG GCCAGCCTGC TTCCGACACC CTGACCAGCG GCAGTGGCAT AGCATAGCCG	TCTGGTTCCA ACCCCCTGG TGGACGCCAG CCGCCGCCGCCGCCAGCCG CAGCTTTCAT CGTCGACCGC CGGGCGCCCT CGCTGAGGCT	GAACCGTCGG GCTGCCCTTC CCCCTTCCCT CGCCGCCGCC GGCGCCGCTC CAGCCCGGCA GGCCGGCTC GGCCGACCCG CAAGGCCAAG	1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680
15		133 Proteir					
13	1	cession #: F 11	AK93901.1	31	41	51	
20	EKAVQGSPKS PRGEAPPPPP PFVPPPPALD EELLEDDEEE	SERPECKSKS SSAPFEAELH PTARPGERPD ELGGPGGVTH LLEDDARALL VCLSAGSDSE	LPPKLRRLYG GAGAAAAAA PEERLGVAGG KEPRRCPVAA	PGGGRLLQGA AAAAAWDTLK PGSAPAAGGG TGAVAAAAAA	AAAAAAAAA ISQAPQVSIS TGTEDDEEEL AVATEGGELS	AAAAATATAG RSKSYRENGA LEDEEDEDEE PKEELLLHPE	60 120 180 240 300 360
25	PHHPALDSAW FGRLFSTMAP	RVQVWFQNRR TAAAAAAAA LTSASTAAAL ILPGTSTGKE	PPSLPPPPGS LRQPTPAVEG	ASLPPSGAPL	GLSTFLGAAV	FRHPAFISPA	420 480 540
30		134 DNA sec	-	ıster			
	1	11	21	31	41	51	
35	TGCTTGAGCA CACGTAGCAC ACAGAACTGA GTCTTTTGTC	TTTTTTTAAA GTGTTATAGC ACACATATTC TTCCTGCAGA TGTATTGCCC	ACTCAGCCCT AGCCATATCA ATATCCTGAG TTGACACCTC	CAGGGCAAAG TGCTGAATGG ATACTTATCA CTCAAGGAAA	ATAAGTCTTC GAATACAGGA AGCTGTTAAA GTATCTAGAA	ACCATTGTCA CTTTGTAGAA GGAGACATCA ATTCTTTGTC	60 120 180 240 300
40	TAGAATAGAA	CCCTCAGACC AAGCACCTTG	AAAACTGTAG	TCTGACTTAA	TAGACACAAA	TATAATGAAA	360 420
40		ATAAGATCCT TGCACAGGAA			GCAAAAGGCA	CAAGCTTCAG	480
45	Nucleic Ac:	135 DNA sec id Accession Lence: 199	#: NW_006.	799			
45	Nucleic Ac:	id Accession	#: NW_006.	799 31 	41 . 1	51 	
45 50	Nucleic According sequents GCCGCGGGAG GCGGCTGGAC CGACGGGTCA TGGCAGGGGA CGCTGGGCAC CGCTGGGCAC	id Accession Lence: 195 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCGCGC	1 #: NM_006' 063 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT	31 GGGGCGCTGC GAGGCGCGC GGAGAGGACG CACGTATGCG GAAACCTATA	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC	60 120 180 240 300
50	Nucleic Act Coding sequil 1 GCCGCGGGAG CGGCTGGAC CGACGGGTCA TGGCAGGGGA CGCTGGGCAC GGGTGGATGG TACTACACCC	id Accession uence: 19 11 AGBAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGGC TCACGGCGGC TCACGTCTGG	#: NM_006' 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC	31 GGGGCGCTGC GAGGCGGCGC GCAGAGGACC CACGTATGCC GAAACCTATA TCCATGCCAT TATCTGAGCC	TGCTGGCGCT TGCTGGCGCT CGTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT	GCTGCTGGCT ACCATGCGGC GCGTTGGCCG GCTCAGCCAC TGATCCCTCC CCTGCAGGCC GGGGAATTCA	120 180 240 300 360 420
	Nucleic Ac: Coding sequil Codesease Cogectegac Cogactegac Cogactegac Cogactegac Cogactegac Cocategac Coca	id Accession lence: 19 11 AGAAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGCC TCACGTCTTGG GTTACTTCGT TTGCCTTGGT TCCAGGCCTC ACATCAAACAA	#: NM_006' 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATGGAATATC GAAGCTGTCT CACATTTGAG GGATGAGGA CTCTATGTGC	31 GGGGCGCTGC GAGGCGGCGC GCACTATGCG GAAACCTATA TCCATGCCAT TTTTGAGGCC GCACCTGTCA TTTGAGAACCC CTGCCATCTCC AACCACCTCT	TGCTGGCGCT CGTTATCAGG CCGAACTCAG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CCTGCTACCT CCTACACTAA GGCAGACTG TCCTCAAGTA	GCTGCTGGCT GCTTGGCCG GCGTTGGCCA GCTCAGCCAC TGATCCCTCC GCGGAATTCA ACACATCCAG CTCAGGTGACT CCAGGAAGTT CAGGTAGTT CCAGGAAGTT CAGGTACT	120 180 240 300 360 420 480 540 600
50	Nucleic Ac: Coding sequil GCCCCGGGAG GCGCTGGAC CGACGGTCA TGGCAGGGGA TGGCAGGGGAC GGGTGGATCG TACTACACCC CCCTATGACA CCCATTGTC GGCTGGGGT CAGGTCGCA AAGGACATCT TTCCGTGACT	id Accession uence: 19 11 AGGAGGCCAT TCACGGCGC GCCTGCGCC TCACGTCGCG GCTTCACGTCGG GTTACTTCGT TTCCCTTGGT TCCAGGCCTC ACATCAAAGA TCATAAACAA TTGGAGACAT	#: NM_006' 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGGT GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT ACCATTTTGAG GGATGAGGCA CTCTATTGGG GGTTTGTGC CTTGGCCTGT	31 GGGGGGGG GAGGGGGG GAGGAGGACG CACGTATGCG GAACCTATA TATCTGAGCC GCACCTGTCA TTTGAGAACC CTGCCATCTC AACCACCTCT AGCAACGCC AACAAGAATG	I TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTT GTGACCTTAG CCTTCTGGAG CTCGCTACACTAA GGACAGACTG CCCACACCCT TCCTCAAGTAA AAGGCGGGAA GACTGTGGTAA GACTGTGGTAA	GCTGCTGGCT GCTGCTGGCG GCGTTGGCCG GCTCAGCCAC CCTGCAGGCC GCGGAATTCA ACACATCCAG CTGGGGAATTC CCAGGAAGTT CAGGTGACT CAGGTGACT CAGGTGCT CTCAGGATGCCTGC GCATTCCGC GCATTCCGC GCATTCCGC GCATTCCGC GCATTCCGC GCATTCGAC TCAGATTCGA	120 180 240 300 360 420 480 540 660 720 780
50 55 60	Nucleic Ac: Coding sequil GCCGCGGGAG GCGCGGGAC CGACGGGTCA TGGCAGGGGAC TGGCAGGGGAC TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGGT CAGGTCGCCA AAGGACATCT TTCGGTGACT GTCGTGACT GTCGTGACT GTCGTGACT CCCTCCTGGC TGAGCCTACC	id Accession uence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGCCGG GCTGCGCT TCACGCCGG GTTACTTCGT TTCCTTGGT TCCAGGCGCT ACATCAAAGA TCATAAACAA TTGAGACAT TCAGGGCCC GGGGAGTGGG TCAGTGGACC GGGGAGTGGA TCAGTGGACC TCAGTGGACC TCAGTTGGT TCAGTGGACC TCAGTGGACC TCAGTGGACC TCAGTGGACC TCAGTGGACC TCAGTGGACT TCAGCCATG	#: NM_006' 163 21 1 GGGCGCGCGC GGAGTCGCAG CATCGTTGT CCAGCTGATT CCAGCTGATT ATCGAATATC GAAGCTGTT CACATTTGAG GGATTAGAG CTCTATGAG CGTTTTTGAG CGTTTTTGTGC CGTTGTGTCT CTTGGCCTG CTGTGGTCGG CCAGAAGCTG CTTCCCTCTT CAGCCTGGGGGGGGGG	31 GGGGCGCTGC GAGGGGGCG GGAGAGGACG GAACCTATA TCCATGCCAT TTTGAGAACC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT AACCACCTCT AACAGATGCCC AACAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCC	I TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTT GCTGCTACACTAA CGCACACCCT TCCTCAAGTAA AAGGCGGGAA GACTGTGGTGCTACCTCAAGTAA CCGGTGTCTACACTAA ACGCGGGAA CACCCT TCCTCAAGTA CCGGTGTCTA CCGGTGTCTA CCGGTGCCCT TCCCACTCCT GTCAGGCCCCT	GCTGCTGGCT GCTTGGCCG GCTTGGCCC GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGAAGTT CAGGTTCCGC GGATGCCTGC GGATGCCTGC CCAGGAAGTT CAGGTTCCGC GGATGCCTGC CCAGCCAGAC CCCAGCCAGAC GGGCCGGTC GGTTCTCTTC	120 180 240 300 360 420 480 540 600 660 720
50 55	Nucleic Ac: Coding sequil GCCGCGGGAG GCGGGTGGAC CGACGGGTCA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGT AAGGACATCT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGTGACAC TGTCTT	id Accession uence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGCGGCT TCACGCGGCT TCCAGTTTGG TTGCCTTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TCATAAACAA TCAGAGACAT CAGGGGTGGA CTGGGAGTGGG TTGAGTGGAT CGCTACTCT TGAGCCCATG GGTAATAAACA	#: NM_006' 63 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGATTCC CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATGAGCA CTCTATGTGG CTTTGTGCT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT CTTCGCCTGT CCAGAAGCTG TTTCCCTCTT CAGCCTGGGG ACATTCCAGT	31 GGGGCGCTGC GAGGGGGCG GGAGAGGACG GAACCTATA TCCATGCCAT TTTGAGAACC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT AACCACCTCT AACAGATGCCC AACAGAATG CCCAATCGGC ATGGCCCAGA CTCTGGGCTCC	I TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTT GCTGCTACACTAA CGCACACCCT TCCTCAAGTAA AAGGCGGGAA GACTGTGGTGCTACCTCAAGTAA CCGGTGTCTACACTAA ACGCGGGAA CACCCT TCCTCAAGTA CCGGTGTCTA CCGGTGTCTA CCGGTGCCCT TCCCACTCCT GTCAGGCCCCT	GCTGCTGGCT GCTTGGCCG GCTTGGCCC GCTCAGCCAC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGGGAAGTT CAGGTTCCGC GGATGCCTGC GGATGCCTGC CCAGGAAGTT CAGGTTCCGC GGATGCCTGC CCAGCCAGAC CCCAGCCAGAC GGGCCGGTC GGTTCTCTTC	120 180 240 300 360 420 480 540 600 660 720 780 840 960
50 55 60	Nucleic Ac: Coding sequil GCOCGGGGAG GCGCGGGAG CGACGGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA CCCATCTGTC GGCTGGGGCT AAGGACATCT TTCGGTGACT GTCGTGACT TCCGTGACT TCCCTCCTGGC TGACCACCACT TGTCTTGTTT Seq ID NO: Protein Ac 1	id Accession uence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGGCGGC GCCTGCGCT TCACGGCGGC TCACGTTGG TTCATTGGT TTGCCTTGGT TCCAGGCGCT TCAGGCAT TCAGGCAGC TCAAAGA TCATAAACAA TTGAGACAT TCAGTGGACC GGGAGTGGG TCAGTGGAC GGGAGTGGA TCAGTGGAC 136 Protei Cession #: 1 1 LLLARAGLRK	#: NM_006' 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTTGT CCAGCTGATT CCAGCTGATT ATCGAATATC GAAGCTGTT CACATTTGAG GGATTAGAG CTCTATGAG CTTTCCCTCT CAGCCTGGAAGCTG ACATTCCAGT A Sequence NP_006790 21 PESQEAAPLS	31 	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCTT GCTGACCTTAG CCTCTTAGACTAA GGACAGACTG CCCACACCCT TCCTCAAGTAA AAGGCGGGAA GACTGTGCTAC CTGCAAGTAC CCGGTGTCTA CCGGCCCT CAGGGCATTC 41 RIVGGEDAEL	GCTGCTGGCT GCTGCTGGCG GCGTTGGCCG GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACTCCAG CTGGTGACT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC GCAGATTCCAGC GGATGCCTGC GCAGCAGAG CACCAATATC CCAGCCAGAC GGGTCCTGC GGTTCTCTT TTCAAAA 51 GRWFWQGSLR	120 180 240 300 360 420 480 540 660 720 780 900 960 1020
50556065	Nucleic Ac: Coding sequil GCOCGGGGAG GCGCGGGAG CGACGGGTCA TGGCAGGGGA TGGCAGGGGA TACTACACCC CCCTATGACA ACCATCTGTC GGCTGGGAC TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGTGACT TTCGTGACT GTCTTCTTC TGTGACT GTCTTCTTT Seq ID NO: Protein Ac: I MGARGALLLA LWDSHVCGVS VSNIYLSPRY EDEALPSPHT	id Accession uence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGTCGCG TCCAGTTTGG TTCACTGGT TCCAGGCGTC ACATCAAAGA TCATAAACAA TCATAAACAA TCAGAGACAT CAGGTGGAC GGGAGTGGG TTCAGTGGAT CAGTATAACA 136 Prote: CCSACTCTT LLLARAGLAC LLLARAGLAC LLSHRWALTA LCHSPYDIAL LQEVQVAIIN YQIGVVSWGV	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG GTGGGATTCC GCACTGCTTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTTGAG GGATTGAGGCA CTCTATTGAG CGTTTTTGAGC GGTTGCTCTT CTGGCCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CTGGCTGT CAGCTGGGG ACATTCCAGT I Sequence NP_006790 21 PESQEAAPLS AHCFETYSDL VKLSAPVTYT NSMCNHLFLK	31 GGGGCGCTGC GAGGCGCGCG GGAGAGGAC GCACTATGCG GAAACCTATA TCCATGCCAT TTTGAGAAC CTGCCATCTC AACCACCTCT AACCACCTCT AACCACCTCT CGCAATGCCC ATTGGGCA CTCTGGGCT CCCACTGCCAA TGGCCCAG TGGCCTGC 31 GPCGRRVITS SDPSGWMVQF KHIQPICLA YSFRKDIFGD	TGCTGGCGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTCTCTGGAG CTCGCTACCTA CCCACACCCT TCCTCAAGTA AAGGCGGGA AAGGCGGGA GACTGTCT CCCACTCCT GTCAGGCCT GTCAGGCATTC CCGGTGTCTA 41 RIVGGEDAEL GQUTSMPSFW STFEFENRTD MVCAGNAQGG	GCTGCTGGCT GCTGCTGGCG GCTTGGCCG GCTCAGCCA GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGAGGCAGT CCAGGAAGTT CCAGGAAGTT CCAGGAAGTT CCAGGAAGTT CCAGATTGGA CACCAATATC CCAGCCAGA GGGGCCGGT GGTCTCTTC TTCAAAA	120 180 240 300 360 420 540 600 720 780 840 900 960 1020
5055606570	Nucleic Ac: Coding sequil Coding sequil GCCGCGGGAG GCCGCGGGAG CCGACGGTCA TGGCAGGGGAA CGCTGGGCAC TACTACACCC CCTATGACA ACGACTCGTC GCTGGGGGT AGCACACT TTCGTGACT AGCACACT TTCGTGACT AGCACACT TCCTTGTT Seq ID NO: Protein Ac LWDSHVCGVS VSNIYLSPRY EDEALPSPHT PLACNKNGLM FFPLLWALPL Seq ID NO: Nucleic Ac Coding seq	id Accession uence: 19 11 AGGAGGCCAT TCAGGAGGCCAT TCAGGAGGCCT TCACGTCGCG GCCTGCGGCT TCACGGCGT TTACTTGGT TTGCCTTGGT TTGCCTTGGT TCCAGGCCTC ACATCAAAGA TCATAAACAA TCATAAACAA TCAGAGACAT CAGGTGGAC GGGGAGTGGG TTGAGTGGAT CGTACTCTT TGAGCCCATG GGTAATAAAC 136 Protein cession #: 1 LLLARAGLRK LLSHRWALTA LCMSPYDIAL LQEVQVAIIN YQIGVVSWGV LGPV 137 DNA sei id Accession uence: 19	#: NM_006* 163 21 GGGCGCGCGC GGAGTCGCAG CATCGTGGT GTGGGATTC CACATGCTTT CACATTTGAG GGATGAGGCA CTCTATTGAG GGATGAGGCA CTCTATGTGC CGTTTGCCTGT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT CTTGGCCTGT CAGAAGCTG CTAGAAGCTG CTAGAAGCTG CTAGAAGCTG CTAGAAGCTG CTAGAAGCTG CAGAAGCTG CAGAAGCTG CAGAAGCTG CAGAAGCTG CAGAAGCTG CAGAAGCTG CAGAAGCTG CAGCTGGGG ACATTCCAGT DESCEAAPLS ACATTCCAGT NECONOMINELE CGCGPNRPGV Quence U#: Eos se	31 GGGGCGCTGC GAGGCGCGCG GGAGAGGACC GCACTATGCG GAAACCTATA TTCTGAGCC TTTGAGAACC TTTGAGAACC CTGCCATCTC AACCACTCT GCAATGCC AACCACTCT GCAATGCC ATGCCAGA TCTGCCAGA TCTGCCAGA TCTGCCAGA TCTGCCAGA TCATGCCTTG 31 GPCGRRVITS SDPSGWMVQF KHIQPICLQA YSFRKDIFGD YTNISHHFEW Quence	TGCTGGCGCT TGCTGGCGGCT CGTTATCAGG CCGAACTCGG GAGTGAGCCT GTGACCTTAG CCTCTCAGGAG CTCGCTACCTAA CCTACACTAA GACAGACTG CCCACACCCT TCCTCAAGTA AAGGCGGGAA GACTGTGGTA CCGGTGCTCA GTGGCATGTC TCCCACTCCT GTCAGGCATTC 41 RIVGGEDAEL GQLTSMPSFW STTEFENRTD MVCAGNAQGG IQKLMAQSGM	GCTGCTGGCT GCTGCTGGCG GCTCAGCCG GCTCAGCCC GCTCAGCCC CCTGCAGGCC GGGGAATTCA ACACATCCAG CTGATTCCCC GGATGCCTGC CAGGAAGTT CAGTTTCCCC GCAGCCAGA CACCAATATC CCAGCCAGAC GGGCCGGTC GGTTCTCTT TTCAAAA 51 GRWPWQGSLR SLQAYYTRYF CNVTGWGYIK KDACFGDSGG SQFDPSWPLL	120 180 240 300 360 420 480 540 660 720 780 960 1020
505560657075	Nucleic Ac: Coding sequil Coding sequil GCCCGGGGAG GCGGGTGGAC CGACGGGTCA TGGCAGGGGAA CGCATGGATGG TACTACACCC CCCTATGAC GCCTGGGGT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TTCGTGACT TAGCACACT CCTCTTGTT Seq ID NO: Protein Act LWDSHVCGVS VSNIYLSPRY EDEALPSPHT PLACKNGLW FFPLLWALPL Seq ID NO: Nucleic Ac Coding seq 1	id Accession uence: 19 11 AGGAGGCCAT TCAGGAAGCC TCACGTCGCG GCCTGCGCCT TCACGGCGCT TCACGGCGCT TCACGGCGCT TCACGGCGCT TCACGGCGCT TCACGGCGT TGCATTGG GTTACTTCGT TGCATAAACA TCATAAACA TCATAAACA TCATAAACA TCAGGCCTC ACATCAAAGA TCATAAACA CAGGTGGAC CGGGAGTGGG TTGATGGAT TGAGCCCATG GGTAATAAAC 116 Protein cession #: 1 LLLARAGLRK LLSRWALTA LGNSPYDIAL LQEVQVAIIN YQIGVVSWGV LGPV 137 DNA secid Accession uence: 19	#: NM_006' 163 21 GGGCGCGCG GGAGTCGCAG CATCGTTGGTT CCAGCTGACT ATCGAATATC GAAGCTGTCT CACATTTGAG GGATGAGCA CTCTATGTGG CTTTGTGTCT CTTGGCTGT CTTGGCTGT TTTCCCTCTT CAGCCTGGGG ACATTCCAGT TTTCCCTCTT CAGCCTGGGG ACATTCCAGT PESQEAAPLS AHCFETYSDL VKLSAPVTYT NSMCMHLFLK GCGRPNRPGV QUENCE n #: Eos se 39 21	31 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TGCTGGCGCT TGCTGGCGGC CGTTATCAGG GAGTGAGCCT GTGACCTTAG CCTTCTGGAG CTCGCTACCT CCTACACTAA GGACAGACTG CCCACACCCT TCCTCAGGTA GACTGTGGTACCT TCCTCAGGTAC GTGCATCT CCACACCCT TCCTCAGGTAC GACTGTGGTA GACTGTGGTA GACTGTGGTA GACTGTGGTA GACTGTGGTA GACTGTGGTA GACTGTGGTA GTGGCATTC TCCACTCCT GTCAGGCCCT CAGGGCATTC 41 RIVGGEDAEL GQLTSMPSFW STFEFENRTD MVCAGNAQGG IQKLMAQSGM .	GCTGCTGGCT GCTGCTGGCCA GCGTTGGCCG GCTCAGCCAC CCTGCAGGCC GGGGAATTCA ACACTCCAG GCTGGTAGCT CCAGGAAGTT CAGTTTCCGC GGATGCCTGC TCAGATTCCAC GGATGCCTGC TCAGATTCCAC GGGCCAGAC CACCAATATC CCAGCCAGAC GGGTCCTCTT TTCAAAA 51 GRWFWQGSLR SLQAYYTRYF CWYTGWGYIK KDACFGDSGG	120 180 240 300 360 420 480 540 660 720 780 960 1020

5	GGGCACTGCT CTGACTTCCA AATATCTATC CTGTCTGCAC TTTGAGTTTG GAGGCACTGC ATGTGCAACC TGTGCTGCAC GCCTGTAACC AGGTCGGCCA AAGCTGATGG	CCCACGTATG TTGAAACTGA TGCCATCCTT TGAGCCCTCG CTGTCACCTA AGAACCGGAC CATCTCCCCA ACCTCTTCCT ATGCCCAAGG AGAATGGACT ATCGGCCCGG CCCAGAGTGG GGGCTCTCCC	CCTTAGTGAT CTGGAGCCTG CTACCTGGGG CACTAAACAC AGACTGCTGG CACCTCCAG CAAGTACAGT CGGGAAGGAT GTGCTACACC CATGTCCAG	CCCTCOGGGT CAGGCCTACT ATCCAGCCCA ATCCAGCCCA ATCAGCCCA GTGACTGGCT GAAGTTCAGG GTCCGCAAGG GCCTGCTTCG ATTGGAGTCC CCAGACCCCT	GGATGGTCCA ACACCCGTTA ATGACATTGC TCTGTCTCCA GGGGGTACAT TCGCCATCAT ACATCTTTGG GTGACTCAGG TGAGCTGGGG ACCACTTTGA	GTTTGGCCAG CTTCGTATCG CTTGGTGAAG GGCCTCCACA CAAAGAGGAT AAACAACTCT AGACATGGTT TGGACCCTTG AGTGGGCTGT GTGGATCCAG	240 300 360 420 480 540 600 660 720 780 840 900
15		138 Protein ession #: E 11		e 31	41	51	
20	LWDSHVCGVS NIYLSPRYLG EALPSPHTLQ	LLLARAGLRK LLSHRWALTA NSPYDIALVK EVQVAIINNS IGVVSWGVGC	AHCFETDLSD LSAPVTYTKH MCNHLFLKYS	PSGWMVQFGQ IQPICLQAST FRKDIFGDMV	LTSMPSFWSL FEFENRTDCW CAGNAQGGKD	QAYYTRYFVS VTGWGYIKED ACFGDSGGPL	60 120 180 240 300
25	I DDMADI DOG						
	Nucleic Aci	139 DNA sec d Accession mence: 131	#: NM_0143				
30	1	11	21	31	41	51	
	TCGCCGCCGG CCGCGGGAGC	TGGGGCCGAA GACCCGGGTG ATGGGCAGGA TCGCTGCTGG	CCTGGGCTCG GGATGCGGGG	GCTTGAAGCG CGCCGCCGCC	GCGGCGGCGC ACCGCGGGGC	ACCGGCACAG TCTGGCTGCT	60 120 180 240
35	CGCCTCCCGG GCCCGCGCCT GAAAACTTTC CCGGAGCGAG	CCGCCCGAAG CGCTTCCCTC CGGGCGCTGC CCCAGGTGGC GGCGTCTTCT	ACCGACTCCC TGCCCCCGCC TCACCCTGGC ACGTGTCAGC	ACGGCGCCCG CCTGGCGTGG GGCCGCGCG CAGGCAGCCC	GCCCGGAGCG GACGCCCGC GACGCCCGC CGGCCGGAGG	GCGGCCCCGC GCGGCTCCCT CCCGGCAGTC AGAGCGCCGC	300 360 420 480
40	GGAGGCCCAG GCGCGGGGGT CTGCGTGCGC	GCGGCGCGT TGCGGGCGCA TACGGCATCA CTGGGCCTCC	GGCTGGAGGC GCTCCAACCG ACCCGGAGCA	GGCTCGCGGC ACTGGCCCGT GATTCAGGGC	GCCCGGATGG TTTGCCGACG GAGGCCCTGT	TGGCCCTGGA GCACCCGCGC CTTACTATCT	540 600 660 720 780
45	CAGCGTGGTG CTGGCGCTCG CCTCAGCCAG	CAGTGGGCGC AGCCTGACAC GAGGACGGCC GCGGAGCTGG AACTTCGACC	GCTGGCTGCC GTCTGCGCCC TGGACCTAGT	CAACCTCACG CCTCCGGGAT ACAATGGACC	GACGTGGTGG GCCGGGGGTG GACTTAATCC	TGCCCGCGCC AGCTGGCCAA TTTTCGACTA	940 960 1020 1080
50 ,	GGACAATGAG CGAGCCGCTG GCTGCACCGC	CGTGCCACCA GCGGGCTTGG TTGCAGTCAG GGACAGGACG GAGCTGGCCG	TGCACGGCTA TGTGCGTGTT CCGCGGCCCG	CCGGGTAGCA CCGCGAGCGG GCTGCTGCGC	GGCATGTGGG ACCGCGCGGC CTCTACCGGC	ACAAGTATAA GCGTCCTGGA GCCACGAGCC	1140 1200 1260 1320 1380
55	CGACTTCCTC TTAGTGTCAC GGGCGGTCGC TAAAAACTTC	GCCAAGCACA CGGGAGGAAA CTCTGCCACT AGCTTTTCAC GAGGACGAAC	TTTTGCACTG AGAGAGAGAT GTCAGGGACC CCACCTGCCC	TAAGGCCAAG CTGGGGCTGG AGCCGGCCAA CTTTCTTTCA	TACGGCCGCC GGTATGGATG CGCCCACCCG ATCCCACGCT	GGTCTGGGAC ATGGGGGGAA CAAAGGTGTC GTTTCCTTTC	1440 1500 1560 1620 1680
60	GTTTGGCCCC TCCCTTTCCG CCAAACAGAG CTGTGTTCTC	TCTTTACTGT CGAGTGGCCG AAAAAGGAAA CGCTGGTGGC CCTTTGTTCC	TCCCTGTGGG ACTTGCGTTT CCCGGAGCAG AGCGCCGCGA	AGATGCACCC GAGCCGTTGA GGCTGTGACA TGGTGAGATC	CATTCTTGGG GCTAATTCTG TTGGCTGGTG ACTGTTCCAA	CCCCCTCAT CAATTTTCTA GAGCCCCTTC GCAGGGGGAC	1740 1800 1860 1920 1980
65	ACAATTTGCC GGTCAGCTGT AATTTTGACA TTGTTTTGAT	ATGCACTAAG ACGATGATGT TTTCATTTTT	CTGACCTCTT TCAAATAATG TCACCAGAAG TATTAAGAAA	GTCATTTTGG AATTTCTTCC GAAAAAAAA AAATTTTATT	CCTGAAGGCT TCCCTCTCGC TCAGTTTTAT TTACAGAATT	ACAAATTCAG AACCGACCAA GCACTTTATT TACCTTCTCT	2280
70	GGAGTTTAAA	GCATAAAGTG ATTTAAAAAA 140 Protein	AAAAAA	ATACTAAACA	AACTTATATT	TCAATAAAAG	2340
	Protein Ac	cession #: 1	NP_055159				
75	RFPLPPPLAW	DARGGSLKTF	RALLTLAAGA	DGPPRQSRSE	PRWHVSARQP	51 ARSGGPAPAP RPEESAAVHG	60 120
80	GVFWSRGLEE YGINPEQIQG SLTRWLPNLT NFDRLVSNLF	QVPPGFSEAQ EALSYYLARL DVVVPAPWRS SLQWDPRVMQ TARRVLELHR	AAAWLEAARG LGLQRHVPPL EDGRLRPLRD RATSNLHRGP	ARMVALERGG ALARVEARGA AGGELANLSQ GGALVFLDNE	CGRSSNRLAR QWAQVQEELR AELVDLVQWT AGLVHGYRVA	FADGTRACVR AAHWTEGSVV DLILFDYLTA GMWDKYNEPL QLLQRRLDPL	180
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30	GATTCTACCA	TCAGAAAAGA	GGCCAAACTT	CTATCATCAT	GGTGGATGTG	AAGTGTCTGA	60
	GTGACTGTAA	ATTGCAGAAC	CAACTTGAGA	AGCTTGGATT	TTCACCTGGC	CCAATACTAC	120
				TAGTACAGTT			180 240
				TGGATGGAGC AATCACATAT			300
35	AGACTACTGC	GCGGAAGACC	AGACTATCGA	GAGCTGGAGA	GAAGAAGGTT	TCCCAGTGGG	360
				CATTGTGGTG			420
				GGAGCAAAGC TGAAGGGCCA			480 540
40	TTGCAGGGAG	CCTTCCCTTG	CACTGTGCTG	CTCTCACAGA	TCGGTGTCTG	GGCTCAGCCA	600
40				GTGTTAAGAG			660
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45 50	Protein Acc 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO:	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA sec	RP_050184.1 21 FSPGPILPST MGLSPKRETT	 RKLYEKKLVQ ARKTRLSRAG	LLVSPPCAPP		60
	Protein Acci 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc	cession #: 1 11 KLQNQLEKLG LQEHQAPESH	RP_050184.1 21 FSPGPILPST MGLSPKRETT Quence #: NM_002:	 RKLYEKKLVQ ARKTRLSRAG	LLVSPPCAPP		60
	Protein Acci 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA sec id Accession	RP_050184.1 21 FSPGPILPST MGLSPKRETT Quence #: NM_002:	 RKLYEKKLVQ ARKTRLSRAG	LLVSPPCAPP		60
50	Protein Acc 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession lence: 74	KP_050184.1 21	 RKLYEKKLVQ ARKTRLSRAG 204.1 31	LLVSPPCAPP EKKVSQWA	 VMNGPRELDG 51	
	Protein Acci 1 	cession #: 1 11	KP_050184.1 21	 RKLYEKKLVQ ARKTRLSRAG	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG	VMNGPRELDG 51 GGACCCCGCT	60 120
50	Protein Acci 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequi 1 AGGTGAACAG TCCGCTGGCA CTGTGCGCTC	cession #: 1 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession cence: 74 11 GTCCTCACGC GCCATGGGCC GCCATGGTCC GCCATGGTCC	KP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCCGCGCGCCC CGGCTGCGTC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA	60 120 180
50	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc Coding sequil AGGTGAACAG TCCGCTGGCA TCTGTGCGCTC TACCCGATTC	cession #: 1 11 KLONQLEKLG LQEHQAPESH 145 DNA secid Accession tence: 74 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA	KP_050184.1 21 1 FSPGPILPST MGLSPKRETT Quence n #: NM_002: 3229 21 1 CCAGCTCCGC CCGGCCCCAG TGGCGCGCGA AGGAGGCCGG	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGGGCCC CGGCTGCGTC GAACCCGGGC	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCTTCG	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT	60 120 180 240
50	Protein Acci 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequi 1 AGGTGAACAG TCCGGTGGCA CTGTGCGCTC TACCCGATTC CGCCCTCCAT GGAGCTCGCT	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession cence: 74 11 GTCCTCACGC GCCTTGATGG CTGGTAGTGG CTGGTAGTGA GGCAGACAG GTGCCCGATG	RP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG CCGGACTGGT	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG GCGCCCCAC GTCTCGCCT AGCCTCTCG GCTCTGGCTG GCTGTGTACC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT	60 120 180 240 300 360
50	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acci Coding sequi AGGTGAACAG TCCGCTGGCA TCCCGGTTC TACCCGATTC CGCCTCCAT GGAGCTCGCT CACTGCCCAC	cession #: 1 11 KLONQLEKLG LQEHQAPESH 145 DNA secid Accession lence: 74 11 GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CGGCAGACAG GTGCCCGATC AAGGATGACT	RP_050184.1 21 1 FSPGPILPST MGLSPKRETT Quence 1 #: NM_002: 3229 21 1 CCAGCTCCGC CCCGGCCCCAG TGGCGGCCCCAG AGGAGGCCGG AGGAGGCCGG AGCAGCAGCA GCTACACCAA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCCC CGGCTGCGTC GAACCCGGGC CCGGACTGGT GAACATCACA	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGTGTACC GTGAAAAATG	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT CCACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA	60 120 180 240 300 360 420
50	Protein Acc 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding seq 1 AGGTGAACAG TCGCTGGCA CTGTGCGCTC TACCCGATTC CGCCTCCAT GGAGCTGCT CACTGCCCAC TCACATTATT	cession #: 1 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession lence: 74 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CGCAGACAG GTGCCCGATG AAGGATGACT GAGGACATGT	RP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCCTGCGCC CGACCGGGCGGCCC GAACCGGGG GCGCTACCTG CCGGACTGGT GAACATCACA GACATCACA GACTGTGGCC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTCG CTCCTGGCTG GCTGTGTACC GTGAAAAATG AGCCAGGGCC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA CTGCAGGCAG CTGCAGGCAG	60 120 180 240 300 360 420 480
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequil AGGTGAACAG TCCGCTGGCA CTGTGCGCTC TACCCGATTC CGCCCTCCAT CGAGCTCCACATTATT AGTTCTGGTC GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG GCGCATGGTG	ression #: 1 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession Lence: 74; GTCCTCACGC GCCATGGGCC GCCATGGTAGGC GTGGTAGTGA GGCAGACAG GTGCCCGATG AAGGACATGT TGTGCCCACC GGCAAGTGCCT GGCAAGTGCT	RP_050184.1 21 1 FSPGPILPST MGLSPKRETT THENCE 1 #: NM_002: 3229 21 CCAGCTCCGC CCAGCCCCAG TGGCGCCCAG AGGAGGCCGG AGCAGGCAGCA GCTACACCAA GTGAGCGGAT GGCTTGGAGT GGCTTGGAGT ACGTACACCA ACGTGCGAGG ACCTTGGAGT ACGTACACCA ACGTGCGAGG	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGGGCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG CCGGACTGGT GAACATCACA GACTGTGGC GGTGCTGTGG CGGTGCTGTGG CAATGACCTA	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCT AGCCTCTCG GCTCTGGCT GCTGTGAAAATG AGCCAGGGCC TCAGGGTCA GGGCTCTGGGCG GAGCTGGACT	VMNGPRELDG 51 GGACCCGGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA CTGCAGCAG AAGACCAGCG CCAGTGATGA	60 120 180 240 300 360 420 480 540 600
50	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequilated accidenced acci	dession #: 1 KLONOLEKLG LOEHQAPESH	RP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCCTC GAACCCGGGC GCGCTACCTG GACCTGGT GAACTGACACACACACACACACACACACACACACACACAC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGTGTACC GTGAAAATG AGCCAGGGCC TCAGGGTCAG GAGCTGGACT GACTACCTGG	S1 GGACCCCGCT GCCTGATGCT TCAACCTCGA GCTACTCGGT GTGCCCAC TGTGCCCAC CTGCAGCAG ACCTGAGCAG ACGTGATGA	60 120 180 240 300 360 420 480 660 660
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequit AGGTGAACAG TCCGCTGGCA CTGTGCGCT CACTGCCACT CACTGCCACT CACTGCCACT CACTGCCACT CCCATTGCCC CTCACTGCCCC CTCACTGCCCC CTCACTGCCCC CTCACTGCCCC CTCACTGCCCC CTCCCACTGCCCC CTCCCACTGCCCC CTGCCAGCCC GTGCCAGCCC GTGCCAGCTG	dession #: 1 KLQNQLEKLG LQEHQAPESH	RP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCTGCGCT GAACCCGGGC GCGCTACCTG CCGGACTGGT GAACATCAC GACTGTGGC GAACATCAC TAGCAACAC CCAGAACAC CCAGAACAC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTCG GCTGTATACC GTGAAAAAT AGCCAGGGCC TCAGGGTCAG GAGCTGGACT GACTACCTCG	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA AGACCAGCA AAGACCAGCA AAGACCAGCA CCAGTGATGA AAGACCACCG CCAGTGATGA AGACCAGCG CCAGTGATGA AGACCAGCGCAT AGACCAGCGCAT AGACCAGCGCAT GCGCCCCCGG	60 120 180 240 300 420 480 540 600 600 720
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Accident Sequence Nucleic	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA set id Accession sence: 74 11 GTCCTCACGC GCCATGGGCC GCCATGGATGA CGCAGAGAGA GAGCAGACAG GTGCCCACC GGCAAGTGCC GGCAAGTGCC TACCACACG GGCAAGTGC TACCACACG GGCAAGGAA AAGGACCAG	RP_050184.1 21	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCCC CGGCTGCGTC GAACCCGGGC GCGCTACCTG GAACATCACA GACTGTGGT GAACATCACA GACTGTGGC CATGACACA TAGCAACACA TAGCAACACT CAGAACACT AATCAGGG AAACCTCTAT	LLVSPPCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCAC GTCTCCGCCT CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCAGGGTCAC GTGAAAAATG AGCCAGGGCC TCAGGGTCAC GACTACCTGG GACTACCTGG ATTGGAGTGAC AAGGAGTGGA ATTGGGTACAC	VMNGPRELDG 51 GGACCCCGCT GCCTGATGCT GCTACTCGGA GCTACTCGGT GTGCCCACT ACCCTGGCCAC CTGCAGGCAG AAGACCAGCG CCAGTGATGAT AGACGGGCAT GCGCCCCGG CCAGTGATGA AGACGGGCAT GCGCCCCGG ACTATCTGA CGATGCAGGT CGATGCAGGT CGATGCAGGT CGATGCAGGT	60 120 180 240 300 420 480 540 600 660 720 780 840
50 55 60 65	Protein Acc 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding seq: 1 AGGTGAACAG TCGCCTGGCA CTGTGCGCT CACCGATTC CACCTGCCAC TCACATTATT AGTTCTGGTC GCGCATGGTC GCGCATGGTC GTGCCAGCT GTGCCAGCT GTGCCAGCT GTGCCAGCT GTGCCAGCT GTGCAGCT GTATAGTTAC AGGCCAGCTTC	dession #: 1 KLQNQLEKLG LQEHQAPESH	RP_050184.1 21 PSPGPILPST MGLSPKRETT QUENCE 1 #: NM_002: 3229 221 CCAGCTCCGC CCAGCTCCGC CCAGCTCCGC AGCAGCCGA AGCAGCCGA AGCAGCCGA AGCAGCCGA AGCAGCCGA AGCAGCCGA AGCAGCCGA AGCAGCCGA GCTACACCAA AGTACACCAA ACTTGGAGG AGATGGAG GCTACACCA ACGTTGGAGT GCTACACCA ACGTTGGAGT GCTACACCA ACGTTGGAGT GCTACACCA ACGTTGCAGG AGATGGAA AGGACCAAGG CCAAAGACAT	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCCGCGCCC CGGCTGCGTC GAACCCGGGC GCGCTGCTG GAACATCACA GACTGTGGC GGTGCTGTGGC GGTGCTGTGGC CAATGACCA CCAGAACAC CCAGAACACT CACCACTGTT	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTCG GCTGTGTACC GTCAAAAAT AGCCAGGGCC TCAGGGTCAG GAGCTGACT GACTACCTGG GTGTACTCG GTGTACTCG AGGAGTGGG ATTGGGTACA ACAGGTGCCC	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA TCTGCAGCAG AGACCAGGCA AGACCAGGCA AGACCAGGCAT AGACGGCAT AGACCAGGCACT CCACTGATGATGA AGACGAGGCACCG ACTTATCTGA CGATGCAGGT CACGGCACCG	60 120 240 300 360 420 480 540 600 720 780 840 900
50 55 60	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Accoding sequilated according sequi	cession #: 1 11 KLQNQLEKLG LQEHQAPESH 145 DNA secid Accession dence: 74 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA GGCAGACAG GTGCCCGATG AAGGACAG GTGCCCGATG AAGGACAG GTGCCCACC GGCAAGTGCT TACCACACAC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACACC GGCAAGTGCT TACCACCACC GGCAAGTGCT TACCACCACC GGCAAGTGCT TACCACCACC GGCAAGTGCT TACCACCACC GGCAAGTGCT TACCACCACC GGCAAGTGCACC GGCACCCACC GGCAAGTCCT TACCACCACC GGCACCCACC GCGCTGTTCT	RP_050184.1 21 1 FSPGPILPST MGLSPKRETT Quence 1 #: NM_002: 3229 21 1 CCAGCTCCGC CCGGCCCCAG TGGCGGCCGAG AGGAGGCGG AGGAGGCGG AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCTGCGCT GAACCCGGGC GGCTACCTG CCGGACTGGT CAACATCACA ACATCACA TAGCAACAC GATTCAGCA CAACACT GATTCAGCG AAACCTCTAT GACTCTAT GACCACACA GATTCAGCG GAACACT GATTCAGCGC AAACCTCTAT CACCATTGTG GGAGGCAGGC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCGGCTG AGCCTCTTCG GCTGTAAAAAT AGCCTGGTAAC GTCAAAGGGC TCAGGGTCAG GAGCTAGACT GACTACTTCG GATTACTTCG AAGGAGTGGA ATTGGGTACT AAGGAGTGGG ATTGGGTACT CGAGAGTGCC GGAGACCTGC GGAGACCTGC	S1 GGACCCGGT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCCCG TGTGCCCACT ACCCTGGCCA AGACCAGCA AAGACCACCG CAGTGATGA AGACCACCG CAGTGATGA AGACGGCAT ACCCCCGG ACTATCTGA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGATGAAGCA CGAGGACCCG GGAGGACGCA CGAGGACCCG GGAGGACGCA	60 120 180 240 300 420 480 600 600 720 780 840 960
50 55 60 65	Protein Acci 1 MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc Coding sequility of the control of the cont	dession #: 1 KLONOLEKLG LOEHQAPESH KLONOLEKLG LOEHQAPESH 145 DNA secid Accession 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG GCGTGTAGTGA AGGACAGG AAGGACAG GTGCCACG GCAAGTGCT TGTGCCCACC GCAAGTGCT TACCACAACG GCACCAGCG TGGAAAGGAA AAGGACCAG ATCCTGCACC GCGGTGTTCT GGCTCGCAGG GGGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCCAGG GCGTGCAGG GCGCACG GCGCACG GCGCACG GCGCACG GCGCACG GCGCACG GCGCACG GCGCACG GCGCACCACC GCGCACCACCACCACCACCACCACCACCACCACCACCACC	RP_050184.1 21 21 PSPGPILPST MGLSPKRETT QUENCE 1 #: NM_002: 3229 221 CCAGCTCCGC CCAGCTCCGC CCAGCTCCGC AGCGCCCAG AGCAGCCGA AGCGCAGCAG AGCAGCCGA AGCAGCCGA AGCAGCCGA GCTACACCAA ACTACACCAA ACATCACAA ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC ACAGCTACAC TGCGAGC CCAAAAACAT TGCTGAGCCCTA TGCGCGCCTA TGCGCGCCCTA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCCC CGGCTGCGTC GAACCCGGGC GCGTACCTG GACTGGT GACTGTGACACACAC CCAGACACAC CAGAACACT TAGCAACACAC GATTCAGCG AAACCTCTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC TTTTGGCAGC GGGCGCCCCC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCTCCGCTT AGCCTCTTCG CTCCTGGTG AGCAAAATG AGCAGGGCC TCAGGGTCAG GAGTACTCG GAGTACTCG AAGGAGTGGG AATGGCC GAGACCTGC GCAATTGCCC TACTACTTCG	S1 GGACCCCGCT GCCTGATGCT TCAACCTCGA GCTACTCGGT GTGCCCACT ACCCGGCA CTGCAGCAG AGACCAGCA AGACCAGCA AGACCAGCA AGACCAGCA CTGCAGCACA CTGCAGCACA CTGCAGCACA CTGCAGCACA CTGCAGCACA CTGCAGCACA CCAGGCACCA GCAGCACCA GCAGCACCA GCAGCACCA GCAGGAGAGCA TGGCAGACCT AGAGGAAAGA	60 120 180 240 300 420 480 540 660 720 780 900 900 900 9020 1080
50 55 60 65	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc Coding sequilated Accident Acci	dession #: 1 KLQNQLEKLG LQEHQAPESH KLQNQLEKLG LQEHQAPESH LS DNA sec id Accession dence: 74 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA CAGCACAGG GTGCCCATC TACCACACG GCCAAGTGCT TACCACACG GCCAAGTGCT TACCACACG GCCACCGCCAGGCAAGGAAAGGA	CP_050184.1 21 21 FSPGPILPST MGLSPKRETT Quence 1 #: NM_002: 3229 21 CCAGCTCCGC CCGGCCCCAG TGGCGCCCAG TGGCGCCCAG TGGCGCCCAG AGCAGCAGCA GCTACACCAA GTGAGCGAGCA GCTACACCAA GTGAGCGAG AGATGTGCAA GTGGCTTCAC ACAGCTACAT AGGACCAAG TGGCTACACT ACGGCTCCAG ACATGTCAC ACAGCTACAT ACGACCAAG ACAGCTACAT AGGACCAAG ACAGCTACAT TGCTGAGCCA ACGTCCTGGT ACTTCCTGGT ATGTCTCAT	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCTGCGCTC CGGCTGCGTC CGACCCGGGC GAACATCAC GATTGTGGC CAATGACTA TAGCAACAC CCAGAACAC GATTCAGGGC AAACCTCTAT CACCATTGTG GGAGGCAGGC TTTTGGCAGC GGGCCCCC GAACCACGC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCTA AGCCTCTTCG GCTGTATACC GTGAAAAAT AGCCAGGGCC TCAGGGTCAG GAGTCACTG GACTACTCG GTGAATACT AACGGGTCAG GAGTACTTCG GATTACTTCG GATTACTTCG GATTACTCC GGAGACCTCC TACTACTTCG GGAACCTCCT	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GCTGCCCCCG TGTGCCCACT ACCCTGGCCA AGACCAGC AGAGCAGCA AGACCAGC CCAGTGATGC ACCTTGCCACT ACCCTGCCCG GAGTGATGA CGATGCAGGT TGCCCCCGG GAGGACGCA TGGCAGCCAC GGAGGACACA TGCCAGCACCA TGGCACCCG GGAGGACACA TCCCTGCTCA	60 120 180 240 360 420 480 660 660 780 960 1020 1020 1140
50 55 60 65 70	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Ac: Coding sequit AGGTGAACAG TCCGCTGGCA CTGTGCGCTC CACCCCAC CACCCCAC CACATCAT AGTTCTGGTC GCGCAGCG CTGCCAGCAGACC CTGCCAGCAGACC AGGCAGCT CACTACATAT CTTGCCAGCT CTGCAGAGC CTGCCAGCT CTGCAGAGC CTGCCACAGC CTGCCAGCT CTGCAGAGC CTGCCAGCT CTGCAGAGC CTGCCAGCT CTGCAGAGC CTGCCAGCT CTGCAGAGC CTGCCAGCT CTGCAGAGC CTGCTACAAC GTATAGTTAC AGGAGCTT CACATTATGGGC GGTGCTGGAG GAACAATGAT GGAAGTAGGG CCCCTCACTC	ression #: 1 KLQNQLEKLG LQEHQAPESH 145 DNA set id Accession 161 Accession 161 Accession 161 Accession 171 GTCCTCACGC GCCATGGGCC GCCATGGACAG GTGCCAGACAG GTGCCAGACAG GTGCCAGACAG GGCAAGTGCT TACCACAACG GCAAGTGCT TACCACAACG GCAAGTGCT TACCACAACG GCACAGCAG TGGAAGGAA AAGGACCAGG GCACAGCAG GCGGTGTTCT GCTCGCAGG GGGTGCCATCT CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CTTCTTCATG CACCACAGCAG CTTCTTCATG	CP_050184.1 21 21 FSPGP1LPST MGLSPKRETT GUENCE 1 #: NM_002: 3229 21 CCAGCTCCGC CCGGCCCCAG TGGCGCCCAG AGCAGGCCGA AGCAGGCCGA AGCTCACCAA AGCTACACAA ACGTTCACCAA ACGTGCAGAG CCAAAAACAT TGCTGAGCCA TGGCGCCCAA ACGTCACCAA ACGTCCAGAC ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCTACAT ACGCCCAAAAACAT TGCTGAGCCAA ACCTCCTGGT ACCTCCTGGT ACCTCCTGAT GCCCCAGTGG	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCCC CGGCTGCTC GAACCCGGGC GCGCTACTG GAACTCTACT GATCTAGCA CAGAACACA CAGAACACT CACTATTGC AAACCTTAT CACCATTGTG GGAGGGGGCGCCCCC GGACCAGGCG CTCTGCCTTTT	LLVSPFCAPP EKKYSQWA 41 GCTCTCGCCG CGCGCCCAC GTCTCCGCCT AGCCTCTTCG CTCCTGGCTG GCTGTACC GTGAAAAATG AGCCAGGGCC TACGGGTCAG GAGTACCTGG AAGGAGTGGAC AAGGAGTGGCC GGAGACCTGC GCAATTGCCC TACTTACTCG GGAACCTCC GGAACCTCC GGAACCTCC	S1 GGACCCCGCT GCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT ACCCTGGCCA TGCAGCACA CTGCAGCACA CTGCAGCACA CACCTGAGCA AGACCAGCA CCAGTGATGA AGACCAGCA CCAGCACCA CCAGCACCA CAGCACCA CAGCACCA CAGGCACCA CAGGCACCA TGCAGGACCA TGGCAGCACA TGGCAGCAT	60 120 180 240 300 420 480 540 660 720 780 900 900 900 9020 1080
50 55 60 65	Protein Acci MVDVKCLSDC AODSDDSEGG Seq ID NO: Nucleic Ac. Coding sequilated accidence accide	dession #: 1 KLQNQLEKLG LQEHQAPESH KLQNQLEKLG LQEHQAPESH LSEN LSEN	CP_050184.1 21 21 FSPGP1LPST MGLSPKRETT GUENCE 1 #: NM_002: 3229 21 CCAGCTCCGC CCGGCCCCAG TGGCGCCCAG TGGCGCCCAG GCTACACCAA GTGAGCAGCA GCTACACCAA GTGAGCGAGCA ACGTGCAGA ACATGCAAC ACAGCTACAT TGCTGAGCAA ACGCTACAT TGCTGAGCAA TGCTGAGCAA ACGCTACAT TGCTGAGCCAA ACGCTACAT TGCTGAGCCA ACGCTACAT TGCTGAGCCA ACGCTACAT TGCTGAGCCAA ACCTCCTGGT ATGTCTCTCAT GCCCCAGTGG ACACTAGGA ACACTAGGTA	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCTGCGCTC CGGCTGCGTC CGACCCGGGC GAACATCAC GATTCAGGC CAATGACTA TAGCAACAC AACCTCTAT CACCATTGTG GAGCAGGC TTTTGGCAGC CGGCCCCC GAACCAGGC CTCTCCCTTT TATTGCTGT TATGCTGT TAGGGGCTCT	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTTCG GCTGTATACC GTGAAAAAT AGCCAGGGCC TCAGGGTCAG GAGTCACTCG GAGTACTTCG GATTACTCG GAGACCTCCT GGAGACCTCCT GGAGACCTCCT GGACACCTCCT GGACACCTCCT GGACCCCCT CGACCCCT CGACCCCCT CGCACCCCT CGACCCCCT CGACCCCCT CGACCCCCT CGACCCCCT CGACCCCCT CGACCCCCT CGACCCCCT CGACCCCCT CTTACACAGC	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GCCCCCCG TGTGCCCCCG TGTGCCCACT ACCCTGGCCA AGACCAGC AGAGCAGCA AGACCAGCG CCAGTGATGA AGACGGCAT GCGCCCCCG GCAGGACGG CCAGGACGCA TGGCAGCC TGGCAGCACT TGCAGGCACT TGCAGACCT TGCAGACCT TCGCAGCAGT TCCAGCAGGT TCCAGCAGGT TCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT TCCCAGCAGGT	60 120 180 240 360 420 480 660 720 780 960 1020 1140 1260 1320
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50 55 60 65 70	Protein Acci MVDVKCLSDC AQDSDDSEGG Seq ID NO: Nucleic Acc Coding sequity AGGTGAACAG TCGCCTGGCA CTGTGCGCT CACCGCATTC CACTGCCCAT CACTGCCCAC TCACATTATT AGTTCTGGTC GCGCATGGTG GTGCCAGCTG TGCCTACACAC GTATAGTTAC AGGCAGCTT ACATATGGC GTGCTACAAC GGTGCTGGAG GAACATGAT GGAACTTGGGC GGTGCTGGAG GAACATGGA CCCTCACTC TGGTGACATC GGGCAAAGTG AATCCATGGA AGCAAATGGA CACATGGAA GCAAATGGA CACATGGAA GCAAATGGA CACATGGAA GCAAATGGAA CGAATGGAA CCACTCACTC CGGTCACTC CGGCAAAGTG AATCCATGGA CACATGGAA CCACTGACTG CACATGGAA CCACATGGAA CCACATGAA CCACATGGAA CCACATGAATGAA CCACATGGAA CCACATGAATGAA CCACATGAATGAAT CCACATGAA CCACATGAATGAA CCACATGAATGAAT CCACATGAAT CCACATT C	dession #: 1 KLONOLEKLG LOEHQAPESH KLONOLEKLG LOEHQAPESH 145 DNA secid Accession 11 GTCCTCACGC GCCATGGGCC GCCATGGGCC GCCATGATGG GTGCCGATG AAGGACAG AAGGACAG GGCACAAGGG ATCCTGCACC GCGAGTGTT TACCACAACG GGCACCAGCG TGGAAAGGAA AAGGACCAG ATCCTGCACC GCGTGCAGG GGTGCATCT CTCTCATG AACGAACTGT CTCTCATG TACCACGAGTGTTCT GGCTCGCAGG GGTGCATCT CTCTCTCATG AACCAGATG TACCACACAGGTGCT CTCTCTATG CAGAAGCTG GGGAGGTGCATCT CTCTCATG TACCAGGATG TACCACTATC GAGAAGCTGG GTGGATGAGAGTGGTGCATGGAGAAGCTGG	RP_050184.1 21 21 PSPGPILPST MGLSPKRETT FURNCE 1 #: NM_002: 3229 221 CCAGCTCCGC CCAGCTCCGC CCAGCTCCGC AGAGCCCAG AGAGCCGGA AGAGCCGGA AGAGCCGGA AGAGCCGGA AGAGCCGGA AGAGCCGAG AGAGCCGAG AGAGCCAA ACAGCTACAC ACACCAC ACACCAC ACACCAC ACACCAC ACACCAC	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCCC CGGACTGCTC GAACCCGGGGC GCGTACCTG GAACTGAT TAGCAACAC TAGCAACACA CCAGAACACT GATTCAGGC GAACCATGGT CACCATTGTG GGAGCAGGC GGGCCCCC GAACCACTTTTGGCAGC CTCTGCCTTT TATTGCTGT TAAGGGGCTT CTTTGCTGT GATGCCCCC GAACCATGTT ATTGCTGT GATGCCACC GAACCATGTT ATTGCTGT AAGGGGCTCCC GAACCATGTT ATTGCTGT AAGGGGCTCC GAACCATGTT ATTGCTGT AAGGGGCTCC GATGCCACC AGACCTTCTA	LLVSPFCAPP EKKYSQWA 41 GCTCTCGCCG CGCGCCCCCC CGCGCCCCCCC CTCCTCGCTG CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCCTGGCTG CTCAGGGTCAG AGCAGGGCC TCAGGGTCAG AAGGAGTGGC AAGGAGTGGCC GGAACCTCCT GGAACCTCCT GGAACCTCCT CGGTTATCTCG GGAACCTCCT TCTTACACAGC TTCGGCTATT GTGGGCAAGCCT	S1 GGACCCCGCT GCCTGATGCT GCTGATGCT GCTACTCGGT GTGCCCACT GCCAGGCAG AGACCAGGCA CTGCAGGCAG AGACCAGGC CCAGTGATGAT AGCCGGCCCCG GCAGGATGAT AGACGGCACT GGATGCAGGT CAGGCACCG GGAGGAGCA TGGCAGGCACT AGAGGAAGA TCCCTGCTCA AGAGGAAGA TCCCTGCTCA TTGAAGGCTT CCCAGCAGGT CCCTCAGTGG CTCCAGCAGGT CCCTCAGTGG CTCCAGCAGGT CCCTCAGTGG CTCCAGCCCC	60 120 180 240 360 420 480 660 720 780 960 1020 1140 1260 1320
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50 55 60 65 70	Protein Acci MVDVKCLSDC AODSDDSEGG Seq ID NO: Nucleic Ac. Coding sequity AGGTGAACAG TCCGCTGCA CTGTGCGCT CACTGCCAC CTGCCACT GGAGCTCGATACAC GTGCCAGCTG TGCCTACTAC GTGCCAGCTG TGCCTACTAC GTGCTACTAC GTATAGTTAC GAGATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT GGAATAGAT CCTTGCTACAC CCCTCACTC CGCCAAATGG CCCTCACTC CGCCAAATGG CCCTCACTC CGCCAAATGGAT CACTTTGCTTG CCAGCTGTG CCACTCTTGCTG CCACTCTTGGAG CCACTCTTGGAG CCACTCTTGGAG CCACTCTTGGAG	dession #: 1 II KLONOLEKLG LOEHQAPESH 145 DNA secid Accession lence: 74 II GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGTAGTGA GTGCCCGATG AAGGATGAT TGTGCCCACC GGCAAGTGAT TGAGGACATGT TACCACACG GGCAAGTGCT TACCACACG GGCAAGTGCT TACCACACG GGCAAGTGCT TACCACACG GGCAAGTGCT TACCACACG GGCACCCAG ATCCTGCACC GGCAGTGTTCT CGCTCGCAGG GGTGCCATCT CTTCTTCATG AACCAGGATG TACATCATC CAGAAGCTGG ACCAGGATGAT ACCAGGATGAT ACCAGGATGAT ACCAGGATGAT ACCAGGATGAGA CTGCGGCCC CTGACCAGG GTGCACCAG ACCAGAGTG A	CP_050184.1 21 21 PSPGPILPST MGLSPKRETT FUENCE 1 #: NM_002: 8229 21 CCAGCTCCGC CCGGCCCCAG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGG AGGAGCCGA GCTACACCA ACTGCGAGC ACTGCAGG AGATGTGCAA AGGACAAG CCAAAAACAT TGCTGAGCA ATGTCTCAC ACAGCTACAT AGGACCAAG ACACTTCAGC ACACTGCGG ACTTCTAC CACTTCAGC ACACTTCACC ACGCCAGTCAC ACACTTCACC CGCCAGTCAC ACACTTCACC ACCGCCAGCCC ACCGCCAGCCC ACCGCCAGCCC	RKLYEKKLVQ ARKTRLSRAG 204.1 31 CCCCTCACGC CCGCGCGCCC CGGCTGCGTC GAACCCGGGC GGACATCACA GACATCACA GACATCACA CCAGAACACT CAGAACACT CAGAACACT CAGAACACT CACATTGIG GGAGGCACCCC GAACCACTGT TATGCAGC CTCTGCCTT TATTGCTGT TAAGGGCC CCCAGACCACT CACACTCTAC CGACCACCCC GAACCACCCCC GAACCACCCCC CTCACCTT TATTGCTGT TAAGGGCCCCC CGACCACCCCC CGACCACCCCC CGACCACCCCC CGACCACCCCC CGACCCCCC CGACCCCCC CAGACCTCTAC CACCCCCCC CGCCCCCCC CGCCCCCCCC CGCCCCCCCC	LLVSPFCAPP EKKVSQWA 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT CTCCTCGTT AGCCTCTCG CTCCTGGTG GCTGTATACC GTGAAAATG AACAGGTCAC GACTACTCG GATACTTCG GATACTTCG GCAATTGCC GAACACTCC GGAACCTCCT GGAACCTCCT GGTTTACTTCG GCAACCTCCT CGTTTTACTTCG CAACACCCC CACAAGACCT TGTGGCAACCC CACAAGACCT CGCTTTGCCCC CACAAGACCT CGCTTTCCCCC CCACAAGACCT CGTGTCCCAC CGCTTTCCCCC CCACAAGACCT CCCCTTCCCCC CCCACAACACC CCCCTTCCCCC CCCCCCCC	S1 GGACCCCGCT GCCTGATGCT TCAACCTGGA GCTACTCGGT GTGCCCACT GCCTGGCCACT ACCCTGGCCA AGACCAGGCA AGACCAGGCA AGACCAGGCA AGACCAGGCA AGACCAGGCA CGAGGAAGA AGACGAGGCA TGCAGGCACCG GGAGGAGGCA TGCAGACCT TGCAGACCT TGCAGACCT TGCAGCACCT TGCAGACCT TGCAGCACCT TGCAGCCT TGCAGCT TGCAGCCT TGCAGCC TGCAGCCT TGCAGCCT TGCAGCCT TGCAGCCT TGCAGCCT TGCAGCCT TGCAGCCT TGCAGCC TGCAGCC TGCAGCC TGCAGC TG	60 120 180 240 300 420 480 660 720 900 900 1080 11200 1260 1380 1440 1500 1500
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			AGCTGGGGAA				2220
			TCGGGGTGAC				2280
			ACCAGGACAA				2340
10			CGCTTAGCAT				2400
10	GGGGACAGTG	ATGGGTGAGT	CTGGCATGAA	AACTGTGGAG	GATGTAGGAA	GCCCCCTCAA	2460
	GTATGAATTC	CAGGTGGGCC	CAATGGGGGA	GGGGCTGGTG	GGCCTGGGGA	CCCTGGTCCT	2520
	AGGTCTGGAG	TGGCCCTACG	AAGTCAGCAA	TGGCAAGTGG	CTGCTGTATC	CCACGGAGAT	2580
			CCTGGCCCTG				2640
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15			AGGGCCCCCC				2760
			CCTGTGCCAC				2820
			TTGTCACCAA				2880
			GAGACTTTGA				2940
	CACCITCATC	GAGGATIACA	GAGACITIGA	CCGAGICCGG	GIAMAIGGCI	COMMONOMOR	
20			CCACCATCAA				3000
20	GGACATTGAC	TCGGAGCTGG	TGGAGGAGCT	GCCGGCCGAA	ATCGAGCTGT	GGCTGGTGCT	3060
			TGCTGCTGCT				3120
			GCACTCGCGC				3180
	GATGAAGAGC	CAGCCGTCAG	AGACAGAGAG	GCTGACCGAC	GACTACTGAG	GGGGCAGCCC	3240
	CCCGCCCCCG	GCCCACCTGG	TGTGACTTCT	TTAAGCGGAC	CCGCTATTAT	CAGATCATGC	3300
25			ATCCGGGAGG				3360
	TGCCCACCAA	GAAGCACTGG	GTGACCAGCT	GCAGACTCG	GGACCAATAC	TACTGACGTC	3420
			CTCCCCCAGT				3480
			GGCCACCACC				3540
			ACATGCTGTC				3600
30			GCCGAGTGCA				3660
50			GCTGGTGCAT				3720
							3780
	AGCCTCTGCC	AGCGCCAGCG	CCAAAACAAG	CCAAAGAGCC	TCCCACCAGA	GCCGGGAGGA	3840
			GACACCTCCC				
35			CTGTCAAAAC				3900
33			CACCCATGCC				3960
			CTGGCGTGCT				4020
			CCTGCATCTC				4080
			GGAAGGAACA				4140
40			GGGATCCTCC				4200
40			AGGAGATGCC				4260
	CAGAAGGCCC	CAGAGAGACC	CTGCAAGACC	ACGGAGGGAG	CCGACACTTG	AATGTAGTAA	4320
	TAGGCAGGGG	GCCCTGCCAC	CCCATCCAGC	CAGACCCCAG	CTGAACCATG	CGTCAGGGGC	4380
	CTAGAGGTGG	AGTTCTTAGC					4440
			TATCCTTGGC	TTTCTGTGCC	AGCCTGGCTC	TGCCCCTCCC	
45	CCATGGGCTG	TGTCCTAAGG	TATCCTTGGC CCCATTTGAG	TTTCTGTGCC AAGCTGAGGC	AGCCTGGCTC TAGTTCCAAA	TGCCCCTCCC AACCTCTCCT	4500
45	CCATGGGCTG GACCCCTGCC	TGTCCTAAGG TGTTGGCAGC	TATCCTTGGC CCCATTTGAG CCACTCCCCA	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500 4560
45	CCATGGGCTG GACCCCTGCC GGGAATTCCC	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT	TATCCTTGGC CCCATTTGAG	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500
45	CCATGGGCTG GACCCCTGCC	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT	TATCCTTGGC CCCATTTGAG CCACTCCCCA	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500 4560
45	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500 4560
	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO:	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500 4560
45 50	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Ac	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT n sequence NP_002195.1	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC	TGCCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA	4500 4560
	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO:	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT	TGCCCCTCCC AACCTCTCCT ACTGTAGCAG	4500 4560
	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT n sequence NP_002195.1 21	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51	4500 4560 4620
	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APPRLMLCALA	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS	TGCCCTCCC AACCTCTCCT ACTGTAGCAG GCGACCAATA 51 1 LFGYSVALHR	4500 4560 4620
50	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1 MGPGPSRAPR QTERQQRYLL	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Frotein cession #: ! 11 APPLIMLCALA LAGAPRELAV	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT 1 Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA	TTTCTGTGCC AAGCTGAGGCC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 vvkEagnpgs DDCERMNITV	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE	4500 4560 4620
	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1 MGPGPSRAPR QTERQQRYLL	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Frotein cession #: ! 11 APPLIMLCALA LAGAPRELAV	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV	TTTCTGTGCC AAGCTGAGGCC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 vvkEagnpgs DDCERMNITV	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE	4500 4560 4620
50	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1 MGPGPSRAPR QTERQQRYLL DMWLGVTVAS	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APPLIMLCALA LAGAPRELAV QGPAGRVLVC	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT 1 Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE	TGCCCTCCC AACCTCTCCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWQTY	4500 4560 4620 60 120
50	CCATGGGTTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Ac: 1	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG	TATCCTTGGC CCCATTTGAG CCACTCCCCA TGTGCCTTCT n sequence nP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS	TTTCTGTGCC AAGCTGAGCC GCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GYEDQRRMVG YFGAPGAYNW	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK	TGCCCTCCC AACCTCTCCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWQTY EWDLSEYSYK	4500 4560 4620 60 120 180
50	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act i MGPGPSRAPR QTERQORYLL DMWLGYTVAS HNEMCNSNTD DPEDQGNLYI	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRILMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI	TATCCTTGGC CCACTTTGAG CCACTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPHRHMGA	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWGTY EWDLSEYSYK DLRRRQVLEG	4500 4560 4620 60 120 180 240
50 55	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc 1 MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: ! 11 APPLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG	TATCCTTGGC CCCATTTGAG CCACTCCCGA TGTGCCTTCT 1 Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY	TTTCTGTGCC AAGCTGAGGCC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 vvkEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG ATYVFMNQAG	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 300
50 55	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act 1 MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APPLIMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI LIALADLINNDG LEVASIGDIN	TATCCTTGGC CCCATTTGAG CCACTTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA ANRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QDGFQDIAVG	TTTCTGTGCC AAGCTGAGGCC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA YFGRKEEVGG APFEGLGKVY	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYUPMNQAG IYHSSKGLL	TGCCCTCCC AACCTCTCCT ACCTGTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 360 420
50	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNITD DPEDQGNLYI SQVGAYTGSA LHGPSGSAFG KLGLPGLATF	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV	TATCCTTGGC CCACTTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DEMFYPDLLV	TTTCTGTGCC AAGCTGAGGC GCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPHRHMGA YFGRKEEVGG APFEGLGKVY GSLSDHIVLL	AGCCTGGCTC TAGTTCCAACA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV VFULSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWQTY EWDLSEYSYK DLRRQVLEG TSFPAHPSLL RQPQQVIHGE KTLVPRPAVL	4500 4560 4620 60 120 180 240 300 360
50 55	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act I	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: ! 11 APPRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG GAPRHRHMGA YFGAPGAYNW GAPRHRHMGA YFERKEEVGG APFEGLGKVYL NITLAYTLEA	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 vvkEaGNPGS DDCERMNITV KCYVRGNDLE KCYVRGNDLE VPLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRLR	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWGTY EWDLSEYSYK DLRRRQVLEG TSFPAHPSLL RQFQQVIHGE KTLVPRPAVL FAGSESAVFH	4500 4560 4620 60 120 240 300 360 420 480 540
50 55	CCATGGGTTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Ac: MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMRC	TGTCCTAAGG TGTTGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN	TATCCTTGGC CCCATTTGAG CCACTTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA ARRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR LRDKLRPIII	TTTCTGTGCC AAGCTGAGGC GCCCAGGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRMVG YFGAPGAYNW GAPRHRHMGA AFFEKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMITIV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYVPMNQAG IYHSSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS	TGCCCTCCC AACCTCTCCT ACCTCTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 300 420 480 540 600
50 55	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act	TGTCCTAAGG TGTTGGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG GYSTMQVGSFI IALADLNNDG GYSTMQVGSFI IALADLNNDG GYSTMQVGSFI IALADLNNDG GYSLGGMDV VQVELCFAYN QKLELLLLMDN FQKECGPDNK	TATCCTTGGC CCACTTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSACNPNYRR QRACKLRPIII CESNLQMRAA	TTTCTGTGCC AAGCTGAGGC GCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPHRHMGA YFGRKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEQQQKLS	AGCCTGGCTC TAGTTCCAACA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPFRLR PDRRLGELR RLQYSRDVRK	TGCCCTCCC AACCTCTCCT ACCTCTCCT ACTGTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 300 420 480 540 660
50 55 60	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMWLGYTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMRC QALENHTEVQ RTSERSGEDA	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APPRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DEMFYPDLLV QSAGNPNYRR LRPKLRPIII CESNLQMRAA FALLLSSVRP	TTTCTGTGCC AAGCTGAGGC GCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG APFERLEGVG APFERLEGVG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEQQKLS FGACQANETI	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KCNSYMIQRK VFLLSQEAGG AIYUFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS RLQYSRDVRK FCELGNPFKR	TGCCCTCCC AACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDDWGTY EWDLSEYSYK DLRRRQVLEG TSFPAHPSLL RQFQQVIHGE KTLVPRPAVL FAGSESAVFH LDAYPILNQA LLLSINVINT NQRMELLIAF	4500 4560 4620 60 120 180 240 360 420 600 600 720
50 55	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Acc I MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMRC QALENHTEVQ RTSERSGEDA EVIGVTLHTR	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDIN GYSLSGQMDIN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST	TATCCTTGGC CCCATTTGAG CCACTTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT UQDLLVGAPY QDGFQDIAVG QEAGNPYPRL LRDKLPPIII CESNLQMRAA PALLLSVRP	TTTCTGTGCC AAGCTGAGGCC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPHRHMGA AFFERKEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVEEQOOKLS PGACQANETI LITLLUDYTL	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG ATYVFMQAG IYHSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS RLQYSRDVRK PCELGNPFKR QTSLSMVNHR	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 360 420 480 660 720 780
50 55 60	CCATGGGTTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act 1 MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPMCC QALENHTEVQ RTSERSGEDA EVIGVTLHTR GESGMKTVED	TGTCCTAAGG TGTTGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG GYSLGGDIN GYSLSGQMDV VQVELCFAYM QKLELLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSELKYEFQ	TATCCTTGGC CCATTTGAG CCACTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR LRPKLRPIII CESNLQMRAA PALLLSSVRP PALLLSSVRP SSHQDNLWPM VGPMGGGLVG	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLL STMYSLPLRM FVSEQQOKLS PGACQANETI LITLLVUGLEW	AGCCTGGCTC TAGTTCCAAA CTTCCACTGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRENDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRL RARPVINIVH DRDRRPPRL RLQYSRDVRK FCELGNPFKR RLQYSRDVNHR PYEVSNGKWL	TGCCCTCCC AACCTCTCCT ACCTCTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 360 360 480 540 660 720 720 780
50 55 60	CCATGGGCTG GACCCCTGCC GACAGCTCCC Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMWLGYTVAS HNEMCNSNTD DPEDQONLYI SQVGAYFGSA LHGPSGSAFE KLGLPGLATF DPALCTATSC GFFSMPEMRC QALENHTEVQ RTSERSGEDA EVIGVTLHTR GESGMKTVED NGSWPCRPFG	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRILMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVGLQLST VGSPLKYEFQ DLIMPLNITL	TATCCTTGGC CCACTTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWA TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG QEMFYPDLLV QSAGNPNYRR LRDKLRPIII LCESNLGMRAA PALLLSSVRP SSEQDNLWPM SCHQDRPSSP	TTTCTGTGCC AAGCTGAGGC GCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPHRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLEA FVSEQOKLS PGACQANETI ILTLUDYTL LGTLVLGLEW QRRRQLDPG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS RLQYSGUVK PCELGNPFKR QTSLSMVNHR PYEVSNGKWL QGGGPPPVTL	TGCCCTCCC AACCTCTCT ACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDWQTY EWDLSEYSYK DLRRRQVLEG TSFPAHPSLL RQPQQVIHGE KTLVPRPAVL FAGSESAVFH LDAYPILNA LLLSINVTNT NQRMELLIAF LQSFFGGTVM LYPTEITVHG AAAKKAKSET	4500 4560 4620 60 120 180 240 360 420 540 600 720 780 900
50 55 60	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act I MGPGPSRAPR QTERQQRYLL DMWLGTTVAS HNEMCNSTIT SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMCC QALENHTEV GRTSERSGEDA EVIGVTLHTR GESGMTTVED NGSWPCRPPG VLTCATGRAH	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APPRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNA HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNITL CVWEECPIPD	TATCCTTGGC CCCATTTGAG CCACTTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LNVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT LHPKNITIVT QOLLVGAPY QDGPQDIAVG DENFYPDLLV QSACNPNYRR LRDKLRPIII CCESNLQMRAA PALLLSVRP SSHQDNLWPM SSHQDNLWPM SSHQDNLWPM SDPGDRPSSP APVVTNVTVK	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHGGA APFEGLGKVY GSLSDHIVLL SMNYSLPLRM FVSEOQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
50556065	CCATGGGCTG GACCCCTGCC GACACTCCC Seq ID NO: Protein Ac: MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYTGSA LHGPSGAFG KLGLPGLATF DPALCTATSC QALENHTEVQ RTSERSGEDA EVIGVTUHTR GESGMKTVED NGSWPCRPFG VLTCATGRAH SIPTIMMENK	TGTCCTAAGG TGTTGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYM QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLIMPLNLTL CVWLECPIPD TTWFSVDIDS	TATCCTTGGC CCCATTTGAG CCCACTTCAGC TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA ARRYTQVLWS TSGGFTQNTV LHPKNITIVT QDGFQDIAVG QDGFQDIAVG QSAGNPNYR QSAGNPNYR LRPKLRPIII CESNLQMRAA FALLLSSVRP VGPMGEGLVG SDPGDRPSS SSEQONLWPM VGPMGEGLVG SDPGDRPSS APVVTNVTVK ELVEELPAEI	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI LITLLVDYTL LGTLVLGLEW QRRRRQLDPG ARVANSTFIE ELWLVLVAVG	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCT ACCTCTCT ACTGTAGCAG GCGACCAATA 51 LFGYSVALHR KNDPGHHIIE LDSSDWQTY EWDLSEYSYK DLRRRQVLEG TSFPAHPSLL RQPQQVIHGE KTLVPRPAVL FAGSESAVFH LDAYPILNA LLLSINVTNT NQRMELLIAF LQSFFGGTVM LYPTEITVHG AAAKKAKSET	4500 4560 4620 60 120 180 240 360 420 540 600 720 780 900
50 55 60	CCATGGGCTG GACCCCTGCC GACACTCCC Seq ID NO: Protein Ac: MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYTGSA LHGPSGAFG KLGLPGLATF DPALCTATSC QALENHTEVQ RTSERSGEDA EVIGVTUHTR GESGMKTVED NGSWPCRPFG VLTCATGRAH SIPTIMMENK	TGTCCTAAGG TGTTGCAGC TCCCCCTCCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYM QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLIMPLNLTL CVWLECPIPD TTWFSVDIDS	TATCCTTGGC CCCATTTGAG CCACTTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LNVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT LHPKNITIVT QOLLVGAPY QDGPQDIAVG DENFYPDLLV QSACNPNYRR LRDKLRPIII CCESNLQMRAA PALLLSVRP SSHQDNLWPM SSHQDNLWPM SSHQDNLWPM SDPGDRPSSP APVVTNVTVK	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI LITLLVDYTL LGTLVLGLEW QRRRRQLDPG ARVANSTFIE ELWLVLVAVG	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
50556065	CCATGGGCTG GACCCCTGCC GGGAATTCCC AACAGCTCCC Seq ID NO: Protein Act I MGPGPSRAPR QTERQORYLL DMWLGYTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMRC QALENHTEV QALENHTEV QRISERSGEDA EVIGVTLHTR GESGMKTVED NGSWPCRPFG VLTCATGRAH SIPTIMMENK RARTRALYEA	TGTCCTAAGG TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APPRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKEGGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLINITL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ	TATCCTTGGC CCCATTTGAG CCCACTTCAC TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVT WQDLLVGAPY QDGPQDIAVG DENFYPDLLV QSACNPNYRR LRDKLRPIII CESNLQMRAA PALLLSVRP SSHQDNLWPM VGDMGEGLVG SDPGGRESS APVVINVTVK ELVEELPAEI PSETERLTDD	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI LITLLVDYTL LGTLVLGLEW QRRRRQLDPG ARVANSTFIE ELWLVLVAVG	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
50556065	CCATGGGCTG GACCCCTGCC GACAGCTCCC Seq ID NO: Protein Ac:	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA SE	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCACTCCCA TGTGCCTTCT a sequence NP_002195.1 21 lmVAAGGCVV PDGYTNRTGA ARRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT LHPKNITIVT QCAGNPNYRR QRAGNPNYRR LRPKLRPIII CESNLQMRAA PALLLSSVRP SSHQDNLWPM VGPMGEGLVG SDPGDRPSSP VGPMGEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA AFFEKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
50556065	CCATGGGCTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Act MGPGPSRAPR QTERQQRYLL DMWLGVTNAS HNEMCNYANS LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMC QALENHTEVQ RTSERSGEDA EVIGVTLHTR GESGMKTVED NGSWPCRPFG VLICATGRAH SIPTINMENK RARTRALYEA Seq ID NO: Nucleic Ac	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC TLETGMCQLG GYTMQVGSFI IALADLNNDG GLSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYFFQ DLINPLNLTL CVMLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR ERDKLRPHIL CESNLQMRAA FALLLSSVRP SSHQDNLWPM VGPMCEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_0059	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA AFFEKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
5055606570	CCATGGGCTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Act MGPGPSRAPR QTERQQRYLL DMWLGVTNAS HNEMCNYANS LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMC QALENHTEVQ RTSERSGEDA EVIGVTLHTR GESGMKTVED NGSWPCRPFG VLICATGRAH SIPTINMENK RARTRALYEA Seq ID NO: Nucleic Ac	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA SE	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR ERDKLRPHIL CESNLQMRAA FALLLSSVRP SSHQDNLWPM VGPMCEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_0059	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL SMNYSLPLRM FVSEOQOKLE ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 501.1	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VPLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DDRRRPFRLR PDRPRLGLRS RLQYSRDVRK PCELGNPFKR QTSLSMVNHR PYEVSNGKWL DYRDFDRVRV AGLLLLGLII	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
50556065	CCATGGGCTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Act MGPGPSRAPR QTERQQRYLL DMWLGVTNAS HNEMCNYANS LHGPSGSAFG KLGLPGLATF DPALCTATSC GFFSMPEMC QALENHTEVQ RTSERSGEDA EVIGVTLHTR GESGMKTVED NGSWPCRPFG VLICATGRAH SIPTINMENK RARTRALYEA Seq ID NO: Nucleic Ac	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC TLETGMCQLG GYTMQVGSFI IALADLNNDG GLSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYFFQ DLINPLNLTL CVMLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR ERDKLRPHIL CESNLQMRAA FALLLSSVRP SSHQDNLWPM VGPMCEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_0059	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA AFFEKEEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AITVFMNQAG IYHSSKGLL RARPVINIVH PDRPRPRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
5055606570	CCATGGGCTG GACCCCTGCC GACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRILMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNITL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74	TATCCTTGGC CCCATTTGAG CCCACTTCAC TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIV LHPKNITIV LGENPYPDLLV QSACNPNYRR LRDKLRPIIL CESNLQMRA PALLLSVRP SSHQDNLWPM VGPMGEGLVG SDPGGRPSS APVVTNVTVK ELVEELPAEI PSETERLTDD quence n #: NM_005: 3274	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL SMNYSLPLRM FVSEOQOKLE ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 501.1	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VPLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DDRRRPFRLR PDRPRLGLRS RLQYSRDVRK PCELGNPFKR QTSLSMVNHR PYEVSNGKWL DYRDFDRVRV AGLLLLGLII	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
5055606570	CCATGGGCTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Act	TGTCCTAAGG TGTTGCAGC TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC TLETGMCQLG GYTMQVGSFI IALADLNNDG GYSLGGIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74 11	TATCCTTGGC CCCATTTGAG CCCACTTCAC TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIV LHPKNITIV LGENPYPDLLV QSACNPNYRR LRDKLRPIIL CESNLQMRA PALLLSVRP SSHQDNLWPM VGPMGEGLVG SDPGGRPSS APVVTNVTVK ELVEELPAEI PSETERLTDD quence n #: NM_005: 3274	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA FVSEQQOKLS PGACQANETI LITLLVDYTL LCTLVUGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 501.1	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRENDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG AIYVFMNQAG AIYVFMNQAG AIYVFMNQAG FYHSSKGLL RARPVINIVH DRDRRPPRLGLRS RLQYSRDVRK FCELGNPFKR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV AGLLLLGLII	TGCCCTCCC AACCTCTCCT AACCTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 350 420 480 600 600 720 780 960
5055606570	CCATGGGCTG GACCCCTGCC GACAGCTCCC AACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST TVGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio vence: 74 11 GTCCTCACGC	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCACTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGPTQNTV LHPKNITIVI LHPKNITIVI LHPKNITIVI CESNLQMRA PALLLSVRP SSHQDNLWPM VGPMGEGLVG SDPGDRYSP APVVTNVTVK ELVEELPAEI PSETERLTDD quence n #: NM_005: 3274 21 CCCAGCTCCGC	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG APPEGLGKVY GSLSDHIVLL NITLAYTLEA SMYSLPLRM FVSEOQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 501.1 31 CCCCCTCACGC	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VPLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DDRRRPFRLR PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGGQBPPVTL DYRDFDRVRV AGLLLLGLII 41 GCCTCTCGCCG	TGCCCTCCC AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 360 420 480 540 660 720 720 720 7840 900 960 1020
505560657075	CCATGGGTTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Ac: MGPGPSRAPR QTERQQRYLL DMWLGVTVAS HNEMCNSNTD DPEDQGNLYI SQVGAYFGSA LHGPSGSAFG KLGLPGLATF DPALCTATSC QALENHTEVQ RTSERSGEDA ACVIGVTLHTR GESGMKTVED NGSWPCRPFG VLTCATGRAH SIPTINMENK RARTRALYEA Seq ID NO: Nucleic Ac Coding seq 1 AGGTGAACAG TCCGCTGGCA	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSF1 IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74 11 GTCCTCACGC	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LWVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QDGFQDIAVG QBAGNPYRR LCESNLQMRAA PALLLSSVRP SSEQDNLWPM VGPMGEGLVG SDPGRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD QUENCE n #: NM_005: 3274 21	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA AYFERKEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEQOOKLS PGACQANETI LITLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCCCCTCACGC CCCCCGCGCCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG ATYVFMQAG IYHSSSKGLL RARPVINIVH PDRPRLGLRS RLQYSRDVRK PCELGNPFKR PCELGNPFKR QTSLSMVNHR PYEVSNGWHL DYRDFDRVRV AGLLLLGLII 41 GCCTCTCGCCG CGCGCCCCAC	TGCCCTCCC AACCTCTCCT AACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 360 420 540 600 720 780 960 1020
505560657075	CCATGGGCTG GACCCCTGCC GACCATGCC GGGAATCCC AACAGCTCCC Seq ID NO: Protein Ac:	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCACTTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA ARRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QDGFQDIAVG QSAGNPNYR QSAGNPNYR QSAGNPNYR CESNLQMRAA PALLLSSVRP VGPMGEGLVG SDPGDRPSS SSHQDNLWPM VGPMGEGLVG SDPGDRPSS APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_005: 3274 21 CCAGCTCCGC CCGGCCCCAG TGGCGCCCAG	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI ILITLUDYTL LGTLVLGLEW QRRRQLDPG ARVANSTFIE ELWLVLVAVG Y 501.1 31 CCCCCTCACGC CCGCGCGCCC CCGCCGCGCCC CCGCCGCGCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMITY KCYVRGDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS RLQYSRDVRK FCELGNPFNR QTSLSMVNHR PYEVSNGKWL GGGGPPPVTL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGCCG GCCGCCCCAC GTCTCCGCCT	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCTCTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 360 360 480 540 660 720 720 7840 900 960 1020
5055606570	CCATGGGTTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC TLETEMCOLG GYTMQVGSFI IALADLINNDG GLSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECSPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74 11 GTCCTCACGC GCCTTGATGG CTGGTAGTGA	TATCCTTGGC CCCATTTGAG CCACTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LMVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY QDGFQDIAVG DENFYPDLLV QSAGNPNYRR ELNDKLRPIII CESNLQMRAA FALLLSSVRP SSHQDNLWPM VGPMCEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_005: 3274 21 CCAGCTCCGC CCGGCCCCAG TGGCGCGCGG AGGAGGCCGG AGGAGGCCGG CCAGTCCCGC CCGGCCCCGG TGGCGCGCGG AGGAGGCCGG	TTTCTGTGCC AAGCTGAGGC GCCCCAGCC GCCCCAGCC TTGTATATAG 31 SAFNLDTRFL YYLCPLTAHK GSEDQRRWG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG GSLSDHIVLL NITLAYTLEA SMYSLPLRM FVSEQQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARWNSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCGCGCGCCCC CGGCTGCGCT CGAACCCCGGCTC GAACCCCGGCTC GAACCCCGGCTC GAACCCCGGCCGCCCC CCCCCCCCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG ATYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPFRLRS RLQYSRDVRK FCELGNPFKR QTSLSMVNHR PYEVSNGKWL GQQGPPPVTL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGCCG CGCGCCCCAC GTCTCCGCCT AGCCTCTTCG	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCTCTCCT ACCTCTCCT CACCTCTCTCT	4500 4560 4620 60 120 180 240 360 420 720 780 960 1020
505560657075	CCATGGGCTG GACCCCTGCC GACAGCTCCC Seq ID NO: Protein Act	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNITL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74 1 GGTCCTCACGC GCCATGGGCC GCCTGTATGG CTGGTAGTGA CCGCAGACAG	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCACTTCCCA TGTGCCTTCT A sequence NP_002195.1 21 LNVAAGGCVV PDGYTNRTGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QCOLLVGAPY QDGFQDIAVG DENFYPDLLV QSACNPNYRR LRDKLRPIII CESNLQMRAA PALLLSVRP SSHQDNLWPM VGPMCEGLVG SDPGDRPSSP APVVTNVTVK ELVESLPAEI PSETERLTDD QUENCE n #: NM_005: 3274 21 CCCAGCTCCGC CCGGCCCCAG TGGCGCCGGA AGGAGCCCGG AGGAGCCCGG AGGAGCCGG AGCAGCCAGC	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA AFFEKEVGG APFEGLGKVY GSLSDHIVLL NITLAYTLEA SMNYSLPLRM FVSEOQOKLS PGACQANETI ILTLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCGCCGCCCC CGGCTGCGTC CGGACCCGGGC GGCTACCTG	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCEMNITV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG ATYVFMONGA IYHSSKGLL RARPVINIVH PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL GGQGPPPVTL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGCCG CGCCCCAC GTCTCCGCCT AGCCTCTCGCTG	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 240 360 420 660 720 780 960 1020
505560657075	CCATGGGCTG GACCCCTGCC GACCATCCC AACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11	TATCCTTGGC CCCATTTGAG CCCATTTGAG CCCATTTGAG CCACTCCCA TGTGCCTTCT a sequence NP_002195.1 21 LMVAAGGCVV PDGYTNATGA ARRYTQVLWS TSGGFTQNTV LHPKNITIVT LHPKNITIVT QDLLVGAPY QDGFQDIAVG QSAGNPNYR QSAGNPNYR LRPKLRPIII CESNLQMRAA PALLLSVER PSSHQDNLWPM VGPMGEGLVG SDPGDRPSSP VGPMGEGLVG SDPGDRPSSP APVVTNVTVK ELVEELPAEI PSETERLTDD Quence n #: NM_005: 3274 21 CCAGCTCCGC CCGGCCCCAG TGGCGCCCGAG TGGCGCCCGAG AGGAGCCCGG AGCGGCCCGAG AGCGGCCCGAG AGCGGCCCGAG AGCGCCCCAAG CCGCCCCAAG AGCGCCCCGAG AGCGGCCCCAAG AGCGCCCCGAG AGCGGCCCCAAG AGCGCCCCAAG AGCGCCCCCAAG AGCCACCCAAA	TTTCTGTGCC AAGCTGAGGC GCCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHRHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNNYSLPLRM FVSEQQOKLS PGACQANETI ILITLUDYTL LGTLVLGLEW QRRRQLDPG ARVANSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCGCGGCCCC GGACCCGGCCCC GCGCTACCTGC CCGCGCTCCTC CCGCGCTCCTGC CCCCGGCTCCTC CCCGCACTGGT	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMITTV KCYVRGNDLE KGNSYMIQRK VFLLSQEAGG AIYVFRWQAG IYHSSSKGLL RARPVINIVH DRDRRPPRLR PDRPRLGLRS RLQYSRDVRK FCELGNPFKR CTSLSMVNHR PYEVSNGKWL GGGGPPFVTL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGCCG CGCCCCCAC GTCTCCGCCT GCCTCTGCCG CTCCTGCTG GCTGTGTACC	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 360 480 540 660 720 900 960 1020
505560657075	CCATGGGCTG GACCCCTGCC GACCCCTGCC AACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TGTTGGCAGC TCCCCCTCAT TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRLMLCALA LAGAPRELAV QGPAGRVLVC TLETGMCQLG GYTMQVGSFI IALADLNNDG GLSVASIGDIN GYSLSGQMDV VQVELCFAYN POWELCFAYN POWECGPDNK HEALLTLVVP DLQVQLQLST VGSPLKYEFQ DLINPLNLTL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio uence: 74 11 GTCCTCACGC GCCATGGGCC GCCTTGATGG CTGGCAGCAGG GTGCCCGATGG AAGGATGACT AAGGATGACTT	TATCCTTGGC CCATTTGAG CCACTTCAGC CCACTTCAGC CCACTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNATGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY WQDGFQDIAVG DENFYPDLLV QSAGNPNYRR LEPKLRPIII CESNLQMRAA PALLLSSVRP SSHQDNLWPM VGPMCBUNG SDPGDRPSP APVVTNVTVK ELVEELPAEI PSETERLTDD QUENCE n #: NM_005: 3274 CCAGCTCCGC CCGGCCCCAG TGGCGGCCGG AGGCGCCGG AGGCGCCGG AGGCGCCGG AGCGCAGA GCTACACCAA	TTTCTGTGCC AAGCTGAGGC GCCCAGCCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRMVG YFGAPGAYNW GAPRHHMGA APFEGLGKVY GSLSDHIVLL NITLAYTLEA SNMYSLPLRM FVSEQQOKLS PGACQANETI LITLLVDYTL LGTLVLGLEW QRRRQLDPG ARVWNSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCGCCGCCC CGGCTGCGTC GAACCCGGGCT CCGGCTGCGTC GAACCCGGGCT CCGGCTGCTC GAACCCGGGT GAACATCACA	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRENDLE KGNSYMIQRK VFLLSQEAGG AIYVFMNQAG IYHSSKGLL RARPVINIVH DRDRRPPRLG RARPVINIVH GCGGPPPVTL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGGCGG GCGCCCCCAC GTCTCCGCCT AGCCTCTTCG CTCTGGCTG GCTGTGTACC GTGAAAAAATG	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCTTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 120 360 420 360 420 720 780 900 960 1020 600 120
505560657075	CCATGGGTTG GACCCTGCC GACACTCCC AACAGCTCCC Seq ID NO: Protein Ac.	TGTCCTAAGG TGTTGCAGC TGTTGGCAGC TCCCCCTCT AGTTTGT 146 Protein cession #: 1 11 APRIMICALA LAGAPRELAV QGPAGRVLVC YLETGMCQLG GYTMQVGSFI IALADLNNDG LSVASIGDIN GYSLSGQMDV VQVELCFAYN QKLELLLMDN FQKECGPDNK HEALLTLVVP DLQVQLQLST TVGSPLKYEFQ DLINPLNITL CVWLECPIPD TTWFSVDIDS KRQKAEMKSQ 147 DNA se id Accessio vence: 74 11 GTCCTCACGC GCCTTGATGG CGCGTTGATGG CGGCTTGATGG CGGCTGAGTGA CGGCGAGACAG GTGCCCGATG CAGGACAGACTGT GAGGACATGT	TATCCTTGGC CCATTTGAG CCACTTCAGC CCACTTCAGC CCACTCCCA TGTGCCTTCT A Sequence NP_002195.1 21 LMVAAGGCVV PDGYTNATGA AHRYTQVLWS TSGGFTQNTV LHPKNITIVT WQDLLVGAPY WQDGFQDIAVG DENFYPDLLV QSAGNPNYRR LEPKLRPIII CESNLQMRAA PALLLSSVRP SSHQDNLWPM VGPMCBUNG SDPGDRPSP APVVTNVTVK ELVEELPAEI PSETERLTDD QUENCE n #: NM_005: 3274 CCAGCTCCGC CCGGCCCCAG TGGCGGCCGG AGGCGCCGG AGGCGCCGG AGGCGCCGG AGCGCAGA GCTACACCAA	TTTCTGTGCC AAGCTGAGGC GCCCAGGCC TTGTATATAG 31 SAFNLDTRFL VYLCPLTAHK GSEDQRRWVG YFGAPGAYNW GAPRHRHMGA YFERKEEVGG APFEGLGKVY GSLSDHIVLL SMNYSLPLRM FVSEOOOKLS PGACQANETI ILTLLVDYTL LGTIVLGLEW QRRRQLDPW ARVWNSTFIE ELWLVLVAVG Y 31 CCCCTCACGC CCGCCGCCC CGGCTGCGTC CCGACCCGGCC CGACCCGGGCCC CGACCCGGGCCC CGGACCTGGTC CCGGACTGGTC CCGGACTGGTC CCGGACTGGTC CCGGACTGGTC CCGGACTGGTC CCGGACTCGGCC CCGGACTGGTC CCGCTCGCC CCGGCTGCTC CCGGACTGGTC CCGGACTGGTC CCGGCTCGCTC CCGGACTGGTC CCGGCTGCTC CCGGACTGGTC CCGCTCTGGCC CCGCTCTGGCC CCGGACTGGTC CCGGACTGGTC CCGGACTGGTC CCGGACTGCT CCGCCTCACGC CCGGCTGCTC CCGGACTGCT CCGCTCCACGC CCGGCTGCTC CCGGACTGCT CCGCTCCACGC CCGGCTGCTC CCGGACTGCT CCGCTCCACC CCGCCTCCACC CCGGCTCCCT CCGGACTGCT CCGCTCCACC CCGCCTCCACC CCGCCTCCACC CCGCCTCCACC CCGGCTCCCT CCGACTGCT CCCCTCCACC CCGCCTCCACC CCGCCTCCACC CCGCCTCCACC CCGCCTCCACC CCGCCCCCC CGGCTCCCT CCGACTGCT CCCCTCCACC CCGCCTCCACC CCGCCCCC CGGCTCCCT CCGCCCC CGCCCCC CGCCCCCC CGCCCCC CGCCCC CGCCCCC CGCCCCC CGCCCC CGCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	AGCCTGGCTC TAGTTCCAAA CTTCCATGGT GCTTCTCACC 41 VVKEAGNPGS DDCERMNITV KCYVRGNDLE KGNSYMIQRK VPLLSQEAGG ATYVFMNQAG IYHSSKGLL RARPVINIVH PDRPRLGLRS RLQYSRDVRK QTSLSMVNHR PYEVSNGKWL DYRDFDRVRV AGLLLLGLII 41 GCTCTCGCCG CGCGCCCAC GTCTCGCCG CTCTGGCTG GCTGTTACC CTCTGGCTG GCTGTAAAAATG AGCCAGGGCCC	TGCCCTCCC AACCTCTCCT AACCTCTCCT ACCGTAGCAG GCGACCAATA 51	4500 4560 4620 60 120 180 360 480 540 660 720 900 960 1020

	CCCCATCCTC	GGCAAGTGCT	A CCTGCGAGG	CAATGACCTA	GAGCTGGACT	CCAGTGATGA	600
					GACTACCTGG		660
					GTGTACTTCG		720
					AAGGAGTGGG		780
5							840
5					ATTGGGTACA ACAGGTGCCC		900
							960
					GGAGACCTGC		
					GCAATTGCCC		1020
10					TACTACTTCG		1080
10					GGAACCTCCT		1140
					GGTTTATCTG		1200
					GGAGCTCCGT		1260
					CTTAGACAGC		1320
1.5					TTCGGCTATT		1380
15					GTGGGAAGCC		1440
	CATTGTGCTG	CTGCGGGCCC	GGCCAGTCAT	CAACATCGTC	CACAAGACCT	TGGTGCCCAG	1500
	GCCAGCTGTG	CTGGACCCTG	CACTTTGCAC	GGCCACCTCT	TGTGTGCAAG	TGGAGCTGTG	1560
	CTTTGCTTAC	AACCAGAGTG	CCGGGAACCC	CAACTACAGG	CGAAACATCA	CCCTGGCCTA	1620
	CACTCTGGAG	GCTGACAGGG	ACCGCCGGCC	GCCCCGGCTC	CGCTTTGCCG	GCAGTGAGTC	1680
20					TGCCAGAAGC		1740
					ATCTCCATGA		1800
					TCCCTGGACG		1860
					CAGTTCCAGA		1920
							1980
25					GCCTTCGTGT		
25					AAATTGCTCC		2040
					GCCCACGAGG		2100
					CCCCCCGGGG		2160
					CGGAACCAGA		2220
20					AGGGACCTTC		2280
30					ATGATCCTCA		2340
	GGACTATACA	CTCCAGACCT	CGCTTAGCAT	GGTAAATCAC	CGGCTACAAA	GCTTCTTTGG	2400
	GGGGACAGTG	ATGGGTGAGT	CTGGCATGAA	AACTGTGGAG	GATGTAGGAA	GCCCCCTCAA	2460
	GTATGAATTC	CAGGTGGGCC	CAATGGGGGA	GGGGCTGGTG	GGCCTGGGGA	CCCTGGTCCT	2520
					CTGCTGTATC		2580
35					GGAGACCTTA		2640
55					CCACAGCGCA		2700
					CTGGCTGCTG		2760
					CACTGTGTGT		2820
					AAGGCACGAG		2880
40							2940
40					GTAAATGGCT		
					AAGACCACGT		3000
					ATCGAGCTGT		3060
					ATCCTCCTGC		3120
15	TGACTTCTTT	AAGCGGACCC	GCTATTATCA	GATCATGCCC	AAGTACCACG	CAGTGCGGAT	3180
45					CCCACCAAGA		3240
					CCCTGATCCC		3300
					CCTCTGACAG		3360
					ACCTCGTCAA		3420
60					CGCTGTGGAC		3480
50	CGAGTGCACT	GCATTCCTGT	GCCCTAGATG	CACGTGGGGC	CCACTGCTCG	TGGACTGTGC	3540
	TGGTGCATCA	CGGATGGTGC	ATGGGCTCGC	CGTGTCTCAG	CCTCTGCCAG	CGCCAGCGCC	3600
	AAAACAAGCC	AAAGAGCCTC	CCACCAGAGC	CGGGAGGAAA	AGGCCCCTGC	AATGTGGTGA	3660
	CACCTCCCCT	TTCACACCTG	GATCCATCTT	GAGAGCCACA	GTCACTGGAT	TGACTTTGCT	3720
					TGGTGGGCCC		3780
55					CGGGGGCACT		3840
					ACCCAGAAGG		3900
					CTCGCAGGGA		3960
					ACTGTGCTGG		4020
					GATGTTGGGA		4080
60					GAAGGCCCCA		4140
30					GGCAGGGGGC		4200
					AGAGGTGGAG		4260
					ATGGGCTGTG		4320
65						TTGGCAGCCC	4380
65						CCCCTCCTTG	4440
	TGCCTTCTTT	GTATATAGGC	TTCTCACCGC	GACCAATAAA	CAGCTCCCAG	TITGT	
	Seq ID NO:	148 Protei	n sequence				
~~	Protein Ac	cession #:	NP_005492.1				
70	1	11	21	31	41	51	
	1	1	1				
	MGPGPSRAPR	APRLMLCALA	LMVAAGGCVV	SAFNLDTRFL	VVKEAGNPGS	LFGYSVALHR	60
						KNDPGHHIIE	120
	DMWLGUTVAS	OGPAGRVI.VC	AHRYTOVLWS	GSEDORRMVG	KCYVRGNDLE	LDSSDDWQTY	180
75						EWDLSEYSYK	240
	DPRDOGNT.VT	GYTMOVGGPT	LHPKNITIUT	GAPRHRHMCA	VELLSOEAGG	DLRRRQVLEG	
	SUACTABLE	TALADIAMO	WODI.I.VCARV	AREBKEENCO	AIYUFMNOAG	TSFPAHPSLL	360
	THUDGOODE	I.CVA CICHT	CONTROLL	ADPECT.CION	TYPEGGRETT	RQPQQVIHGE	420
						KTLVPRPAVL	
80						FAGSESAVFH	
30							
						LDAYPILNQA	
						LLLSINVINI	660
						NORMELLIAF	
0.5						LQSFFGGTVM	
85	GESGMKTVED	VGSPLKYEFO	VGPMGEGLVG	LGTLVLGLEW	PYEVSNGKWL	LYPTEITVHG	840
						_	

	NGSWPCRPPG	DLINPLNLTL	SDPGDRPSSP	QRRRRQLDPG	GGQGPPPVTL	AAAKKAKSET	900	
			APVVTNVTVK ELVEELPART			NGWATLFLRT LLLWKCDFFK	960 1020	
5			RYPPPGSTLP					
3	Sea ID NO:	149 DNA sec	nuence					
	Nucleic Act	id Accession	#: NM_0064	24.1				
	Coding sequ	ence:	21	31	41	51		
10				TOCK TOCK		COGREGOGE	50	
			GGCCGCCGCC ATTGGGAGAT				60 120	
			CACTGCCCCT				180	
15			CAAGATTGAA GGATGACCCC				240 300	
			CACCAAAGGG				360	
			ATTTCTCTAC AGGAAAAATG				420 480	
20	ATGTCCAACC	CTTTGTTGGG	GCTGGTGATC	GGGGTGCTGG	TGACCGTCTT	GGTGCAGAGC	540	
20			CGTTGTCAGC				600 660	
	GCGCTCATGC	AGGTGGGAGA	TCGGAGTGAG	TTCAGAAGAG	CTTTTGCAGG	AGCCACTGTC	720	
			GTCCGTGTTG GCTTATAGTG				780 840	
25	GCCCCAGATC	TTCTGAAAGT	CATCACTAAG	CCCTTCACAA	AGCTCATTGT	CCAGCTGGAT	900	
			TECANTANA			TCCCTCGACT	960 1020	
						GACCATGAAG		
30			CATCGCCAAA				1140	
50			CATCTTGCTC				1200 1260	
	AAGAAGACCA	TCAACACTGA	TTTCCCCTTT	CCCTTTGCAT	GGTTGACTGG	CTACCTGGCC		
						CACGTCGGCC ACTCACGCTG		
35	GGCTCCAACA	TCGGCACCAC	CACCACCGCC	ATCCTGGCCG	CCTTAGCCAG	CCCTGGCAAT	1500	
						CTCCGGCATC GGGGCTGGGC		
						CTTCTTCCTG		
40	ATCCCGCTGA	CGGTGTTTGG	CCTCTCGCTG	GCCGGCTGGC	GGGTGCTGGT	TGGTGTCGGG	1740	
40			CATCCTGGTA ACTCCAGAAC			GATGCGCTCG	1800 1860	
	CTGAAGCCCT	GGGATGCCGT	CGTCTCCAAG	TTCACCGGCT	GCTTCCAGAT	GCGCTGCTGC	1920	
			CCGCGCGTGC			CAAGTGCTGC TGTCCCTGTC	1980 2040	
45						TGAGGTCCCT		
						TGTCAGGGAT		
			CCATTAGCGA			CCCTTTCACC	2220	
50	Fog ID NO.	150 Protein						
50		cession #: 1			•			
	1	11	21	31	41	51		
<i></i>	MAPWPELGDA	QPNPDKYLEG	AAGQQPTAPD	KSKETNKTON	TEAPVTKIEL	lpsystatli	60	
55			KWSERDTKGK				120	
			LMOVGDRSEF			VSSSLLTVRA LLPVEVATHY	180 240	
						EKAKNKSLVK	300	
60			IMIVKILGSV			QHIFVNFHLP FAWLTGYLAI	360 420	
	LVGAGMTFIV	QSSSVFTSAL	TPLIGIGVIT	IERAYPLTLG	SNIGTTTTAI	Laalaspgna	480	
			LWYPIPFTRL PUVFIIILUL			fyliifffli Nflplwmrsl	540 600	
65	KPWDAVVSKP	TGCFQMRCCY	CCRVCCRACC	LLCGCPKCCR		AQEGQDVPVK	660	
65	APETFONITI	SREAQGEVPA	SDSKTECTAL					
		151 DNA se						
		id Accessionuence: 11						
70	1	11	21	31 .	41	51		
)	1	CGGGGCGGGC) NGCCGCTGCC	TGGGCACTAT	CGAGGTGAAG	60	
			TOGTOGGTTT				120	
75	GAGGAGTTTT	ATGGATTACT	ACAACATGTT	CATAAGATCC	CCAATGTTGA	CGTTTTGGTA	180	
, 3			AGACTTACTA ACTGCTTAGG				240 300	
	TACAGTGCCT	TTGGTACAGA	CACGCTAATA	AAGAAGAAGA	ATGTTTTAAC	CAACGTATTG	360	
			AAAGCCACAT CGTGGATATT			AGACTTTAGA GGTACGTCTT	420 480	
80	TACAAATACG	GCACGGAGAA	ACCCCTAGGA	TTCTACATCC	GGGATGGCTC	CAGTGTCAGG	540	
						TGTCCCAGGA	600 660	
						AGTTAATGGC AAATAGCCGT	720	
85	AACCTCATCA	·TAACAGTGAG	ACCGGCAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTCGG	780	
0.5	ACTICITGGCA	GITCUGGICA	GTCTACTGAT	MACAGCCTTC		ACAGCAGATT	840	
					32	.6	•	

5	AATGGAGTGC ACACAGATAG AGCTTAGCAG	CACAGCAGAT AGCTAAGCTT CCATAGCAAG	TCCAAAAGCT TGAGTCTGGA	AGCGAAGAAG GTTCCTAATA CAGAATGGCT ACGGAATTTG ACATTATGA	CTGAGAGCCT TTATTCCCTC	GGAGTCATTA TAATGAAGTG	900 960 1020 1080
		152 Proteir ession #: X		31	41	51	
10	 MNRSHRHGAG GYADIHGDLL RPDNHRKKPH	SGCLGTMEVK PINNDDNYHK IVISMPQDFR	. SKFGAEFRRF AVSTANPLLR PVSSIIDVDI	 SLERSKPGKF IFIQKKEEAD LPETHRRVRL	 EEFYGLLQHV YSAFGTDTLI YKYGTEKPLG	HKIPNVDVLV KKKNVLTNVL FYIRDGSSVR	60 120 180
15	NLIITVRPAN	QRNNVVRNSR VPNTESLESL	TSGSSGQSTD	VNDEVLEVNG NSLLGYPQQI QNGFIPSNEV	EPSFEPEDED	SEEDDIIIED	240 300 360
20	Nucleic Aci	153 DNA sec d Accession mence: 234	#: NM_0030	064.2			
	1	11	21	31	41	51 I	
25	TGCCCTGGGA AGTCTGTCCT	ACTCTGGCAC CCTAAGAAAT	CTTGGGCTGT CTGCCCAGTG	CAGCGGCCTC GGAAGGCTCT CCTTAGATAC	GGAAAGTCCT AAGAAACCTG	TCAAAGCTGG AGTGCCAGAG	60 120 180
30	GGATCCTGTT TGGCCAATGT	GACACCCCAA TTGATGCTTA	ACCCAACAAG ACCCCCCCAA	TTGTCCTGAC GAGGAAGCCT TTTCTGTGAG GAAATCCTGC	GGGAAGTGCC ATGGATGGCC	CAGTGACTTA AGTGCAAGCG	240 300 360 420
	ATTCCTGCCA .CCTGAGACTT	TATGGAGGAG GGCTCCACCA	GCTCTGGAGT CTGATATCCT	CCTGCTCTGT CCTTTGGGGA AAATAAACGA	GTGGTCCAGG AAGGCTTGGC	TCCTTTCCAC ACACAGCAGG	480 540
35		154 Protein cession #: N					
	1	11	21	31 1	41	51 i	
40		KCLDPVDTPN		KAGVCPPKKS VTYGQCLMLN			60 120
	Seq ID NÓ:	155 DNA sec	quence				
45		ld Accession Lence: 199.	1 #: NM_0013	306.1			
	1	11	21	31	41	51	
	AATTCGGCAC	 GAGGGCAGGT	GCAGGCGCAC	 GCGGCGAGAG	CGTATGGAGC	CGAGCCGTTA	60
50				TCCCCGCACC			120 180
	GGCCTTGCCG	CGGCAGCCAT	GTCCATGGGC	CTGGAGATCA	CGGGCACCGC	GCTGGCCGTG	240 300
	ATCGGCAGCA	ACATCATCAC	GTCGCAGAAC	GCGTTGCCCA ATCTGGGAGG	GCCTGTGGAT	GAACTGCGTG	360
55				GTGTACGACT GTGGCCATCC			420 480
55	CTAGTGGCGC	TGGTGGGCGC	CCAGTGCACC	AACTGCGTGC	AGGACGACAC	GGCCAAGGCC	540
	AAGATCACCA GTGTCCTGGT	TCGTGGCAGG	CGTGCTGTTC	CTTCTCGCCG GACTTCTACA	ACCCCGTGGT	GCCCGAGGCG	600 660
60				GTGGGCTGGG CCCCCACGCG			720 780
00	AAGGTCGTCT	ACTCCGCGCC	GCGCTCCACC	GGCCCGGGAG	CCAGCCTGGG	CACAGGCTAC	840
				GCAGGGAGAC CGCGCACCAG			900 960
65				AGGAAGCCCC		TGGGGCAGCT GGACCAACCT	1020 1080
05	GCATGGACTG	TGAAACCTCA	CCCTTCTGGA	GCACGGGGCC	TGGGTGACCG	CCAATACTTG	1140
				TAAAAGCCTC		GGGACCGGCA	1200
70	Seq ID NO:	156 Protei		31	41	51	
	I .	ı			1	1	60
75	MQCKVYDSLL GVLFLLAALL	ALPQDLQAAR TLVPVSWSAN	ALIVVAILLA TIIRDFYNPV		AQCTNCVQDD AGLYVGWAAA	TAKAKITIVA ALQLLGGALL	120 180
80	Nucleic Ac	157 DNA se id Accessio uence: 15	n #: NM_005				
	1	11 	21 	31 	41	51 ·	
85	ATGCCCCTAG CAGGACTCCA	GTCTCCTGTG	GCTGGGCCTA	GCCCTGTTGG	GGGCTCTGCA GCAAGGTCCC	TGCCCAGGCC TCTGCAGCAG	60 120
					. 32		

5	ATTCTCAGAG GACAAGAGCT AGGACTTTTG CCTGGATTAA GTGTTCTTCA ACCAAGGAGC	ACAACCAATT AAGACAAAGA ACAATGTCAC TTCCAGGTTG CGAGTTACCT AGAAAGTTTC TGACTTCGGA ACCACATCGT	CCCGCAAAAG CTCCGTCCTG CCAGCCCGGC CGTCCGAGTG TCAAAACAGG ACTAAAGGAG	ATGTATGCCA TTTAGGAAAA GAGTTCACGC GTGAGCACCA GAGTACTTCA AACTTCATCC	CCATCTATGA AGAAGTGTGA TGGGCAACAT ACTACAACCA AGATCACCCT GCTTCTCCAA	GCTGAAAGAA CTACTGGATC TAAGAGTTAC GCATGCTATG CTACGGGAGA ATATCTGGGC	180 240 300 360 420 480 540
10		158 Protein ession #: N 11		31	41	51	
15	ILREDKDPQK	ALLGALHAQA MYATIYELKE VSTNYNQHAM PIDQCIDG	DKSYNVTSVL	FRKKKCDYWI	RTFVPGCQPG	EFTLGNIKSY	60 120 180
20	Nucleic Act	159 DNA sec	#: NM_006	353.1			
	1	ience: 268 11 	21 	31 	41 ^	51 	
25	ATCGGGCAGA CATGAGGATT	GCTCGGGTTC GGTCTCACAG CTGCAGTTAA AAGGGGTTCG	CAGCCAAGGA TCCTGCTTGC	ACCTGGGGCC TČTGGCAACA	CGCTCCTCCC GGGCTTGTAG	CCCTCCAGGC GGGGAGAGAC	60 120 180 240
30	AGCCCACTGC GGAGGGCTGT	CGGCTACTCT CTCAAGCCCC GAGCAGACCC AACAAAGACC	GCTACATAGT GGACAGCCAC	TCACCTGGGG TGAGTCCTTC	CAGCACAACC CCCCACCCCG	TCCAGAAGGA GCTTCAACAA	300 360 420 480
35	CAGCTGCCTC CTTGCGATGC	TGGGCTGTGC ATTTCCGGCT GCCAACATCA GACACCATGG	GGGGCAGCAC CCATCATTGA	GTCCAGCCCC GCACCAGAAG	CAGTTACGCC TGTGAGAACG	TGCCTCACAC CCTACCCCGG	540 600 660 720
	CCAGGATCCG GGACTGGATC	GGGGGCCCTC TGTGCGATCA CAGGAGACGA	CCCGAAAGCC TGAAGAACAA	TGGTGTCTAC TTAGACTGGA	ACGAAAGTCT CCCACCCACC	GCAAATATGT ACAGCCCATC	780 840 900
40	CAAGACCCTC AATCAACCTG GACTCTGGGA	TCCACTTGGT TACGAACATT GGGTTCGAAA ATGACAACAC ATATCAAGGT	CTTTGGGCCT TCAGTGAGAC CTGGTTTGTT	CCTGGACTAC CTGGATTCAA CTCTGTTGTA	AGGAGATGCT ATTCTGCCTT TCCCCAGCCC	GTCACTTAAT GAAATATTGT	960 1020 1080 1140
45	Protein Acc	160 Proteir cession #: N	NP_006844.1	22	41		
50		11 LATGLVGGET					60
50	SITWAVRPLT	HLGQHNLQKE LSSRCVTAGT VQEGGKDSCQ	SCLISGWGST	SSPQLRLPHT	LRCANITIIE	HQKCENAYPG	120 180 240

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

1	1.	A method of detecting an ovarian cancer-associated transcript in a cell
2	from a patient, the m	ethod comprising contacting a biological sample from the patient with a
3	polynucleotide that s	electively hybridizes to a sequence at least 80% identical to a sequence
4	as shown in Tables 1	-26.
1	2.	The method of claim 1, wherein the biological sample comprises
2	isolated nucleic acids	3.
1	3.	The method of claim 2, wherein the nucleic acids are mRNA.
1	4.	The method of claim 2, further comprising the step of amplifying
2	nucleic acids before	the step of contacting the biological sample with the polynucleotide.
i	. 5.	The method of claim 1, wherein the polynucleotide comprises a
2	sequence as shown in	n Tables 1-26.
1	6.	The method of claim 1, wherein the polynucleotide is immobilized on
2	a solid surface.	
1 -	7.	The method of claim 1, wherein the patient is undergoing a therapeutic
2	regimen to treat ovar	ian cancer.
1	8.	The method of claim 1, wherein the patient is suspected of having
2	ovarian cancer.	·
1	. 9.	An isolated nucleic acid molecule consisting of a polynucleotide
2	sequence as shown i	n Tables 1-26.
1	10.	The nucleic acid molecule of claim 9, which is labeled.
1	· 11.	An expression vector comprising the nucleic acid of claim 9.
1	12.	A host cell comprising the expression vector of claim 11.
1	13.	An isolated polypeptide which is encoded by a nucleic acid molecule
2	having polynucleotic	de sequence as shown in Tables 1-26.

1		14.	An antibody that specifically binds a polypeptide of claim 13.
1	ı	15. .	The antibody of claim 14, further conjugated to an effector component.
1 2	fluorescent lal	16. bel.	The antibody of claim 15, wherein the effector component is a
_	1140100011111		
1		17.	The antibody of claim 15, wherein the effector component is a
2	radioisotope o	or a cyto	otoxic chemical.
1		18.	The antibody of claim 15, which is an antibody fragment.
1		19.	The antibody of claim 15, which is a humanized antibody
1		20.	A method of detecting an ovarian cancer cell in a biological sample
2	from a patient	t, the m	ethod comprising contacting the biological sample with an antibody of
3	claim 14.		
1		21	The weether of a falsing 20 verboroin the antihody is firsther conjugated to
1	on officiation on	21.	The method of claim 20, wherein the antibody is further conjugated to
2	an effector co	mponer	it.
1		22.	The method of claim 21, wherein the effector component is a
2	fluorescent la	bel.	
1		23.	A method for identifying a compound that modulates an ovarian
2	cancer-associ	ated pol	lypeptide, the method comprising the steps of:
3		(i) cor	ntacting the compound with an ovarian cancer-associated polypeptide,
4	the polypeptic	de enco	ded by a polynucleotide that selectively hybridizes to a sequence at least
5	80% identical	l to a se	quence as shown in Tables 1-26; and
6		(ii) de	termining the functional effect of the compound upon the polypeptide.
1		24.	A drug screening assay comprising the steps of
2		(i) adı	ministering a test compound to a mammal having ovarian cancer or a cell
3	isolated there	from;	
4		(ii) co	emparing the level of gene expression of a polynucleotide that selectively
5	hybridizes to	a seque	ence at least 80% identical to a sequence as shown in Tables 1-26 in a

6 treated cell or mammal with the level of gene expression of the polynucleotide in a control

- 7 cell or mammal, wherein a test compound that modulates the level of expression of the
- 8 polynucleotide is a candidate for the treatment of ovarian cancer.

(19) World Intellectual Property Organization

International Bureau





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PCT

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English

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 US

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 US

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 US

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 12 April 2002 (12.04.2002)
 US

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(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

INTERNATIONAL SEARCH REPORT

International application No.

	PC1/US02/1929/	l				
A. CLASSIFICATION OF SUBJECT MATTER						
IPC(7) : C12Q 1/68; C07H 21/04		ľ				
US CL : 435/6, 91.1; 536/23.1		i				
According to International Patent Classification (IPC) or to both nat	tional classification and IPC					
B. FIELDS SEARCHED						
Minimum documentation searched (classification system followed b	y classification symbols)					
U.S.: 435/6, 91.1; 536/23.1						
Documentation searched other than minimum documentation to the	extent that such documents are included in	the fields searched				
Electronic data base consulted during the international search (name	e of data base and, where practicable, sear	ch terms used)				
Please See Continuation Sheet		1				
C. DOCUMENTS CONSIDERED TO BE RELEVANT						
Category * Citation of document, with indication, where ap	poropriate, of the relevant passages	Relevant to claim No.				
X WU, D. et al. Characterization and Molecular Clonic		1-5, 9-12				
		1-5, 3-12				
Y Vol. 266, No. 25, pages 16778-16785, see especially		6				
	page 10776, coi. 1, page 10763, Fig.					
7, Fig. 8.						
Y US 5,700,637 A (SOUTHERN) 23 December 1997 ((23.12.1997) see whole document.	. 6				
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Further documents are listed in the continuation of Box C.	See patent family annex.					
Special categories of cited documents:	"T" later document published after the inte					
	date and not in conflict with the applic					
"A" document defining the general state of the art which is not considered to be of particular relevance	principle or theory underlying the inve	ention				
or particular relevance	"X" document of particular relevance; the	claimed invention cannot be				
"E" earlier application or patent published on or after the international filing date	considered novel or cannot be consider					
	when the document is taken alone					
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as	"Y" document of particular relevance; the	claimed invention cannot be				
specified)	considered to involve an inventive step					
	combined with one or more other such	documents, such combination				
"O" document referring to an oral disclosure, use, exhibition or other means	being obvious to a person skilled in the	e art				
"P" document published prior to the international filing date but later than the	"&" document member of the same patent	family				
priority date claimed	accurate memoer of the same patern	iaiii.y				
	Data of mailing of the international con-	sh sonos				
Date of the actual completion of the international search	Date of mailing of the international seam					
08 November 2004 (08.11.2004)	1 / 04/0	PEC 2004				
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Mail Stop PCT, Atm: ISA/US	I XXXXX I < NUXC	en of				
Commissioner for Patents	Jernanne S Siction	r /)				
P.O. Box 1450	\d./	//				
Alexandria, Virginia 22313-1450	Teléphone No. 571-272-0500	//				
Facsimile No. (703) 305-3230						

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/19297

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons: 1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely: 2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically: 3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a). Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet) This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet 1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite
because they relate to subject matter not required to be searched by this Authority, namely: 2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically: 3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a). Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet) This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet 1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically: 3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a). Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet) This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet 1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
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This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet 1.
Please See Continuation Sheet 1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite
payment of any additional fee.
As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-12, directed to heparin binding growth factor binding protein
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT	
BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LAC Groups 1-12000, claim(s) 1-12, drawn to nucleic acids and methods of detecting nu corresponds to each of the genes or nucleic acids set forth in tables 1-26. Therefore for search, Group I and claims 1-12 will be searched to the extent that they apply to to elect and pay for additional groups for search, applicant is requested to indicate to	cleic acids. It is noted that each group named above e, if applicant does not choose to pay additional fees b heparin binding growth factor. If applicant wishes
Groups 12001-24000, claim(s) 13 and 23, drawn to polypeptides and methods of de named above corresponds to proteins encoded by each of the genes or nucleic acids wishes to elect and pay for additional groups for search, applicant is requested to in elected.	set forth in tables 1-26. Therefore, if applicant
Groups 24001-36000, claim(s) 14-22, drawn to antibodies and methods of using and corresponds to an antibody that binds a protein encoded by each of the genes or nucleapplicant wishes to elect and pay for additional groups for search, applicant is required are elected.	eleic acids set forth in tables 1-26. Therefore, if
Groups 36001-48000, claim(s) 24, drawn to drug screening assays. It is noted that gene expression of each of the genes or nucleic acids set forth in tables 1-26. If applied for search, applicant is requested to indicate which nucleic acid from tables 1-26 are	plicant wishes to elect and pay for additional groups
The inventions listed as Groups 1-48000 do not relate to a single general inventive of Rule 13.2, they lack the same or corresponding special technical features for the for 12000 (see e.g., claim 1) include genes or nucleic acid sequences which are both stother nucleic acids in the tables. As such the products of groups 1-12000 do not relack a special technical feature that is the same as or that corresponds to a special technical feature linking the recited Groups, as would be necessarian.	llowing reasons: The products claimed in groups 1- ructurally and functionally unrelated to any of the present a contribution over the prior art, the claims echnical feature of the other claimed inventions. Thus
Groups 1-36000 are additionally drawn to multiple distinct products lacking the san nucleic acids of Groups 1-12000 are composed of nucleotides and function in, e.g., amplification. The polypeptides of groups 12001-24000, which are composed of ar polynucleotides or antibodies and can function in, e.g. catalysis of reactions. While groups 24001-36000 are polypeptides, in this instance the polypeptides of groups 12 polypeptides of groups 24001-36000 encompasses antibodies including IgG which constant and variable regions, and including framework regions which act as a scaf (CDRs) that function to bind an epitope, and can function, e.g. in eliciting an immu 24000 and the antibodies of groups 24001-36000 are structurally distinct molecules from each other in structure, function, and effect, they do not belong to a recognize "common property or activity" and a common structure, as would be required to significant molecules.	methods of nucleic acid hybridization or mino acids are structurally distinct molecules from e the inventions of both groups 12001-24000 and 2001-24000 are single chain molecules whereas the comprises 2 heavy and 2 light chains containing fold for the 6 complementarity determining regions ane response. Thus the polypeptides of groups 12001 As the products of the different sets of groups differed class of chemical compounds, or have both a
Further, the methods of Groups 36001-48000 do not require either the peptides of 24001-36000. Further, the methods of groups 36001-48000 (involve administering require different process steps than the methods or nucleic acids of groups 1-12000 require the method steps of groups 36001-48000. In addition to differences in object that the claims of the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences in the present groups are not directed to the detection or identification to differences are not directed to the detection or identification to differences are not directed to the detection	a test compound) have different objectives and Further, the methods of groups 1-12000 do not ectives, effects, and method steps, it is again noted

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Continuation of B. FIELDS SEARCHED Item 3: medline, caplus, NCBI search terms: heparin binding growth factor binding protein			
medline, caplus, NCBI			
search terms: heparin binding growth factor binding protein			
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Form PCT/ISA/210 (second sheet) (July 1998)